

; PRIOR APPLICATION NUMBER: US/09/657,346
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 175
; SEQ ID NO 32
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-293-783-32

Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2275 GGTTTCACCGTGTAGCCAG 2294
||| ||||| ||||| ||||| |||||
Db 1 GGTTTCACCATGTGTGCAG 20

RESULT 1520
US-10-293-783-33
; Sequence 33, Application US/10293783
; Publication No. US20030130222A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST EXP
; FILE REFERENCE: ISPH-0544
; CURRENT APPLICATION NUMBER: US/10/293,783
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US/09/800,631
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US/09/657,346
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 175
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-293-783-33

Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2146 TCTGGCTCACTCAAGCTC 2165
||| ||||| ||||| ||||| |||||
Db 1 TCTGGCTCACTCAACCTC 20

RESULT 1521
US-10-293-783-49
; Sequence 49, Application US/10293783
; Publication No. US20030130222A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST EXP
; FILE REFERENCE: ISPH-0544
; CURRENT APPLICATION NUMBER: US/10/293,783
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US/09/800,631
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US/09/657,346
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 175
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-293-783-49

Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2342 AAAGTCTGGGATTACAGGC 2361
||| ||||| ||||| ||||| |||||
Db 1 AAGTAGCTGGGATTACAGGC 20

RESULT 1522
US-10-293-783-66
; Sequence 66, Application US/10293783
; Publication No. US20030130222A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST EXE
; FILE REFERENCE: ISPH-0544
; CURRENT APPLICATION NUMBER: US/10/293,783
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US/09/800,631
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US/09/657,346
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 175
; SEQ ID NO 66
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-293-783-66

Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2285 TGTAGCCAGGATGCTCG 2304
||| ||||| ||||| ||||| |||||
Db 1 TGTGGCCAGGCTGCTCG 20

RESULT 1523
US-10-119-431-42
; Sequence 42, Application US/10119431
; Publication No. US20030152939A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Zhong, Mei
; APPLICANT: Khramtsov, Nikolai
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Padigaru, Muraidhara
; APPLICANT: Anderson, David
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: NOVEL SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING
; TITLE OF INVENTION: THEM
; FILE REFERENCE: Cura-29 CIP1
; CURRENT APPLICATION NUMBER: US/10/119,431
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/103,195
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/282,548
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/412,231
; PRIOR FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1

```
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Chemically
; OTHER INFORMATION: Synthesized
US-10-119-431-42

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2104 CCGAGTCTTGCTGCTGTACC 2123
Db 1 CAGAGTCTTGCTGCTGTCTCC 20

RESULT 1524
US-10-345-092-62/c
; Sequence 62, Application US/10345092
; Publication No. US20030165506A1
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnol
; TITLE OF INVENTION: No. US20030165506A1el alpha-catenin expressed in heart and testis
; FILE REFERENCE: FVR/aTc/V067
; CURRENT APPLICATION NUMBER: US/10/345,092
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: 00202472.7
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/218,309
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: lower primer
US-10-345-092-62

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2095 TTTTGGACCGAGTCTTGC 2114
Db 20 TTTTGGACCGAGTCTGC 1

RESULT 1525
US-10-210-951-198/c
; Sequence 198, Application US/10210951
; Publication No. US20030170228A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Pitti, Robert M.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stone, Donna M.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
; FILE REFERENCE: P2931R1C1
; CURRENT APPLICATION NUMBER: US/10/210,951
```

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; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/014699
; PRIOR FILING DATE: 1996-04-01
; PRIOR APPLICATION NUMBER: 60/026943
; PRIOR FILING DATE: 1996-09-23
; PRIOR APPLICATION NUMBER: 60/059121
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/062037
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: 60/063755
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063045
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/066511
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 258
; SEQ ID NO 198
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe.
US-10-210-951-198

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 48 TCGAAAGATGAGCAAGAA 67
Db 20 TCGAGGGATGAGCAAGAA 1

RESULT 1526
US-10-289-845-16
; Sequence 16, Application US/10289845
; Publication No. US20030170679A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Linda
; APPLICANT: Wagner, Susanne
; APPLICANT: Parodi, Luis
; TITLE OF INVENTION: Single Nucleotide Polymorphisms in GH-1
; FILE REFERENCE: 00791.US1
; CURRENT APPLICATION NUMBER: US/10/289,845
; CURRENT FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-289-845-16

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2176 GGCTTCGCACCATTCCTCG 2195
Db 1 GGATTCACGCCATTCCTCG 20

RESULT 1527
US-10-211-884-198/c
```

Sequence 199, Application US/10211884
Publication No. US20030175900A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
APPLICANT: Pan, James
APPLICANT: Pitti, Robert M.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stone, Donna M.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
FILE REFERENCE: P293IRIC1
CURRENT APPLICATION NUMBER: US/10/211,884
CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: 60/014699
PRIOR FILING DATE: 1996-04-01
PRIOR APPLICATION NUMBER: 60/026943
PRIOR FILING DATE: 1996-09-23
PRIOR APPLICATION NUMBER: 60/059121
PRIOR FILING DATE: 1997-07-17
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/062037
PRIOR FILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: 60/063755
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063045
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/066511
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066772
PRIOR FILING DATE: 1997-11-24
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 258
SEQ ID NO 198
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide Probe.
US-10-211-884-198

Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 48 TCGGAAGATGGAGCAAGAA 67
||||| ||||||| |||||
Db 20 TCGGAGGATGGAGAAAGAA 1

RESULT 1528
US-10-331-907-78
Sequence 78, Application US/10331907
Publication No. US20030181660A1
GENERAL INFORMATION:
APPLICANT: Todd, John A
Hess, John W
Caskey, Charles T
Cox, Roger D
Gerhold, David
Hammond, Holly
Hey, Patricia
Kawaguchi, Yoshihiko
Merriman, Tony R

Metzker, Michael L
TITLE OF INVENTION: No. US20030181660A1e1 LDL-Receptor
NUMBER OF SEQUENCES: 455
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon and Vanderhye
STREET: 1100 No. US20030181660A1th Glebe Road, Eighth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: US
ZIP: VA 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA: US/10/331,907
FILING DATE: 31-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/402,923A
FILING DATE: 14-Feb-2001
APPLICATION NUMBER: PCT/GB98/01102
FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/043,553
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 60/048,740
FILING DATE: 05-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: B.J.Sadoff
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 620-81
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4091
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 78:
US-10-331-907-78
Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2293 AGGATGCTCTCGATCTCCTG 2312
||||| ||||||| |||||||
Db 1 AGGCTGCTCTCAACTCCTG 20
RESULT 1529
US-10-331-907-240/c
Sequence 240, Application US/10331907
Publication No. US20030181660A1
GENERAL INFORMATION:
APPLICANT: Todd, John A
Hess, John W
Caskey, Charles T
Cox, Roger D
Gerhold, David
Hammond, Holly
Hey, Patricia
Kawaguchi, Yoshihiko
Merriman, Tony R
Metzker, Michael L
TITLE OF INVENTION: No. US20030181660A1e1 LDL-Receptor
NUMBER OF SEQUENCES: 455
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon and Vanderhye
STREET: 1100 No. US20030181660A1th Glebe Road, Eighth Floor
CITY: Arlington

STATE: Virginia
COUNTRY: US
ZIP: VA 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/331,907
FILING DATE: 31-Dec-2002
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/402,923A
FILING DATE: 14-Feb-2001
APPLICATION NUMBER: PCT/GB98/01102
FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/043,553
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 60/048,740
FILING DATE: 05-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: B.J.Sadoff
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 620-81
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4091
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 240:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 240:
US-10-331-907-240

Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2103 ACCGAGTCTGCTCTGTTC 2122
||| ||||| ||||| ||||| |||||
Db 20 ACAGGGTCTGCTCTGTTC 1

RESULT 1530
US-10-005-344-341/c
; Sequence 341, Application US/10005344
; Publication No. US20030203862A1
; GENERAL INFORMATION:
; APPLICANT: Loren J. Miraglia
; APPLICANT: Pamela Nero
; APPLICANT: Mark J. Graham
; APPLICANT: Brett P. Monia
; APPLICANT: Erich Koller
; APPLICANT: Mingyi Chiang
; APPLICANT: Mano Manoharan
; TITLE OF INVENTION: Antisense Modulation of mdm2 expression.
; FILE REFERENCE: ISPH-0622
; CURRENT APPLICATION NUMBER: US/10/005,344
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 09/048,810
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/280,805
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 379
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 341
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide

US-10-005-344-341

Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 978 GATCTTGATGCTGCTGTAAG 997
||||| ||||| ||||| ||||| |||||
Db 20 GATCTTGACGATGCGTAAG 1

RESULT 1531
US-10-005-344-351/c
; Sequence 351, Application US/10005344
; Publication No. US20030203862A1
; GENERAL INFORMATION:
; APPLICANT: Loren J. Miraglia
; APPLICANT: Pamela Nero
; APPLICANT: Mark J. Graham
; APPLICANT: Brett P. Monia
; APPLICANT: Erich Koller
; APPLICANT: Mingyi Chiang
; APPLICANT: Mano Manoharan
; TITLE OF INVENTION: Antisense Modulation of mdm2 expression.
; FILE REFERENCE: ISPH-0622
; CURRENT APPLICATION NUMBER: US/10/005,344
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 09/048,810
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/280,805
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 379
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 351
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-005-344-351

Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1638 GGTGACCTAAATAATGTTG 1657
||| ||||| ||||| ||||| |||||
Db 20 GGGCGGCTAAATAATGCTG 1

RESULT 1532
US-10-446-373-98
; Sequence 98, Application US/10446373
; Publication No. US20030204076A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE EXPRESSION
; FILE REFERENCE: RTS-0232
; CURRENT APPLICATION NUMBER: US/10/446,373
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: US/09/953,318
; PRIOR FILING DATE: 2001-09-13
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 98
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-446-373-98

Query Match 0.6%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 1.4e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2234 CACCACACCTGGCTAATTTT 2253
 ||||| || ||||| |||||
 Db 1 CACCATGCCGGCTAATTTT 20

RESULT 1533
 US-10-211-858-198/c
 ; Sequence 198, Application US/10211858
 ; Publication No. US20030211096A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Marsters, Scot A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Pitti, Robert M.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stone, Donna M.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
 ; FILE REFERENCE: P2931R1C1
 ; CURRENT APPLICATION NUMBER: US/10/211,858
 ; CURRENT FILING DATE: 2002-08-02
 ; PRIOR APPLICATION NUMBER: 60/014699
 ; PRIOR FILING DATE: 1996-04-01
 ; PRIOR APPLICATION NUMBER: 60/026943
 ; PRIOR FILING DATE: 1996-09-23
 ; PRIOR APPLICATION NUMBER: 60/059121
 ; PRIOR FILING DATE: 1997-07-17
 ; PRIOR APPLICATION NUMBER: 60/059352
 ; PRIOR FILING DATE: 1997-09-19
 ; PRIOR APPLICATION NUMBER: 60/062037
 ; PRIOR FILING DATE: 1997-10-10
 ; PRIOR APPLICATION NUMBER: 60/063755
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063045
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063046
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/066511
 ; PRIOR FILING DATE: 1997-11-24
 ; PRIOR APPLICATION NUMBER: 60/066772
 ; PRIOR FILING DATE: 1997-11-24
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 258
 ; SEQ ID NO 198
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic Oligonucleotide Probe.
 US-10-211-858-198

Query Match 0.6%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 1.4e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 48 TCGGAAGATGGAGCAAGAA 67
 ||||| ||||| |||||
 Db 20 TCGGAGGATGGAGAAAGAA 1

RESULT 1534
 US-10-181-875-71/c
 ; Sequence 71, Application US/10181875

; Publication No. US20030216333A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Isis Pharmaceuticals, Inc.
 ; APPLICANT: Brett P. Monia
 ; APPLICANT: Robert McKay
 ; APPLICANT: Madeline M. Butler
 ; APPLICANT: Jacqueline Wyatt
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 ALPHA EXPRESS
 ; FILE REFERENCE: RTSP-0356
 ; CURRENT APPLICATION NUMBER: US/10/181,875
 ; CURRENT FILING DATE: 2002-07-22
 ; PRIOR APPLICATION NUMBER: 09/488,856
 ; PRIOR FILING DATE: 2000-01-21
 ; NUMBER OF SEQ ID NOS: 88
 ; SEQ ID NO 71
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-10-181-875-71

Query Match 0.6%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 1.4e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2146 TCTTGGCTCACTGCAAGCTC 2165
 ||||| ||||| ||||| |||||
 Db 20 TCTCGGGTCACTGCAACCTC 1

RESULT 1535
 US-10-094-749-3312
 ; Sequence 3312, Application US/10094749
 ; Publication No. US20030219741A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ISOGAI, TAKAO
 ; APPLICANT: SUGIYAMA, TOMOYASU
 ; APPLICANT: OTSUKI, TETSUJI
 ; APPLICANT: WAKAMATSU, AI
 ; APPLICANT: SATO, HIROYUKI
 ; APPLICANT: ISHII, SHIZUKO
 ; APPLICANT: YAMAMOTO, JUN-ICHI
 ; APPLICANT: ISONO, YUUKO
 ; APPLICANT: HIO, YURI
 ; APPLICANT: OTSUKA, KAORU
 ; APPLICANT: NAGAI, KEIICHI
 ; APPLICANT: IRIE, RYOTARO
 ; APPLICANT: TAMECHIKA, ICHIRO
 ; APPLICANT: SEKI, NAOHIKO
 ; APPLICANT: YOSHIKAWA, TSUTOMU
 ; APPLICANT: OTSUKA, MOTOYUKI
 ; APPLICANT: NAGAHARI, KENJI
 ; APPLICANT: MASUHO, YASUHIKO
 ; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
 ; FILE REFERENCE: 084335/0160
 ; CURRENT APPLICATION NUMBER: US/10/094,749
 ; CURRENT FILING DATE: 2002-03-12
 ; PRIOR APPLICATION NUMBER: 60/350,435
 ; PRIOR FILING DATE: 2002-01-24
 ; PRIOR APPLICATION NUMBER: JP 2001-328381
 ; PRIOR FILING DATE: 2001-09-14
 ; NUMBER OF SEQ ID NOS: 3381
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3312
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized primer sequence
 US-10-094-749-3312

Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2086 TTTTGAGACCGAGTCCT 2115
|||||
Db 1 TTTTGAGACAGATTGCGT 20

RESULT 1536
US-10-282-174-215
; Sequence 215, Application US/10282174
; Publication No. US20030224380A1
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bertram, Lars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; FILE REFERENCE: 37481-3308
; CURRENT APPLICATION NUMBER: US/10/282,174
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/337,052
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/368,919
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 215
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-282-174-215

Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2344 AGTGTGGGATTACGCAT 2363
|||||
Db 1 AGTGTGGGATTATAGGCTT 20

RESULT 1537
US-10-282-174-234
; Sequence 234, Application US/10282174
; Publication No. US20030224380A1
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bertram, Lars
; APPLICANT: Saunders, Aleister J.

; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; FILE REFERENCE: 37481-3308
; CURRENT APPLICATION NUMBER: US/10/282,174
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/337,052
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/368,919
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 234
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-282-174-234

Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2321 ATCCGCCACCTCGGCTCC 2340
|||||
Db 1 ATCCGCCACCTGGACTTC 20

RESULT 1538
US-10-160-807-22
; Sequence 22, Application US/10160807
; Publication No. US20030224514A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PPAR-DELTA EXPRESSION
; FILE REFERENCE: RTS-0189
; CURRENT APPLICATION NUMBER: US/10/160,807
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 296
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-160-807-22

Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2341 CAAAGTGTGGGATTACAGG 2360
|||||
Db 1 CAAGTAGCTGGGATTACAGG 20

RESULT 1539
US-10-160-807-175/c
; Sequence 175, Application US/10160807

```

; Publication No. US20030224514A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PPAR-DELTA EXPRESSION
; FILE REFERENCE: RYS-0189
; CURRENT APPLICATION NUMBER: US/10/160,807
; CURRENT FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 296
; SEQ ID NO 175
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-160-807-175

```

```

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 2341 CAAAGTCTGGATTACAGG 2360
Db 20 CAAGTAGCTGGATTACAGG 1

```

```

RESULT 1540
US-10-388-263-680
; Sequence 680, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
; APPLICANT: Cowsert, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Sasnor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 680
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-680

```

```

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 2275 GGTTTACCGTGTAGCCAG 2294
Db 1 GGTTTACCATTGTGTGTCAG 20

```

```

RESULT 1541
US-10-388-263-681
; Sequence 681, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
; APPLICANT: Cowsert, Lex M.
; APPLICANT: Baker, Brenda F.

```

```

; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Sasnor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 681
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-681

```

```

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

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QY 2146 TCTTGGCTCACTGCAAGCTC 2165
Db 1 TCTCGGCTCACTACAACCTC 20

```

```

RESULT 1542
US-10-388-263-697
; Sequence 697, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
; APPLICANT: Cowsert, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Sasnor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 697
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-697

```

```

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 2342 AAGTCTGGATTACAGGC 2361
Db 1 AAGTAGCTGGATTACAGGC 20

```

```
RESULT 1543
US-10-388-263-714
; Sequence 714, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
; APPLICANT: Cowsett, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Saemor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 714
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-714

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2285 TGTAGCCAGGAGTGCTCG 2304
||||| ||||| ||||| |||||
Db 1 TGTGGCCAGGAGTGCTCG 20

RESULT 1544
US-10-177-798-40/c
; Sequence 40, Application US/10177798
; Publication No. US20030235912A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF ORPHAN G-PROTEIN COUPLED RECEPTOR GPRC5B
; FILE REFERENCE: PTD-0047
; CURRENT APPLICATION NUMBER: US/10/177,798
; CURRENT FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 70
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-177-798-40

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 981 CTTGATGCTGGTGAAGTGA 1000
||||| ||||| ||||| |||||
Db 20 CCTGATGCTGGTGAAGTGA 1

RESULT 1545
US-10-199-676-54/c
; Sequence 54, Application US/10199676
```

```
; Publication No. US20040014051A1
; GENERAL INFORMATION:
; APPLICANT: Vickie L. Brown-Driver
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF BREAST CANCER-1 EXPRESSION
; FILE REFERENCE: PTD-0017
; CURRENT APPLICATION NUMBER: US/10/199,676
; CURRENT FILING DATE: 2002-07-18
; NUMBER OF SEQ ID NOS: 84
; SEQ ID NO 54
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-199-676-54

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2097 TTTGAGACCGAGTCTTGCTC 2116
||||| ||||| ||||| |||||
Db 20 TTTGAGACAGGGTCTTACTC 1

RESULT 1546
US-10-199-676-79
; Sequence 79, Application US/10199676
; Publication No. US20040014051A1
; GENERAL INFORMATION:
; APPLICANT: Vickie L. Brown-Driver
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF BREAST CANCER-1 EXPRESSION
; FILE REFERENCE: PTD-0017
; CURRENT APPLICATION NUMBER: US/10/199,676
; CURRENT FILING DATE: 2002-07-18
; NUMBER OF SEQ ID NOS: 84
; SEQ ID NO 79
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-199-676-79

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2097 TTTGAGACCGAGTCTTGCTC 2116
||||| ||||| ||||| |||||
Db 1 TTTGAGACAGGGTCTTACTC 20

RESULT 1547
US-10-210-556-77
; Sequence 77, Application US/10210556
; Publication No. US20040023904A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowsett
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTPRA EXPRESSION
; FILE REFERENCE: PTD-0015
; CURRENT APPLICATION NUMBER: US/10/210,556
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 227
; SEQ ID NO 77
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
```

US-10-210-556-77

Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2292 CAGGATCGTCTCGATCTCCT 2311
|||||
DB 1 CAGGCTGGTTTCGAACCTCT 20

RESULT 1548

US-10-210-556-195/c
; Sequence 195, Application US/10210556
; Publication No. US20040023904A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowart
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTTPRA EXPRESSION
; FILE REFERENCE: PTS-0015
; CURRENT APPLICATION NUMBER: US/10/210,556
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 227
; SEQ ID NO 195
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-210-556-195

Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2292 CAGGATCGTCTCGATCTCCT 2311
|||||
DB 20 CAGGCTGGTTTCGAACCTCT 1

RESULT 1549

US-10-237-614-17/c
; Sequence 17, Application US/10237614
; Publication No. US20040048259A1
; GENERAL INFORMATION:
; APPLICANT: SOMIARI, RICHARD IDEM
; APPLICANT: SOMIARI, STELLA BASSEY
; APPLICANT: JACOBS, F. NICHOLAS
; APPLICANT: JORDAN, RICK
; TITLE OF INVENTION: MULTIPLE-GENE DIAGNOSTIC PROBES AND ASSAY KITS AND
; TITLE OF INVENTION: METHOD FOR THE ASSESSMENT OF MULTIPLE MARKERS FOR
; TITLE OF INVENTION: BREAST CANCER PROGNOSIS
; FILE REFERENCE: 13168.0006
; CURRENT APPLICATION NUMBER: US/10/237,614
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-237-614-17

Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2236 CCACACCTGGCTAATTTT 2255
|||||
DB 20 CCAGACTTGGCTAATTTAT 1

RESULT 1550

US-10-147-299A-11
; Sequence 11, Application US/10147299A
; Publication No. US20040058323A1
; GENERAL INFORMATION:
; APPLICANT: KO, ALBERT I.
; APPLICANT: HAAKE, DAVID A.
; APPLICANT: REIS, MITERMAYER GALVAO
; APPLICANT: MATSUNAGA, JAMES
; APPLICANT: CRODA, JULIO HENRIQUE ROSA
; APPLICANT: SIQUEIRA, ISADORA CRISTINA
; APPLICANT: RILEY, LEE W.
; APPLICANT: BAROCCHI, MICHELE
; APPLICANT: YOUNG, TRACY ANN
; TITLE OF INVENTION: DOMAINS PRESENT IN LEPTOSPIRA SPECIES
; FILE REFERENCE: 3673-19
; CURRENT APPLICATION NUMBER: US/10/147,299A
; CURRENT FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-147-299A-11

Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1446 GATGATAAAATTACACAAGC 1465
|||||
DB 1 GATTTTAAAGTTACACAAGC 20

RESULT 1551

US-10-655-847-22
; Sequence 22, Application US/10655847
; Publication No. US20040063129A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PPAR-DELTA EXPRESSION
; FILE REFERENCE: RTS-0189
; CURRENT APPLICATION NUMBER: US/10/655,847
; CURRENT FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: US/10/160,807
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 296
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-655-847-22

Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2341 CAAAGTCTGGGATTACAGC 2360
|||||
DB 1 CAAGTAGCTGGGATTACAGC 20

RESULT 1552

```
US-10-655-847-175/c
; Sequence 175, Application US/10655847
; Publication No. US20040063129A1
; GENERAL INFORMATION:
; APPLICANT: William M. Garde
; APPLICANT: Susan M. Freier
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PPAR-DELTA EXPRESSION
; FILE REFERENCE: RTS-0189
; CURRENT APPLICATION NUMBER: US/10/655,847
; CURRENT FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: US/10/160,807
; PRIOR FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 296
; SEQ ID NO 175
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-655-847-175

Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2341 CAAAGTGTGGGATTACAGG 2360
    ||| ||||| ||||| |||||
Db 20 CAAGTAGCTGGGATTACAGG 1

RESULT 1553
US-10-683-386-42/c
; Sequence 42, Application US/10683386
; Publication No. US20040063137A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, VOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOKOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; FILE REFERENCE: 0163-0758-0X
; CURRENT APPLICATION NUMBER: US/10/683,386
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US/09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-42

Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2048 TTTTTCCTTAATATGAT 2067
    ||||| ||||| ||||| |||||
Db 20 TTTTTCCTTAATATATAT 1

RESULT 1554
US-10-728-509-150

; Sequence 150, Application US/10728509
; Publication No. US20040077583A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/10/728,509
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US/09/908,147
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 150
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-728-509-150

Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2347 GCTGGGATTACAGCATGAG 2366
    ||||| ||||| ||||| |||||
Db 1 GCTGGGATTAAAGCGTGGC 20

RESULT 1555
US-10-304-116-92
; Sequence 92, Application US/10304116
; Publication No. US20040101857A1
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF CYTOKINE-INDUCIBLE KINASE EXPRESSION
; FILE REFERENCE: RTS-0397
; CURRENT APPLICATION NUMBER: US/10/304,116
; CURRENT FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 138
; SEQ ID NO 92
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-304-116-92

Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2100 GAGACCGAGTCTGCTCTGT 2119
    ||||| ||||| ||||| |||||
Db 1 GAGATCGAGTCTCGCTCTGT 20

RESULT 1556
US-10-304-116-138/c
; Sequence 138, Application US/10304116
; Publication No. US20040101857A1
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF CYTOKINE-INDUCIBLE KINASE EXPRESSION
; FILE REFERENCE: RTS-0397
; CURRENT APPLICATION NUMBER: US/10/304,116
; CURRENT FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 138
; SEQ ID NO 138
; LENGTH: 20
; TYPE: DNA
```

```
; ORGANISM: H. sapiens
; FEATURE:
US-10-304-116-138

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2100 GAGACCGAGTCTGTCTGT 2119
|||||
Db 20 GAGATGGAGTCTGCTCTGT 1

RESULT 1557
US-10-303-325-84
; Sequence 84, Application US/10303325
; Publication No. US20040102395A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: MODULATION OF IAP-LIKE EXPRESSION
; FILE REFERENCE: RTS-0434
; CURRENT APPLICATION NUMBER: US/10/303,325
; CURRENT FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 84
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-303-325-84

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2109 TCTTGTCTCTGTACCCAGGC 2128
|||||
Db 1 TCTCGTCTCTGTACCCGGC 20

RESULT 1558
US-10-303-325-150/c
; Sequence 150, Application US/10303325
; Publication No. US20040102395A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: MODULATION OF IAP-LIKE EXPRESSION
; FILE REFERENCE: RTS-0434
; CURRENT APPLICATION NUMBER: US/10/303,325
; CURRENT FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 150
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-303-325-150

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2109 TCTTGTCTCTGTACCCAGGC 2128
|||||
Db 20 TCTCGTCTCTGTACCCGGC 1

RESULT 1559
US-10-688-706-682/c
; Sequence 682, Application US/10688706

; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 682
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-682

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1346 CAAACTGGAAACTCAACAC 1365
|||||
Db 20 CAAACTGTAATAACTTAAAC 1

RESULT 1560
US-10-318-819A-74
; Sequence 74, Application US/10318819A
; Publication No. US20040115645A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF DRK2 EXPRESSION
; FILE REFERENCE: PTS-0069
; CURRENT APPLICATION NUMBER: US/10/318,819A
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 133
; SEQ ID NO 74
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-318-819A-74

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2107 AGTCTTGCTCTGTACCCAG 2126
|||||
Db 1 AGTGTGCTCTGTGCGCCAG 20

RESULT 1561
US-10-318-819A-126/c
; Sequence 126, Application US/10318819A
; Publication No. US20040115645A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF DRK2 EXPRESSION
; FILE REFERENCE: PTS-0069
; CURRENT APPLICATION NUMBER: US/10/318,819A
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 133
; SEQ ID NO 126
; LENGTH: 20
; TYPE: DNA
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; ORGANISM: H. sapiens
; FEATURE:
US-10-318-819A-126

Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2107 AGCTTGCTCTGTTACCCAG 2126
Db 20 AGTGTGCTCTGTCGCCAG 1

RESULT 1562
US-10-671-395-656/c
; Sequence 656, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 656
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-656

Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2150 GGCTCACTGCAAGCTCTGCC 2169
Db 20 GGCTCACTGCAAGCTCTGCC 1

RESULT 1563
US-10-671-395-668/c
; Sequence 668, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 668
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-668

Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2107 AGCTTGCTCTGTTACCCAG 2126
Db 20 AGTGTGCTCTGTCGCCAG 1

RESULT 1562
US-10-671-395-656/c
; Sequence 656, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 656
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-656

Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2150 GGCTCACTGCAAGCTCTGCC 2169
Db 20 GGCTCACTGCAAGCTCTGCC 1

RESULT 1563
US-10-671-395-668/c
; Sequence 668, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 668
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-668

Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2149 TGGCTCACTGCAAGCTCTGC 2168
Db 20 TGGCTCACTGCAAGCTCTGC 1

RESULT 1564
US-10-671-395-696/c
; Sequence 696, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 696
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-696

Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2351 GGATTACAGGCATGAGCCAC 2370
Db 20 GGATTACAGGCATGAGCCAC 1

RESULT 1565
US-10-671-395-863/c
; Sequence 863, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 863
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-863

Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2235 ACCACACCTGGCTAATTTT 2254
Db 20 ACCATACCCAGCTAATTTT 1

RESULT 1566
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US-10-671-395-949/c
; Sequence 949, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 949
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-949

Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2120 TACCCAGGCTGGAGTGCGT 2139
| | | | | | | | | | | | | | | | | |
Db 20 TGCCCAAGCTGGAGTGAGT 1

RESULT 1567
US-10-671-395-987/c
; Sequence 987, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 987
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-987

Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2234 CACACACCTGGCTAAATTT 2253
| | | | | | | | | | | | | | | | | |
Db 20 CACCATACCCAGCTAAATTT 1

RESULT 1568
US-10-671-395-1060/c
; Sequence 1060, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE

; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1060
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1060

Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2119 TTACCCAGGCTGGAGTGCG 2138
| | | | | | | | | | | | | | | | | |
Db 20 TTGCCCAAGCTGGAGTGAG 1

RESULT 1569
US-10-671-395-1224/c
; Sequence 1224, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1224
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1224

Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2258 ACTTTTAGTAGACAGCGGT 2277
| | | | | | | | | | | | | | | | | |
Db 20 ATTTTGTAGTAGACGCGGT 1

RESULT 1570
US-10-671-395-1261/c
; Sequence 1261, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; NUMBER OF SEQ ID NOS: 1809

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1261
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1261

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2118 GTTACCCAGGCTGGAGTGCA 2137
Db 20 GTTGCCCAAGCTGGAGTGAA 1

RESULT 1571
US-10-671-395-1269/c
; Sequence 1269, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1269
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1269

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2350 GGGATTACGCGCATGACCCA 2369
Db 20 GGGATGACGCGCATGAATCA 1

RESULT 1572
US-10-671-395-1448/c
; Sequence 1448, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1448
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1448

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2195 GCCTCAGCCTCCCAATTAGC 2214
Db 20 GCCTCAGCCTCCTGAGTAGC 1

RESULT 1573
US-10-671-395-1453/c
; Sequence 1453, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1453
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1453

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2196 CCTCAGCCTCCCAATTAGCT 2215
Db 20 CCTCAGCCTCCTGAGTAGCT 1

RESULT 1574
US-10-671-395-1517/c
; Sequence 1517, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1517
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1517

Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2319 TGATCGCCACCTCGGCCT 2338
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||||| || |||||||
Db      20 TGATCCACCGGCTCGGCCT 1

RESULT 1575
US-10-671-395-1562/c
; Sequence 1562, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1562
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1562
Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2318 GTGATCCGCCACCTCGGCC 2337
Db      20 GTGATCCACCGGCTCGGCC 1

RESULT 1576
US-10-671-395-1563/c
; Sequence 1563, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1563
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1563
Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2320 GATCCGCCACCTCGGCCTC 2339
Db      20 GATCCACCGGCTCGGCCTC 1

RESULT 1577
US-10-671-395-1630/c
; Sequence 1630, Application US/10671395
```

```
Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1630
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1630
Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2190 CTCCTGCCTCAGCCTCCCAA 2209
Db      20 CACCGGCTCGGCTCCCAA 1

RESULT 1578
US-10-671-395-1680/c
; Sequence 1680, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1680
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1680
Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2321 ATCCGCCACCTCGGCCTCC 2340
Db      20 ATCCACCGGCTCGGCCTCC 1

RESULT 1579
US-10-671-395-1713/c
; Sequence 1713, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
```

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; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1713
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
;   OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1713

```

```
Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

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RESULT 1580
US-10-671-395-1723/c
; Sequence 1723, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Glaxo, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809.
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1723
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1723

```

```
Query Match          0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```

RESULT 1581
US-10-671-395-1736/c
; Sequence 1736, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1736

```

```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1736
```

Query Match 0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

RESULT 1582
US-10-671-395-1742/c
; Sequence 1742, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: ANTISENSE EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1742
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1742

```

```
Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```

RESULT 1583
US-10-671-395-1745/c
; Sequence 1745, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K.
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1745
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human pGE2 antisense
US-10-671-395-1745

```

```
Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2285 TGTAGCCAGGATGGTCTCG 2304
      ||||| ||||| ||||| |||||
Db 20 TGTGCCAGGAGGGTCTCG 1

RESULT 1584
US-10-671-395-1751/c
; Sequence 1751, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671.395
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1751
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1751

Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2322 TCGCCACCTCGGCTCCC 2341
      ||||| ||||| ||||| |||||
Db 20 TCCACGGCTCGGCTCCC 1

RESULT 1585
US-10-819-244-87/c
; Sequence 87, Application US/10819244
; Publication No. US20040171575A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERPERON GAMMA RECEPTOR 2 EXPRESSION
; FILE REFERENCE: RTS-0235
; CURRENT APPLICATION NUMBER: US/10/819,244
; CURRENT FILING DATE: 2004-04-06
; PRIOR APPLICATION NUMBER: US/09/843,377
; PRIOR FILING DATE: 2001-04-26
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 87
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-819-244-87

Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2108 GTCTTGCTCTGTACCCAGG 2127
      ||||| ||||| ||||| |||||
Db 20 GTCTTGCACTGTGCCCCAGG 1
```

```
RESULT 1586
US-10-819-244-89
; Sequence 89, Application US/10819244
; Publication No. US20040171575A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERFERON GAMMA RECEPTOR 2 EXPRESSION
; FILE REFERENCE: RTS-0235
; CURRENT APPLICATION NUMBER: US/10/819,244
; CURRENT FILING DATE: 2004-04-06
; PRIOR APPLICATION NUMBER: US/09/843,377
; PRIOR FILING DATE: 2001-04-26
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 89
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-819-244-89

Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2189 TCTCTGCTCGCTCCCA 2208
      ||||| ||||| ||||| |||||
Db 1 TCTCTTGCACTCGCTCTCA 20

RESULT 1587
US-10-776-013-45
; Sequence 45, Application US/10776013
; Publication No. US20040226056A1
; GENERAL INFORMATION:
; APPLICANT: MYRIAD GENETICS, INC.
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEUROLOGICAL DISORDERS AND
; FILE REFERENCE: 1600.24
; CURRENT APPLICATION NUMBER: US/10/776,013
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 09/948904
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 09/466139
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/113534
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/124120
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/141243
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/975072
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 10/194967
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 60/304775
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 695
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 45
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-776-013-45

Query Match      0.6%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
```

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1460 ACAAGCTTCACATCAAG 1479
Db 1 ACAAGCTTCAGTCAAG 20

RESULT 1588

US-10-010-802-81
; Sequence 81, Application US/10010802
; Publication No. US20030078220A1
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals
; APPLICANT: Chew, Anne
; APPLICANT: Denton, R. Rex
; APPLICANT: Duda, Amy
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Stephens, J. Claiborne
; APPLICANT: Windemuth, Andreas
; TITLE OF INVENTION: Drug Target Isoenes: Polymorphisms in the Interleukin
; FILE REFERENCE: MWH-0002US2 IL4R alpha
; CURRENT APPLICATION NUMBER: US/10/010.802
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/US00/19094
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-010-802-81

Query Match 0.6%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2126 GCCTGGAGTCAGTG 2140
Db 1 GCCTGGAGTCAGTG 15

RESULT 1589

US-10-092-885-46/c
; Sequence 46, Application US/10092885
; Publication No. US20030190618A1
; GENERAL INFORMATION:
; APPLICANT: SAMAL, BABRU
; APPLICANT: LI, YUAN
; APPLICANT: HERMIDA, LEANDRO C.
; APPLICANT: HOPPA, NANCY L.
; APPLICANT: JOHE, KARL K.
; TITLE OF INVENTION: METHOD FOR GENERATING FIVE PRIME BIASED TANDEM TAG
; FILE REFERENCE: 0109015/026
; CURRENT APPLICATION NUMBER: US/10/092.885
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-885-46

Query Match 0.6%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAGTGCT 2349
Db 15 GCCTCCCAAGTGCT 1

RESULT 1590
US-10-092-885-48/c
; Sequence 48, Application US/10092885
; Publication No. US20030190618A1
; GENERAL INFORMATION:
; APPLICANT: SAMAL, BABRU
; APPLICANT: LI, YUAN
; APPLICANT: HERMIDA, LEANDRO C.
; APPLICANT: HOPPA, NANCY L.
; APPLICANT: JOHE, KARL K.
; TITLE OF INVENTION: METHOD FOR GENERATING FIVE PRIME BIASED TANDEM TAG
; FILE REFERENCE: 0109015/026
; CURRENT APPLICATION NUMBER: US/10/092.885
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-885-48

Query Match 0.6%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAGTGCT 2349
Db 15 GCCTCCCAAGTGCT 1

RESULT 1591

US-10-156-306-1660
; Sequence 1660, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1660
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-1660

Query Match 0.6%; Score 15; DB 1; Length 17;
Best Local Similarity 73.3%; Pred. No. 1.5e+03;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2147 CTTGGCTCACTGCAA 2161
Db 1 CUUGGCUCACUGCAA 15

RESULT 1592

US-10-156-306-1670
; Sequence 1670, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBHB01-664-A (400/050)

; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1670
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-1670

Query Match 0.6%; Score 15; DB 1; Length 17;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2187 ATTCTCTCGCTCAG 2201
||:||||:||||
Db 3 AUUCCUGCCUCAG 17

RESULT 1593
US-10-156-306-1674
; Sequence 1674, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1674
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-1674

Query Match 0.6%; Score 15; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2192 CCTGCTCAGCCCTCC 2206
||:||||:||||
Db 1 CCUGCCUCAGCCUCC 15

RESULT 1594
US-10-156-306-2408
; Sequence 2408, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2408
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-2408

Query Match 0.6%; Score 15; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2269 AGACAGGGTTTCACC 2283

Db 2 AGACAGGGUUCACC 16
|||||||:||||
RESULT 1595
US-10-238-700-664
; Sequence 664, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Leve
; FILE REFERENCE: 400/057 (MBH01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 664
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-664

Query Match 0.6%; Score 15; DB 1; Length 17;
Best Local Similarity 73.3%; Pred. No. 1.5e+03;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1228 CTTTCATGCAATGAA 1242
||:||||:||||
Db 3 CUUUGCAUGAAA 17

RESULT 1596
US-10-238-700-698
; Sequence 698, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Leve
; FILE REFERENCE: 400/057 (MBH01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 698
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-698

Query Match 0.6%; Score 15; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2347 GCTGGGATTACAGC 2361
||:||||:||||
Db 3 GCUUGGAUACAGC 17

RESULT 1597
US-10-061-201-696
; Sequence 696, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:

```
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 696
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-696
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Query Match 0.6%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 913 TAATAAGGGAGATAT 927
||| ||||| ||||| |||||
Db 2 TAATAAGGGAGATAT 16
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RESULT 1598
US-10-061-201-697
; Sequence 697, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
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; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 697
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-697
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Query Match 0.6%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 913 TAATAAGGGAGATAT 927
||| ||||| ||||| |||||
Db 1 TAATAAGGGAGATAT 15
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```
RESULT 1599
US-10-336-472-138
; Sequence 138, Application US/10336472
; Publication No. US20040043929A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.
; APPLICANT: Ballinger, Robert A.
; APPLICANT: Baumgartner, Jason C.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Chant, John S.
; APPLICANT: Berghs, Constance
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gilbert, Jennifer A.
; APPLICANT: Gunther, Erik
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Rastelli, Luca
; APPLICANT: MacDougall, John R.
; APPLICANT: Mishra, Vishnu
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Smithson, Glennda
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Stone, David J.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Ort, Tatiana
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-533C
; CURRENT APPLICATION NUMBER: US/10/336,472
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: 09/746,491
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 10/005,041
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 10/023,681
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 10/024,212
; PRIOR FILING DATE: 2001-12-18
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; PRIOR APPLICATION NUMBER: 10/055,569
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 10/080,334
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/092,900
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 10/136,826
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 10/236,417
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/345,092
; PRIOR FILING DATE: 2002-01-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: CuraSegList version 0.1
; SEQ ID NO 138
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
US-10-336-472-138

Query Match          0.6%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 CCTGGCCCGGAGAGT 186
Db 1 CCTGGCCCGGAGAGT 15

RESULT 1600
US-10-255-434-9
; Sequence 9, Application US/10255434
; Publication No. US20030129626A1
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Kirsten V.
; APPLICANT: Hyldig-Nielsen, Jens J.
; TITLE OF INVENTION: Methods, Kits And Compositions Pertaining To The
; TITLE OF INVENTION: Suppression Of Detectable Probe Binding To Randomly
; FILE REFERENCE: BP0101-US
; CURRENT APPLICATION NUMBER: US/10/255,434
; CURRENT FILING DATE: 2002-09-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:Synthetic
; OTHER INFORMATION: Oligomer Sequence
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic Probe
US-10-255-434-9

Query Match          0.6%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2347 GCTGGGATTACAGC 2361
Db 3 GCTGGGATTACAGC 17

RESULT 1601
US-10-255-434-21/c
; Sequence 21, Application US/10255434
; Publication No. US20030129626A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Kirsten V.
; APPLICANT: Hyldig-Nielsen, Jens J.
; APPLICANT: Williams, Brett F.
; TITLE OF INVENTION: Methods, Kits And Compositions Pertaining To The
; TITLE OF INVENTION: Suppression Of Detectable Probe Binding To Randomly
; FILE REFERENCE: BP0101-US
; CURRENT APPLICATION NUMBER: US/10/255,434
; CURRENT FILING DATE: 2002-09-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 21
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:Synthetic
; OTHER INFORMATION: Oligomer Sequence
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic Probe
US-10-255-434-21

Query Match          0.6%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2347 GCTGGGATTACAGC 2361
Db 16 GCTGGGATTACAGC 2

RESULT 1602
US-10-108-260A-5312/c
; Sequence 5312, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5312
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized
US-10-108-260A-5312

Query Match          0.6%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 736 TTCAGGAGAGAAAC 750
Db 18 TTCAGGAGAGAAAC 4

RESULT 1603
US-10-007-078-84/c
; Sequence 84, Application US/10007078
; Publication No. US20030105042A1
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF EIF2C1 EXPRESSION
; FILE REFERENCE: RTS-0236
; CURRENT APPLICATION NUMBER: US/10/007,078
; CURRENT FILING DATE: 2001-11-08
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US-10-671-395-1438

Query Match 0.6%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2347 GCTGGGATTACAGC 2361
Db 17 GCTGGGATTACAGC 3

RESULT 1608

US-10-671-395-1511/c
; Sequence 1511, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1511
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1511

Query Match 0.6%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2347 GCTGGGATTACAGC 2361
Db 18 GCTGGGATTACAGC 4

RESULT 1609

US-10-671-395-1558/c
; Sequence 1558, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1558
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1558

Query Match 0.6%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2347 GCTGGGATTACAGC 2361

Db 19 GCTGGGATTACAGC 5

RESULT 1610

US-10-671-395-1568/c
; Sequence 1568, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1568
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-1568

Query Match 0.6%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2347 GCTGGGATTACAGC 2361
Db 20 GCTGGGATTACAGC 6

RESULT 1611

US-09-784-423-69/c
; Sequence 69, Application US/09784423
; Patent No. US20020012924A1
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; Bacher, Jeffery W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM REPEAT DNA MARKERS
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97 (DOS text format)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/784,423
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/018,584
; FILING DATE: 04-Feb-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Grady J. Frenchick
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 16026.9180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-3501

```

; TELEFAX: (608) 257-2275
; INFORMATION FOR SEQ ID NO: 69
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 69
US-09-784-423-69

Query Match          0.6%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2110 CTTGCTCTCTGTTACCCAGG 2127
Db 18 CTTGCTCTCTGTTACCCAGG 1

RESULT 1612
US-09-935-223-7
; Sequence 7, Application US/09935223
; Publication No. US20020086983A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: Fadd-Like Anti-Apoptotic Molecules, Methods Of Using The Same, And
; FILE REFERENCE: TU02499
; CURRENT APPLICATION NUMBER: US/09/935,223
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 09/723,450
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/276,993
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/859,167
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Novel Sequence
US-09-935-223-7

Query Match          0.6%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2293 AGGATGGTCTCGATCTCC 2310
Db 1 AGGATGGTCTCGAATCTCC 18

RESULT 1613
US-09-982-262B-4/c
; Sequence 4, Application US/09982262B
; Publication No. US20030077565A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Christopher K. Mirabelli
; TITLE OF INVENTION: OLIGONUCLEOTIDE MODULATION OF CELL ADHESION
; FILE REFERENCE: ISPH-0612
; CURRENT APPLICATION NUMBER: US/09/982,262B
; CURRENT FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 09/659,288
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 09/128,496
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: 08/440,740
; PRIOR FILING DATE: 1995-05-12
; PRIOR APPLICATION NUMBER: 08/063,167

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; PRIOR FILING DATE: 1993-05-17
; PRIOR APPLICATION NUMBER: 07/969,151
; PRIOR FILING DATE: 1993-02-10
; PRIOR APPLICATION NUMBER: 08/007,997
; PRIOR FILING DATE: 1993-01-21
; NUMBER OF SEQ ID NOS: 86
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-982-262B-4

Query Match          0.6%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2322 TCCGCCACCTCGGCCTC 2339
Db 18 TCCTCCACCTCAGCCTC 1

RESULT 1614
US-10-351-951-71/c
; Sequence 71, Application US/10351951
; Publication No. US20030203380A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Stefan E.
; TITLE OF INVENTION: GENE LINKED TO OSTEOARTHRITIS
; FILE REFERENCE: 2345.2043-004
; CURRENT APPLICATION NUMBER: US/10/351,951
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 10/057,312
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 60/431,538
; PRIOR FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer that hybridizes to the human MATN3 gene
US-10-351-951-71

Query Match          0.6%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2319 TGATCCGCCACCTCGGC 2336
Db 18 TGATCTCTCCACCTTGGC 1

RESULT 1615
US-10-454-663-4/c
; Sequence 4, Application US/10454663
; Publication No. US20040033977A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Christopher K. Mirabelli
; TITLE OF INVENTION: OLIGONUCLEOTIDE MODULATION OF CELL ADHESION
; FILE REFERENCE: ISPH-0744
; CURRENT APPLICATION NUMBER: US/10/454,663
; CURRENT FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: 09/982,262
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 09/659,288
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 09/128,496
; PRIOR FILING DATE: 1998-08-03

```

; PRIOR APPLICATION NUMBER: 08/440,740
; PRIOR FILING DATE: 1995-05-12
; PRIOR APPLICATION NUMBER: 08/063,167
; PRIOR FILING DATE: 1993-05-17
; PRIOR APPLICATION NUMBER: 07/969,151
; PRIOR FILING DATE: 1993-02-10
; PRIOR APPLICATION NUMBER: 08/007,997
; PRIOR FILING DATE: 1993-01-21
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-454-663-4

Query Match 0.6%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2322 TCGCCACCTCGGCCTC 2339
||| ||||| ||||| |||||
Db 18 TCTCCACCTCAGCCTC 1

RESULT 1616
US-10-627-757-40
; Sequence 40, Application US/10627757
; Publication No. US20040091914A1
; GENERAL INFORMATION:
; APPLICANT: KOUCHI YASUHIRO
; APPLICANT: MASASGO AKINORI
; APPLICANT: TAKAHATI TAKAYUKI
; TITLE OF INVENTION: GENE ASSAY METHOD FOR PREDICTING GLAUCOMA ONSET RISK
; FILE REFERENCE: Q76319
; CURRENT APPLICATION NUMBER: US/10/627,757
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: JP P2002-226612
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Designed DNA based on OPTN gene
US-10-627-757-40

Query Match 0.6%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2321 ATCGCCACCTCGGCCT 2338
||| ||||| ||||| |||||
Db 1 ATCCACCCACCTCGACCT 18

RESULT 1617
US-10-473-126-613/c
; Sequence 613, Application US/10473126
; Publication No. US20040234973A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
; FILE REFERENCE: proliferative disorders
; CURRENT APPLICATION NUMBER: US/10/473,126
; CURRENT FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 613
; LENGTH: 18

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Detection oligonucleotide for CDH3
US-10-473-126-613

Query Match 0.6%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2235 ACCACACCTGGCTAATTT 2252
||| ||||| ||||| |||||
Db 18 ACCACACCTGGCTAATTT 1

RESULT 1618
US-09-784-423-64/c
; Sequence 64, Application US/09784423
; Patent No. US20020012924A1
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; Bacher, Jeffery W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
REPEAT DNA MARKERS
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
; COMPUTER: IBM compatible PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97 (DOS text format)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/784,423
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/018,584
; FILING DATE: 04-Feb-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Grady J. Frenchick
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 16026.9180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-3501
; TELEFAX: (608) 257-2275
; INFORMATION FOR SEQ ID NO: 64
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 64
US-09-784-423-64

Query Match 0.6%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2106 GAGTCTGTCTGTATTACC 2123
||| ||||| ||||| |||||
Db 19 GAGTCTGTCTGTATTACC 2

RESULT 1619
US-10-444-925-599/c
; Sequence 599, Application US/10444925

Publication No. US20040009946A1
GENERAL INFORMATION:
APPLICANT: Lewis, Stephen Patrick
APPLICANT: Klinghoffer, Richard
APPLICANT: Wilson, Linda K.
TITLE OF INVENTION: MODULATION OF PTP1B SIGNAL TRANSDUCTION
FILE REFERENCE: 200125.441
CURRENT APPLICATION NUMBER: US/10/444,925
NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 599
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Small interfering RNA
US-10-444-925-599

Query Match 0.6%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 802 CAATTAGTGAGACAGAAG 819
| | | | | | | | | | | | | | | | | | |
Db 19 CCATTAGTGAGACACAAG 2

RESULT 1620
US-10-636-065-128
Sequence 128, Application US/10636065
Publication No. US20040127694A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: LaCasse, Eric
APPLICANT: Baird, Stephen
APPLICANT: Holcik, Martin
APPLICANT: Young, Sean
TITLE OF INVENTION: Antisense TAP Nucleic Acids and Uses
TITLE OF INVENTION: Thereof
FILE REFERENCE: 07891/025005
CURRENT APPLICATION NUMBER: US/10/636,065
CURRENT FILING DATE: 2003-08-07
PRIOR APPLICATION NUMBER: 09/672,717
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 231
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 128
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: based on Homo sapiens
US-10-636-065-128

Query Match 0.6%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1093 TTAGTGAAGAGGACAAG 1110
| | | | | | | | | | | | | | | | | | |
Db 2 TTAGTGAAGAGGAAAG 19

RESULT 1621
US-10-670-011-10
Sequence 10, Application US/10670011
Publication No. US20040209832A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid

APPLICANT: Pavco, Pamela
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: 400/132 (MBHB02-742-G)
CURRENT APPLICATION NUMBER: US/10/670,011
CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: PCT/US03/05022
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US60/393,796
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: US60/399,348
PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: US60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US60/440,129
PRIOR FILING DATE: 2003-01-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 427
SOFTWARE: PatentIn version 3.2
SEQ ID NO 10
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r
US-10-670-011-10

Query Match 0.6%; Score 14.8; DB 1; Length 19;
Best Local Similarity 27.8%; Pred. No. 1.5e+03;
Matches 5; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

Qy 2046 TTTTCTTCTTAATAT 2063
| | | | | | | | | | | | | | | | | | |
Db 2 UUCUUUUUUUAACAU 19

RESULT 1622
US-10-670-011-106/c
Sequence 106, Application US/10670011
Publication No. US20040209832A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
APPLICANT: Pavco, Pamela
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: 400/132 (MBHB02-742-G)
CURRENT APPLICATION NUMBER: US/10/670,011
CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: PCT/US03/05022
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US60/393,796
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: US60/399,348

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; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 427
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 106
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-670-011-106

Query Match          0.6%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2046 TTTTCTTTCTTAAATAT 2063
      |||||||
Db 18 TTCTTTTCTTAAACAT 1

RESULT 1623
US-09-764-887-575/c
; Sequence 575, Application US/09764887
; Patent No. US20020042096A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PAIL3
; CURRENT APPLICATION NUMBER: US/09/764,887
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 658
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 575
; LENGTH: 66
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-887-575

Query Match          0.6%; Score 14.8; DB 1; Length 66;
Best Local Similarity 59.5%; Pred. No. 9.6e+02;
Matches 25; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 1031 AGTTGACATCAGTTTGTAGTGTAGTGTAGTGTAGTGTAGTGTCTCT 1072
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 58 AGTTTGACACAGCGCTGTGTAATATGTGTGAACCCGCTCTCT 17

RESULT 1624
US-10-073-961-575/c
; Sequence 575, Application US/10073961
; Publication No. US20030077602A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PAIL3C1
; CURRENT APPLICATION NUMBER: US/10/073,961
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/764,887
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
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; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/234,274
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/234,223
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,369
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/224,519
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/249,299
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,368
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/251,856
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/251,868
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/229,344
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 60/229,343
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,345
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,287
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,513
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; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/249,218
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,208
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,213
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,212
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,207
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,245
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,244
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,217
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,211
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,215
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,264
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,214
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,297
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/232,400
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/231,242
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,081
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,080
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,414
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,244
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,064
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/233,063
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,397
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,399
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,401
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/241,808
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,826
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,786
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,221
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,475
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08

Query Match 0.6%; Score 14.6; DB 1; Length 87;
Best Local Similarity 54.7%; Pred. No. 8.1e+02;
Matches 29; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1107 CAAGAACTCTCAGATGAAGATGATGAGGTATATCAAGTTACTGTGTATCAGGC 1159
Db 72 CCAGCACTTTGGAGGCAGAGCGGGTGGATCAGAGTCAGGAGTTTGAGAC 20

RESULT 1627
US-10-212-872-962/c

; Sequence 962, Application US/10212872
; Publication No. US20030215893A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008C2
; CURRENT APPLICATION NUMBER: US/10/212,872
; CURRENT FILING DATE: 2002-08-07
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 962
; LENGTH: 87
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-872-962

Query Match 0.6%; Score 14.6; DB 1; Length 87;
Best Local Similarity 54.7%; Pred. No. 8.1e+02;
Matches 29; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1107 CAAGAACTCTCAGATGAAGATGATGAGGTATATCAAGTTACTGTGTATCAGGC 1159
Db 72 CCAGCACTTTGGAGGCAGAGCGGGTGGATCAGAGTCAGGAGTTTGAGAC 20

RESULT 1628

US-09-739-909-4
; Sequence 4, Application US/09739909
; Publication No. US20030022163A1
; GENERAL INFORMATION:
; APPLICANT: Mandrekar, Michelle N.
; APPLICANT: Tereba, Allan
; APPLICANT: Shultz, John W.
; TITLE OF INVENTION: Detection of Repetitive Nucleic Acid Sequences
; FILE REFERENCE: US CIP of PRO-104.0
; CURRENT APPLICATION NUMBER: US/09/739,909
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 09/358,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 09/383,316
; PRIOR FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-739-909-4

Query Match 0.6%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2146 TCTTGGCTCACTGCAA 2161
Db 1 TCTGGCTCACTGCAA 16

RESULT 1629

US-09-739-909-5
; Sequence 5, Application US/09739909
; Publication No. US20030022163A1
; GENERAL INFORMATION:
; APPLICANT: Mandrekar, Michelle N.
; APPLICANT: Tereba, Allan
; APPLICANT: Shultz, John W.
; TITLE OF INVENTION: Detection of Repetitive Nucleic Acid Sequences
; FILE REFERENCE: US CIP of PRO-104.0
; CURRENT APPLICATION NUMBER: US/09/739,909
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 09/358,972
; PRIOR FILING DATE: 1999-07-21

; PRIOR APPLICATION NUMBER: 09/383,316
; PRIOR FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-739-909-5

Query Match 0.6%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2146 TCTGGCTCACTGCAA 2161
||| |||||
Db 1 TCTGGCTCACTGCAA 16

RESULT 1630
US-09-739-909-6
; Sequence 6, Application US/09739909
; Publication No. US20030022163A1
; GENERAL INFORMATION:
; APPLICANT: Mandrekar, Michelle N.
; APPLICANT: Tereba, Allan
; APPLICANT: Shultz, John W.
; TITLE OF INVENTION: Detection of Repetitive Nucleic Acid Sequences
; FILE REFERENCE: US CIP of PRO-104.0
; CURRENT APPLICATION NUMBER: US/09/739,909
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 09/358,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 09/383,316
; PRIOR FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-739-909-6

Query Match 0.6%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2351 GGATTACAGCGTGAG 2366
||| |||||
Db 1 GGATTACAGCGTGAG 16

RESULT 1631
US-10-255-434-5/c
; Sequence 5, Application US/10255434
; Publication No. US20030129626A1
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Kirsten V.
; APPLICANT: Hyldig-Nielsen, Jens J.
; TITLE OF INVENTION: Methods, Kits And Compositions Pertaining To The
; TITLE OF INVENTION: Suppression Of Detectable Probe Binding To Randomly
; TITLE OF INVENTION: Distributed Repeat Sequences In Genomic Nucleic Acid
; FILE REFERENCE: BP0101-US
; CURRENT APPLICATION NUMBER: US/10/255,434
; CURRENT FILING DATE: 2002-09-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:Synthetic
; OTHER INFORMATION: Oligomer Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic Probe
; OTHER INFORMATION: Sequence
US-10-255-434-5

Query Match 0.6%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2326 CCCACCTCGGCTCCC 2341
||| |||||
Db 15 CCGGCTCGGCTCCC 1

RESULT 1632
US-10-255-434-17
; Sequence 17, Application US/10255434
; Publication No. US20030129626A1
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Kirsten V.
; APPLICANT: Hyldig-Nielsen, Jens J.
; TITLE OF INVENTION: Methods, Kits And Compositions Pertaining To The
; TITLE OF INVENTION: Suppression Of Detectable Probe Binding To Randomly
; TITLE OF INVENTION: Distributed Repeat Sequences In Genomic Nucleic Acid
; FILE REFERENCE: BP0101-US
; CURRENT APPLICATION NUMBER: US/10/255,434
; CURRENT FILING DATE: 2002-09-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:Synthetic
; OTHER INFORMATION: Oligomer Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic Probe
; OTHER INFORMATION: Sequence
US-10-255-434-17

Query Match 0.6%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2326 CCCACCTCGGCTCCC 2341
||| |||||
Db 1 CCGGCTCGGCTCCC 16

RESULT 1633
US-10-091-281-60
; Sequence 60, Application US/10091281
; Publication No. US20030190617A1
; GENERAL INFORMATION:
; APPLICANT: RAYMOND, VINCENT
; APPLICANT: SI, ERWIN
; APPLICANT: MORISSETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 13587.338
; CURRENT APPLICATION NUMBER: US/10/091,281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Putative B2TF/E2.01 motif

US-10-091-281-60

Query Match 0.6%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 285 AAACCCCGGTGGTGA 300
|||||
DB 1 AAACCCCGGTGGTGA 16

RESULT 1634

US-10-092-885-43/c
; Sequence 43, Application US/10092885
; Publication No. US20030190618A1

; GENERAL INFORMATION:
; APPLICANT: SAMAL, BABRU

; APPLICANT: LI, YUAN

; APPLICANT: HERMIDA, LEANDRO C.

; APPLICANT: HOPPA, NANCY L.

; APPLICANT: JOHE, KARL K.

; TITLE OF INVENTION: METHOD FOR GENERATING FIVE PRIME BIASED TANDEM TAG

; FILE REFERENCE: LIBRARIES OF CDNAS

; CURRENT APPLICATION NUMBER: US/10/092,885

; CURRENT FILING DATE: 2002-03-06

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 43

; LENGTH: 16

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-092-885-43

Query Match 0.6%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2352 GATTACAGCGTGAGC 2367
|||||
DB 16 GATTACAGCGTGAGC 1

RESULT 1635

US-10-092-885-55/c

; Sequence 55, Application US/10092885

; Publication No. US20030190618A1

; GENERAL INFORMATION:
; APPLICANT: SAMAL, BABRU

; APPLICANT: LI, YUAN

; APPLICANT: HERMIDA, LEANDRO C.

; APPLICANT: HOPPA, NANCY L.

; APPLICANT: JOHE, KARL K.

; TITLE OF INVENTION: METHOD FOR GENERATING FIVE PRIME BIASED TANDEM TAG

; FILE REFERENCE: LIBRARIES OF CDNAS

; CURRENT APPLICATION NUMBER: US/10/092,885

; CURRENT FILING DATE: 2002-03-06

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 55

; LENGTH: 16

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-092-885-55

Query Match 0.6%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGACAGG 2275
|||||
DB 16 TTTTAGTAGACAGG 1

RESULT 1636

US-09-866-108-7367

; Sequence 7367, Application US/09866108

; Patent No. US20020048800A1

; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 60/266,860

; PRIOR FILING DATE: 2001-02-05

; NUMBER OF SEQ ID NOS: 15752

; SOFTWARE: Aecomica Sequence Listing Engine

; SEQ ID NO 7367

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108-7367

Query Match 0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 818 AGAAATTCAGATGAA 833
|||||
DB 2 AGAAATTCAGATGAA 17

RESULT 1637

US-09-866-108-7369

; Sequence 7369, Application US/09866108

; Patent No. US20020048800A1

; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AROMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 7369
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7369

Query Match 0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 819 GAAATTCAGATGAAT 834
|||||:|||||
Db 1 GAAATTCAGTGAAT 16

RESULT 1638
US-09-776-474-380
; Sequence 380, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Boohar, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK
; FILE REFERENCE: MHB00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02

; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 380
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-380

Query Match 0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 1.6e+03;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 935 AAGAAGCAGTAGCAGT 950
|||||:|||||
Db 2 AAGACAGUCGAGU 17

RESULT 1639
US-09-776-474-692
; Sequence 692, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Boohar, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK
; FILE REFERENCE: MHB00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 692
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-692

Query Match 0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 1.6e+03;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 938 AAGCAGTAGCAGTGAA 953
|||||:|||||
Db 1 AAGCAGUCGAGUGAA 16

RESULT 1640
US-10-060-998-413/c
; Sequence 413, Application US/10060998
; Publication No. US20030104530A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: HUMAN SODIUM-HYDROGEN EXCHANGER LIKE PROTEIN 1
; FILE REFERENCE: PB01108
; CURRENT APPLICATION NUMBER: US/10/060,998
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/343,331
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 3056

; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 413
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-998-413

Query Match 0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1766 TGTGCTAACTTATTC 1781
DB 17 TGTGCTGACTTATTC 2

RESULT 1641
US-10-060-998-415/c
; Sequence 415, Application US/10060998
; Publication No. US20030104530A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: HUMAN SODIUM-HYDROGEN EXCHANGER LIKE PROTEIN 1
; FILE REFERENCE: PB01108
; CURRENT APPLICATION NUMBER: US/10/060,998
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/343,331
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 3056
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 415
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-998-415

Query Match 0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1765 TTGTGCTAACTTATTT 1780
DB 16 TTGTGCTGACTTATTT 1

RESULT 1642
US-10-156-306-524
; Sequence 524, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 524
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-524

Query Match 0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 18.8%; Pred. No. 1.6e+03;
Matches 3; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 2045 TTTTTCCTTTCTTAAA 2060
DB 2 UUUUUUUUUUUUUAAA 17

RESULT 1643
US-10-156-306-525
; Sequence 525, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 525
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-525

Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 18.8%; Pred. No. 1.6e+03;
Matches 3; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 2045 TTTTTCCTTTCTTAAA 2060
DB 1 UUUUUUUUUUUUUAAA 16

RESULT 1644
US-10-156-306-534
; Sequence 534, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 534
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-534

Query Match 0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 1.6e+03;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2113 GCTCTGTTATCCAGGC 2128
DB 2 GCUCUGUCCAGGC 17

RESULT 1645
US-10-156-306-573
; Sequence 573, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; FILE REFERENCE: MBH01-664-A (400/050)

```

; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 573
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-573

```

Query Match 0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. NO. 1.6e+03;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2192 CTGCCTCAGCCTCCC 2207
||:||||:||||:
Db 2 CCUGCCUUGGCCUCCC 17

RESULT 1646
US-10-156-306-1680
; Sequence 1680, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.

Query Match 0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 1.6e+03;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2351 GGATTACAGGCATGAG 2366
Db 2 GGAUUCACGGCAUGUG 17

RESULT 1647
US-10-156-306-1691
; Sequence 1691, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.

Query Match 0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 1.6e+03;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2266 TAGAGACAGGGTTCA 2281

Db 2 UAAAGACAGGGUUCA 17

RESULT 1648
US-10-156-306-1692
; Sequence 1692, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:

Query Match 0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 56.2%; Pred. No. 1.6e+03;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy	2273	AGGGTTT	CACCGTGT	2288
Db	1	AGGGUUU	CACCAUGU	16

RESULT 1649
US-10-156-306-2391
; Sequence 2391, Application US/10156306
; Publication No. US20030119017A1

```
Query Match          0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 1.6e+03;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

Qy 2125 AGGCTGGAGTGCAGTG 2140
|||||:||||:|
Db 1 AGGCTGGAGTGCAGTG 16

RESULT 1650
US-10-156-306-2404
; Sequence 2404, Application US/10156306
; Publication No. US20030119017A1

APPLICANT: McSwiggen, James
 TITLE OF INVENTION: Enzymatic Nucleic Acid
 FILE OF INVENTION: Levels of IKK-Gamma
 FILE REFERENCE: MBH01-664-A (400/050)
 CURRENT APPLICATION NUMBER: US/10/156.306

FILE REFERENCE: MBHB01-664-A (400/050)
CURRENT APPLICATION NUMBER: US/10/156.306

; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2404
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-2404

Query Match 0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.6e+03;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2356 ACAGGCGTGGCCACC 2371
|||||||:|||||
Db 1 ACAGGCGTGGCCACC 16

RESULT 1651
US-10-238-700-364/c
; Sequence 364, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/057 (MBHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 364
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-364

Query Match 0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 450 ACTTATCTATGAAAG 465
|||||||:|||||
Db 16 AGTTATCTATGAAAG 1

RESULT 1652
US-10-238-700-712
; Sequence 712, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/057 (MBHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 712
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-712

Query Match 0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 1.6e+03;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2268 GAGACAGGTTTCACC 2283
|||||||:|||||
Db 1 GAGACGGGUUUCACC 16

RESULT 1653
US-10-061-201-693
; Sequence 693, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 693
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-693

Query Match 0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 910 GTGTAATAAGGAGAT 925
|||||||:|||||
Db 2 GTTTAATAAGGAGAT 17

RESULT 1654
US-10-339-793-52
; Sequence 52, Application US/10339793
; Publication No. US20030180764A1
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: Shang, Jin
; APPLICANT: Bowen, Benjamin
; TITLE OF INVENTION: GENES AFFECTED BY CHOLESTEROL TREATMENT AND DURING ADIPOGENESIS
; FILE REFERENCE: 37-000310US
; CURRENT APPLICATION NUMBER: US/10/339,793
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 443
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 17
; TYPE: DNA

; ORGANISM: Homo sapiens
US-10-339-793-52

Query Match 0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2320 GATCCGCCACCTCGG 2335
||||| |||||||
Db 1 GATCCACCCACCTCGG 16

RESULT 1655

US-10-723-361-7367
; Sequence 7367, Application US/10723361
; Publication No. US20040137589A1

; GENERAL INFORMATION:
; APPLICANT: GU Yizhong

; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26

; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine

; SEQ ID NO 7367
; LENGTH: 17
; TYPE: DNA

; ORGANISM: Homo sapiens
US-10-723-361-7367

Query Match 0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 818 AGAAATTCAGATGAA 833
||||| |||||||
Db 2 AGAAATTCAGTTGAA 17

RESULT 1656

US-10-723-361-7369
; Sequence 7369, Application US/10723361
; Publication No. US20040137589A1

; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART A.
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26

; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine

; SEQ ID NO 7369
; LENGTH: 17
; TYPE: DNA

; ORGANISM: Homo sapiens
US-10-723-361-7369

Query Match 0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 819 GAAATTCAGATGAAT 834
||||| |||||||
Db 1 GAAATTCAGTTGAAT 16

RESULT 1657

US-10-498-462-2243
; Sequence 2243, Application US/10498462
; Publication No. US20040259175A1

; GENERAL INFORMATION:
; APPLICANT: Guo, Jinjiao

; TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1
; FILE REFERENCE: PB01102
; CURRENT APPLICATION NUMBER: US/10/498,462

; CURRENT FILING DATE: 2004-06-10
; PRIOR APPLICATION NUMBER: US 60/339,764

; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/US02/37506

; PRIOR FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 3320

; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2243
; LENGTH: 17
; TYPE: DNA

; ORGANISM: Homo sapiens
US-10-498-462-2243

Query Match 0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 38 GCCCTGTGTGCGGAA 53
|||||
Db 2 GCCCTGTGTGCGGA 17

RESULT 1658

US-10-498-462-2245
; Sequence 2245, Application US/10498462
; Publication No. US20040259175A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Jinjiao
; TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1
; FILE REFERENCE: PB01102
; CURRENT APPLICATION NUMBER: US/10/498,462
; CURRENT FILING DATE: 2004-06-10
; PRIOR APPLICATION NUMBER: US 60/339,764
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/US02/37506
; PRIOR FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 3320
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 2245
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-498-462-2245

Query Match 0.6%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 39 CCCTGTGTGCGGAA 54
|||||
Db 1 CCCTGTGTGCGGAA 16

RESULT 1659

US-09-881-012-1/c
; Sequence 1, Application US/09881012
; Publication No. US20020192655A1
; GENERAL INFORMATION:
; APPLICANT: Ginns, Edward I.
; APPLICANT: Egeland, Janice A.
; APPLICANT: Paul, Steven M.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Susceptibility and Resistance Genes for
; TITLE OF INVENTION: Bipolar Affective Disorder
; FILE REFERENCE: 015280-248110US
; CURRENT APPLICATION NUMBER: US/09/881,012
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US/09/175,158
; PRIOR FILING DATE: 1998-10-19
; PRIOR APPLICATION NUMBER: US 60/062,924
; PRIOR FILING DATE: 1997-10-20
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D6S344 forward primer
US-09-881-012-1

Query Match 0.6%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2118 GTTACCCAGGCTGGAG 2133
|||||
Db 16 GTGACCCAGGCTGGAG 1

RESULT 1660
US-09-881-012-1/c
; Sequence 1, Application US/09881012
; Publication No. US20040248086A9
; GENERAL INFORMATION:
; APPLICANT: Ginns, Edward I.
; APPLICANT: Egeland, Janice A.
; APPLICANT: Paul, Steven M.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Susceptibility and Resistance Genes for
; TITLE OF INVENTION: Bipolar Affective Disorder
; FILE REFERENCE: 015280-248110US
; CURRENT APPLICATION NUMBER: US/09/881,012
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US/09/175,158
; PRIOR FILING DATE: 1998-10-19
; PRIOR APPLICATION NUMBER: US 60/062,924
; PRIOR FILING DATE: 1997-10-20
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D6S344 forward primer
US-09-881-012-1

Query Match 0.6%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2118 GTTACCCAGGCTGGAG 2133
|||||
Db 16 GTGACCCAGGCTGGAG 1

RESULT 1661

US-09-881-012-83/c
; Sequence 83, Application US/09881012
; Publication No. US20020192655A1
; GENERAL INFORMATION:
; APPLICANT: Ginns, Edward I.
; APPLICANT: Egeland, Janice A.
; APPLICANT: Paul, Steven M.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Susceptibility and Resistance Genes for
; TITLE OF INVENTION: Bipolar Affective Disorder
; FILE REFERENCE: 015280-248110US
; CURRENT APPLICATION NUMBER: US/09/881,012
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US/09/175,158
; PRIOR FILING DATE: 1998-10-19
; PRIOR APPLICATION NUMBER: US 60/062,924
; PRIOR FILING DATE: 1997-10-20
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 83
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D4S422 forward primer
; NAME/KEY: modified base
; LOCATION: (8)...(8)
; OTHER INFORMATION: n = g,a,c or t
US-09-881-012-83

	Query Match	0.6%; Score 14.4; DB 1; Length 18;	
	Best Local Similarity	93.8%; Pred. No. 1.6e+03;	
	Matches	15; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
	US-09-775-479-9		
Qy	2098 TTGAGACCGAGTCTTCG 2114		
Db	18 TTGAGACGGANTCTTCG 2		
	RESULT 1662		
	US-09-881-012-83/c		
	; Sequence 83, Application US/09881012		
	; Publication NO. US20040248086A9		
	; GENERAL INFORMATION:		
	; APPLICANT: Ginns, Edward I.		
	; APPLICANT: Egeland, Janice A.		
	; APPLICANT: Paul, Steven M.		
	; APPLICANT: The Government of the United States of America		
	; APPLICANT: as represented by The Secretary of the		
	; APPLICANT: Department of Health and Human Services		
	; TITLE OF INVENTION: Susceptibility and Resistance Genes for		
	; TITLE OF INVENTION: Bipolar Affective Disorder		
	; FILE REFERENCE: 015280-248110US		
	; CURRENT APPLICATION NUMBER: US/09/881,012		
	; CURRENT FILING DATE: 2001-06-13		
	; PRIOR APPLICATION NUMBER: US/09/175,158		
	; PRIOR FILING DATE: 1998-10-19		
	; PRIOR APPLICATION NUMBER: US 60/062,924		
	; PRIOR FILING DATE: 1997-10-20		
	; NUMBER OF SEQ ID NOS: 240		
	; SOFTWARE: FastSeq for Windows Version 3.0		
	; SEQ ID NO 83		
	; LENGTH: 18		
	; TYPE: DNA		
	; ORGANISM: Artificial Sequence		
	; FEATURE:		
	; NAME/KEY: modified base		
	; LOCATION: (8)...(8)		
	; OTHER INFORMATION: n = g,a,c or t		
	US-09-881-012-83		
	Query Match	0.6%; Score 14.4; DB 1; Length 18;	
	Best Local Similarity	88.2%; Pred. No. 1.6e+03;	
	Matches	15; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
	US-09-775-479-9		
Qy	2098 TTGAGACCGAGTCTTCG 2114		
Db	18 TTGAGACGGANTCTTCG 2		
	RESULT 1663		
	US-09-775-479-9		
	; Sequence 9, Application US/09775479		
	; Publication NO. US20040067197A1		
	; GENERAL INFORMATION:		
	; APPLICANT: LECLERC, Guy		
	; APPLICANT: MARTEL, Rmi		
	; TITLE OF INVENTION: RADIOLABELLED DNA CARRIER, METHOD OF		
	; TITLE OF INVENTION: RADIOLABELLED DNA CARRIER, METHOD OF PREPARATION AND		
	; TITLE OF INVENTION: THERAPEUTIC USES THEREOF		
	; FILE REFERENCE: 12168-IUS-2		
	; CURRENT APPLICATION NUMBER: US/09/775,479		
	; CURRENT FILING DATE: 2001-02-02		
	; PRIOR APPLICATION NUMBER: 09/318,106		
	; PRIOR FILING DATE: 1999-05-24		
	; PRIOR APPLICATION NUMBER: 08/756,728		
	; PRIOR FILING DATE: 1996-11-26		
	; NUMBER OF SEQ ID NOS: 24		
	; SOFTWARE: FastSeq for Windows Version 3.0		
	; SEQ ID NO 9		
	; LENGTH: 18		

! NAME/KEY: misc feature
! OTHER INFORMATION: antisense primer D8S1828
US-09-242-772-30

Query Match 0.6%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2099 TGAGACGAGCTTGC 2114
||||| |||||||
Db 16 TGAGACGAGCTTGC 1

RESULT 1666
US-10-320-646-20/C
! Sequence 20, Application US/10320646
! Publication No. US20030143687A1
! GENERAL INFORMATION:
! APPLICANT: MAGAININ PHARMACEUTICALS, INC.
! TITLE OF INVENTION: Biological Variability of Asthma
! Associated Factors Useful in Treating and Diagnosing
! Atopic Allergies Including Asthma and Related Disorders
! NUMBER OF SEQUENCES: 36
! CORRESPONDENCE ADDRESS:
! ADDRESSEE: Morgan, Lewis & Bockius LLP
! STREET: 1800 M St., NW
! CITY: Washington
! STATE: DC
! COUNTRY: USA
! ZIP: 20036
! MEDIUM TYPE: Floppy disk
! COMPUTER: IBM PC compatible
! OPERATING SYSTEM: PC-DOS/MS-DOS
! SOFTWARE: Patent In Release #1.0, Version #1.30
! CURRENT APPLICATION DATA:
! APPLICATION NUMBER: US/10/320,646
! FILING DATE: 17-Dec-2002
! PRIOR APPLICATION DATA:
! APPLICATION NUMBER: US/09/596,377
! FILING DATE: 16-Jun-2000
! APPLICATION NUMBER: US 60/032,224
! FILING DATE: 02-DEC-1996
! APPLICATION NUMBER: US 08/980,872
! FILING DATE: 01-DEC-1997
! APPLICATION NUMBER: PCT/US97/21992
! FILING DATE: 02-DEC-1997
! ATTORNEY/AGENT INFORMATION:
! NAME: Michael S. Tuscan
! REGISTRATION NUMBER: 43,210
! REFERENCE/DOCKET NUMBER: 36870-5057-US
! TELECOMMUNICATION INFORMATION:
! TELEPHONE: 202 467 7000
! TELEFAX: 202 467 7176
! INFORMATION FOR SEQ ID NO: 20:
! SEQUENCE CHARACTERISTICS:
! LENGTH: 19 base pairs
! TYPE: nucleic acid
! STRANDEDNESS: single
! TOPOLOGY: linear
! MOLECULE TYPE: other nucleic acid
! SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-320-646-20

Query Match 0.6%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2322 TCCGCCCACTCGGCC 2337
||||| |||||||
Db 18 TCCGCCCACTCGGCC 3

RESULT 1667
US-10-294-228-24
! Sequence 24, Application US/10294228
! Publication No. US20040018176A1
! GENERAL INFORMATION:
! APPLICANT: Tolentino, Michael J.
! APPLICANT: Reich, Samuel Jotham
! TITLE OF INVENTION: Compositions and Methods for siRNA
! TITLE OF INVENTION: Inhibition of Angiogenesis
! FILE REFERENCE: 43826-1
! CURRENT APPLICATION NUMBER: US/10/294,228
! CURRENT FILING DATE: 2002-11-14
! PRIOR APPLICATION NUMBER: US 60/398,417
! PRIOR FILING DATE: 2002-07-24
! NUMBER OF SEQ ID NOS: 80
! SOFTWARE: FastSeq for Windows Version 4.0
! SEQ ID NO 24
! LENGTH: 19
! TYPE: DNA
! ORGANISM: Artificial Sequence
! FEATURE:
! OTHER INFORMATION: Targeting Sequence
US-10-294-228-24

Query Match 0.6%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 51 GAAAGATGGAGCAAGA 66
||||| |||||||
Db 2 GAAAGATAGCAAGA 17

RESULT 1668
US-10-294-228-25
! Sequence 25, Application US/10294228
! Publication No. US20040018176A1
! GENERAL INFORMATION:
! APPLICANT: Tolentino, Michael J.
! APPLICANT: Reich, Samuel Jotham
! TITLE OF INVENTION: Compositions and Methods for siRNA
! TITLE OF INVENTION: Inhibition of Angiogenesis
! FILE REFERENCE: 43826-1
! CURRENT APPLICATION NUMBER: US/10/294,228
! CURRENT FILING DATE: 2002-11-14
! PRIOR APPLICATION NUMBER: US 60/398,417
! PRIOR FILING DATE: 2002-07-24
! NUMBER OF SEQ ID NOS: 80
! SOFTWARE: FastSeq for Windows Version 4.0
! SEQ ID NO 25
! LENGTH: 19
! TYPE: DNA
! ORGANISM: Artificial Sequence
! FEATURE:
! OTHER INFORMATION: Targeting Sequence
US-10-294-228-25

Query Match 0.6%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 51 GAAAGATGGAGCAAGA 66
||||| |||||||
Db 1 GAAAGATAGCAAGA 16

RESULT 1669
US-10-674-124A-27098/C
! Sequence 27098, Application US/10674124A
! Publication No. US2004019797A1
! GENERAL INFORMATION:
! APPLICANT: INOKO, Hidetoshi
! APPLICANT: TAMIYA, Gen

; TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE
; FILE OF INVENTION: GENETIC POLYMORPHISM MARKERS
; FILE REFERENCE: ORIN-003CIP
; CURRENT APPLICATION NUMBER: US/10/674,124A
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 10/257,511
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: PCT/JP00/07621
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: JP2000-112699
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: JP2002-327516
; PRIOR FILING DATE: 2002-09-28
; PRIOR APPLICATION NUMBER: JP2002-383869
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 27110
; SEQ ID NO 27098
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-674-124A-27098

Query Match 0.6%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2231 TGCACACACCTGGC 2246
Db 16 TGCACACACATCTGGC 1

Search completed: January 26, 2005, 12:41:49
Job time : 60 secs

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OM nucleic - nucleic search, using sw model

Run on: January 25, 2005, 16:20:19 ; Search time 100 Seconds
(without alignments)
3.683 Million cell updates/sec

Title: US-09-966-724B-2-COPY

Perfect score: 2372

Sequence: 1 GCACCGCGGAGCTGGCTG.....ATTACAGGCATGAGCCACCG 2372

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 3105 seqs, 77640 residues

Total number of hits satisfying chosen parameters: 6210

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 2000 summaries

Database : rng.db.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	88.8	3.7	100	1	AAK73008 Human immune/haema
C 2	88.8	3.7	100	1	AAL03022 Human reproductive
C 3	87.8	3.7	100	1	AAK69883 Human immune/haema
C 4	86.4	3.6	100	1	AAC13296 Human secreted pro
C 5	86.4	3.6	100	1	AAC14608 Human secreted pro
C 6	85.2	3.6	98	1	AAL07382 Human reproductive
C 7	85.2	3.6	98	1	AAL07385 Human reproductive
C 8	85.2	3.6	98	1	ABL98854 Human testicular a
C 9	85.2	3.6	98	1	ABL98851 Human testicular a
C 10	83.6	3.5	99	1	AAS34440 Human DNA for a no
C 11	82.6	3.5	100	1	AAS28286 Genomic sequence #
C 12	82.6	3.5	100	1	ADG41482 Human respiratory
C 13	81.6	3.4	96	1	AAK85166 Human immune/haema
C 14	81.5	3.4	100	1	AAK90852 Human digestive sy
C 15	81.4	3.4	99	1	AAK72850 Human immune/haema
C 16	81.2	3.4	94	1	AAC23951 Human secreted pro
C 17	80.6	3.4	95	1	AAC28711 Human secreted pro
C 18	80	3.4	100	1	AAC11043 Human secreted pro
C 19	78.4	3.3	88	1	ADJ12759 DNA fragment of a
C 20	78.4	3.3	90	1	AAC23570 Human secreted pro
C 21	78	3.3	86	1	AAC14994 Human secreted pro
C 22	75.8	3.2	87	1	AAL37410 Human musculooskele
C 23	75.8	3.2	87	1	ABX60398 CDNA encoding nove
C 24	75.8	3.2	87	1	ADJ31148 Human musculooskele
C 25	74.2	3.1	87	1	AAK79823 Human immune/haema
C 26	73	3.1	73	1	AAK35141 Nucleotide sequenc
C 27	73	3.1	73	1	AAD65023 Human mouse double
C 28	72.8	3.1	76	1	AAC13689 Human secreted pro
C 29	72.6	3.1	87	1	AAK75687 Human immune/haema
C 30	72.6	3.1	87	1	AAK76817 Human immune/haema
C 31	72.6	3.1	87	1	AAK82025 Human immune/haema
C 32	72.6	3.1	87	1	AAK75689 Human immune/haema
C 33	72.6	3.1	87	1	AAK76646 Human immune/haema

C	34	72.6	3.1	87	1	AAK75688 Human immune/haema
C	35	72.6	3.1	87	1	AAS28528 Genomic sequence #
C	36	72.6	3.1	87	1	ADG41724 Human respiratory
C	37	71.4	3.0	84	1	AAC12517 Human secreted pro
C	38	71	3.0	79	1	AAC24033 Human secreted pro
C	39	71	3.0	87	1	AAI99210 Human excretory re
C	40	71	3.0	87	1	AAI99210 Human excretory re
C	41	71	3.0	87	1	AAI99211 Human immune/haema
C	42	71	3.0	87	1	AAK87263 Human immune/haema
C	43	71	3.0	87	1	AAK84994 Human immune/haema
C	44	71	3.0	87	1	AAK87262 Human immune/haema
C	45	71	3.0	87	1	AAK78040 Human immune/haema
C	46	71	3.0	87	1	AAK84995 Human immune/haema
C	47	71	3.0	87	1	AAK68262 Human immune/haema
C	48	71	3.0	87	1	AAK84992 Human immune/haema
C	49	71	3.0	87	1	AAK68855 Human immune/haema
C	50	71	3.0	87	1	AAK68854 Human immune/haema
C	51	71	3.0	87	1	AAS28332 Genomic sequence #
C	52	71	3.0	87	1	AAI63561 Human kidney relat
C	53	71	3.0	87	1	AAI63558 Human kidney relat
C	54	71	3.0	87	1	AAI63560 Human kidney relat
C	55	71	3.0	87	1	ABZ74272 Secreted protein g
C	56	71	3.0	87	1	ADA98801 Human secreted pro
C	57	71	3.0	87	1	ADG41528 Human respiratory
C	58	71	3.0	87	1	ABZ67838 Human secreted pro
C	59	70.8	3.0	84	1	ABK45727 cDNA encoding colo
C	60	70.2	3.0	92	1	AAK11340 Human secreted pro
C	61	69.4	2.9	87	1	AAS36366 Human cardiovascular
C	62	69.4	2.9	87	1	AAK91304 Human digestive sy
C	63	69.4	2.9	87	1	AAK91305 Human digestive sy
C	64	69.4	2.9	87	1	AAK91307 Human digestive sy
C	65	69.4	2.9	87	1	AAK86755 Human immune/haema
C	66	69.4	2.9	87	1	AAK75934 Human immune/haema
C	67	69.4	2.9	87	1	AAK81974 Human immune/haema
C	68	69.4	2.9	87	1	AAK81975 Human immune/haema
C	69	69.4	2.9	87	1	AAK75935 Human immune/haema
C	70	69.4	2.9	87	1	AAK81973 Human immune/haema
C	71	69.4	2.9	87	1	AAK83799 Human immune/haema
C	72	69.4	2.9	87	1	AAK86753 Human immune/haema
C	73	69.4	2.9	87	1	AAK36467 Human musculooskele
C	74	69.4	2.9	87	1	AAK36466 Human musculooskele
C	75	69.4	2.9	87	1	AAK36464 Human musculooskele
C	76	69.4	2.9	87	1	AAK02848 Human reproductive
C	77	69.4	2.9	87	1	AAK02849 Human reproductive
C	78	69.4	2.9	87	1	AAK07338 Human reproductive
C	79	69.4	2.9	87	1	AAS32132 Human liver associ
C	80	69.4	2.9	87	1	AAS32134 Human liver associ
C	81	69.4	2.9	87	1	AAS32131 Human liver associ
C	82	69.4	2.9	87	1	ABN90487 Human liver antige
C	83	69.4	2.9	87	1	ABN90489 Human liver antige
C	84	69.4	2.9	87	1	ABN90486 Human liver antige
C	85	69.4	2.9	87	1	ABX59454 CDNA encoding nove
C	86	69.4	2.9	87	1	ABX59455 CDNA encoding nove
C	87	69.4	2.9	87	1	ABX59452 CDNA encoding nove
C	88	69.4	2.9	87	1	ADJ47060 Human cardiovascular
C	89	69.4	2.9	87	1	ADJ15402 Human liver-relate
C	90	69.4	2.9	87	1	ADJ15399 Human liver-relate
C	91	69.4	2.9	87	1	ADJ15400 Human liver-relate
C	92	69.4	2.9	87	1	ADJ30205 Human musculooskele
C	93	69.4	2.9	87	1	ADJ30202 Human musculooskele
C	94	69.4	2.9	87	1	ADJ30204 Human musculooskele
C	95	68.3	2.9	90	1	AAK83861 Human immune/haema
C	96	68.3	2.9	90	1	AAK85686 Human immune/haema
C	97	67.8	2.9	87	1	AAK90874 Human digestive sy
C	98	67.8	2.9	87	1	ABA15851 Human nervous syst
C	99	67.8	2.9	87	1	ABA15852 Human nervous syst
C	100	66.2	2.8	87	1	AAK65876 Human immune/haema
C	101	66.2	2.8	87	1	AAK65878 Human immune/haema
C	102	66	2.8	82	1	AAK76883 Human immune/haema
C	103	64.4	2.7	80	1	ADJ12544 Mutant human BRCA1
C	104	62.2	2.6	81	1	AAC11941 Human secreted pro
C	105	60	2.5	60	1	AAK39842 Human spliced tran
C	106	60	2.5	61	1	ABZ09613 Human oligonucleot

C 107	60	2.5	68	1	ABZ73066	Tumour suppression	C 180	41.4	1.7	51	1	AAI76989	Human clone cg4292
C 108	58.4	2.5	68	1	ABZ09678	Human oligonucleot	C 181	41.4	1.7	51	1	AAI77230	Human clone cg4397
C 109	58.4	2.5	68	1	ABZ79131	Tumour suppression	C 182	41.4	1.7	51	1	AAI73071	Human silent SNP c
C 110	56.8	2.4	68	1	ABZ09289	Human oligonucleot	C 183	41.4	1.7	51	1	AAI76193	Human silent SNP c
C 111	56.8	2.4	68	1	ABZ78742	Tumour suppression	C 184	41.4	1.7	51	1	AAI79866	Human nonconservat
C 112	56.2	2.4	69	1	AAAS57672	cDNA #348 encoding	C 185	41.4	1.7	51	1	AAI74978	Human silent SNP c
C 113	54.4	2.3	65	1	AAAC12925	Human secreted pro	C 186	41.4	1.7	51	1	AAI74450	Human silent SNP c
C 114	52	2.2	60	1	ABZ09729	Human oligonucleot	C 187	41.4	1.7	51	1	AAI75457	Human silent SNP c
C 115	52	2.2	60	1	ABZ79182	Tumour suppression	C 188	41.4	1.7	51	1	AAI76650	Human silent SNP c
C 116	52	2.2	60	1	AD112543	Mutant human BRCA1	C 189	41.4	1.7	51	1	AAI76653	Human silent SNP c
C 117	51.6	2.2	66	1	AAK91064	Human digestive sy	C 190	41.4	1.7	51	1	AAI76184	Human silent SNP c
C 118	51.6	2.2	66	1	AAAS32099	Human liver associ	C 191	41.4	1.7	51	1	AAI79688	Human conservative
C 119	51.6	2.2	66	1	ABN90454	Human liver antige	C 192	41.4	1.7	51	1	AAH90585	Human clone cg4308
C 120	51.6	2.2	66	1	ADJ15367	Human liver-relate	C 193	41.4	1.7	51	1	AAH90175	Human clone cg4286
C 121	51	2.2	64	1	AAAC11032	Human secreted pro	C 194	41.4	1.7	51	1	AAH89507	Human coding seque
C 122	50.2	2.1	64	1	AAAC15723	Human secreted pro	C 195	41.4	1.7	51	1	AAH89485	Human coding seque
C 123	50	2.1	50	1	ABZ04758	Human leukocyte ge	C 196	41.4	1.7	51	1	AAH89308	Human coding seque
C 124	50	2.1	50	1	ADP10274	50-mer oligonucleo	C 197	41.4	1.7	51	1	AAH89304	Human coding seque
C 125	50	2.1	51	1	AAI69056	Activated T-cell d	C 198	41.4	1.7	51	1	AAH89519	Human coding seque
C 126	49.4	2.1	51	1	AAAL32116	Human SNP oligonuc	C 199	41.4	1.7	51	1	ABL00076	Human silent nonco
C 127	48.4	2.0	51	1	AAAI7488	Human Alu subfam	C 200	41.4	1.7	51	1	ADK19850	Human mannosyl tra
C 128	47.8	2.0	51	1	AAI77877	Human silent SNP c	C 201	41.2	1.7	47	1	AAZ66299	Human map-related
C 129	47.8	2.0	51	1	AAI79838	Human nonconservat	C 202	41.2	1.7	47	1	AAZ66299	Human map-related
C 130	47.8	2.0	51	1	AAI79700	Human conservative	C 203	41.2	1.7	51	1	AAAL31459	Human SNP oligonuc
C 131	47.8	2.0	51	1	AAH89466	Human coding seque	C 204	41.2	1.7	51	1	AAI79699	Human conservative
C 132	47.6	2.0	63	1	AAK85885	Human immune/haema	C 205	41.2	1.7	51	1	AAH37800	Human SNP flanking
C 133	47.6	2.0	63	1	AAK85881	Human immune/haema	C 206	40.8	1.7	51	1	AAI78300	Human silent SNP c
C 134	47.2	2.0	52	1	ABZ09432	Human oligonucleot	C 207	40.8	1.7	52	1	ABZ09024	Human oligonucleot
C 135	47.2	2.0	52	1	ABZ78885	Tumour suppression	C 208	40.8	1.7	52	1	ABZ78477	Tumour suppression
C 136	47	2.0	47	1	AAZ69526	Human map-related	C 209	40.6	1.7	51	1	AAI78039	Human silent SNP c
C 137	46.8	2.0	51	1	AAAI77489	Human Alu subfam	C 210	40.6	1.7	51	1	AAI79512	Human silent SNP c
C 138	46.8	2.0	59	1	ABK45620	cDNA encoding colo	C 211	40.4	1.7	50	1	AAH89833	Human coding seque
C 139	46.6	2.0	47	1	ABK41287	Human USF2 gene bi	C 212	40.4	1.7	51	1	AAI77228	Human clone cg4397
C 140	46.4	2.0	54	1	AAI68926	Activated T-cell d	C 213	40.4	1.7	51	1	ADCI6930	Human single nucle
C 141	46.2	1.9	51	1	AAI77876	Human silent SNP c	C 214	40.4	1.7	51	1	AAI79771	Human nonconservat
C 142	46.2	1.9	51	1	AAI79701	Human conservative	C 215	40.4	1.7	51	1	AAI75514	Human silent SNP c
C 143	46.2	1.9	51	1	AAI79839	Human nonconservat	C 216	40.4	1.7	51	1	AAI73068	Human silent SNP c
C 144	46.2	1.9	51	1	AAH89467	Human coding seque	C 217	40	1.7	48	1	ADB73481	Human breakpoint r
C 145	46.2	1.9	51	1	AAH40328	Human SNP flanking	C 218	40	1.7	51	1	AAI79647	Human silent SNP c
C 146	46.2	1.9	51	1	ABL00161	Human silent nonco	C 219	40	1.7	51	1	AAI73305	Human silent SNP c
C 147	45.8	1.9	51	1	AAH39992	Human SNP flanking	C 220	40	1.7	51	1	AAH39524	Human SNP flanking
C 148	45.8	1.9	57	1	AAAC29627	Human secreted pro	C 221	40	1.7	51	1	ABZ09598	Human oligonucleot
C 149	45.6	1.9	57	1	AAK83961	Human immune/haema	C 222	40	1.7	51	1	ABZ79051	Tumour suppression
C 150	45.2	1.9	51	1	AAI77324	Human silent SNP c	C 223	39.8	1.7	51	1	AAI77231	Human clone cg4397
C 151	45.2	1.9	51	1	AAI79589	Human silent SNP c	C 224	39.8	1.7	51	1	AAAC14922	Human secreted pro
C 152	44.6	1.9	51	1	AAH89302	Human coding seque	C 225	39.8	1.7	51	1	AAI74451	Human silent SNP c
C 153	44.6	1.9	51	1	AAH40072	Human SNP flanking	C 226	39.8	1.7	51	1	AAI75652	Human silent SNP c
C 154	44.2	1.9	49	1	AD112542	Mutant human BRCA1	C 227	39.8	1.7	51	1	AAI75456	Human silent SNP c
C 155	43.6	1.8	51	1	AAI79588	Human silent SNP c	C 228	39.8	1.7	51	1	AAI77410	Human silent SNP c
C 156	43.6	1.8	51	1	AAI77325	Human silent SNP c	C 229	39.8	1.7	51	1	AAI75454	Human silent SNP c
C 157	43.2	1.8	51	1	AAI73532	Human silent SNP c	C 230	39.8	1.7	51	1	AAI77409	Human silent SNP c
C 158	43	1.8	51	1	AAA77442	Human Alusubfamily	C 231	39.8	1.7	51	1	AAI74979	Human silent SNP c
C 159	43	1.8	51	1	AAA76988	Human clone cg4292	C 232	39.8	1.7	51	1	AAI73070	Human silent SNP c
C 160	43	1.8	51	1	AAI76185	Human silent SNP c	C 233	39.8	1.7	51	1	AAH90586	Human clone cg4308
C 161	43	1.8	51	1	AAI76192	Human silent SNP c	C 234	39.8	1.7	51	1	AAH89305	Human coding seque
C 162	43	1.8	51	1	AAI79867	Human nonconservat	C 235	39.8	1.7	51	1	AAH89317	Human coding seque
C 163	43	1.8	51	1	AAI79689	Human conservative	C 236	39.8	1.7	51	1	AAH89553	Human coding seque
C 164	43	1.8	51	1	AAH90176	Human clone cg4286	C 237	39.8	1.7	51	1	AAH89518	Human coding seque
C 165	43	1.8	51	1	AAH89484	Human coding seque	C 238	39.8	1.7	51	1	AAH89309	Human coding seque
C 166	43	1.8	51	1	AAH89506	Human coding seque	C 239	39.8	1.7	51	1	AAH89566	Human coding seque
C 167	43	1.8	51	1	AAH89303	Human coding seque	C 240	39.8	1.7	51	1	ABL00112	Human silent nonco
C 168	43	1.8	51	1	ADK19860	Human mannosyl tra	C 241	39.6	1.7	51	1	AAI79698	Human conservative
C 169	42.6	1.8	49	1	AAK65537	Human immune/haema	C 242	39.4	1.7	41	1	ABZ20666	Human G protein su
C 170	42.6	1.8	49	1	AAK62905	Human genomic DNA	C 243	39.4	1.7	41	1	ABZ49551	Human glutathione-
C 171	42.2	1.8	51	1	AAI79513	Human silent SNP c	C 244	39.4	1.7	41	1	ABZ43959	Human glutathione-
C 172	42	1.8	50	1	ADG84273	Human TMD0621 prom	C 245	39.4	1.7	51	1	AAI79580	Human silent SNP c
C 173	42	1.8	51	1	AAI75515	Human silent SNP c	C 246	39.4	1.7	51	1	AAH89818	Human coding seque
C 174	42	1.8	51	1	AAI73069	Human silent SNP c	C 247	39.2	1.7	44	1	AD112541	Mutant human BRCA1
C 175	42	1.8	51	1	AAI79770	Human nonconservat	C 248	39.2	1.7	51	1	AAI78301	Human silent SNP c
C 176	41.6	1.8	51	1	AAI79646	Human silent SNP c	C 249	39	1.6	49	1	AD112532	Mutant human BRCA1
C 177	41.6	1.8	51	1	AAI73533	Human silent SNP c	C 250	39	1.6	51	1	AAI78038	Human silent SNP c
C 178	41.6	1.8	52	1	AAAC22417	Human secreted pro	C 251	38.9	1.6	51	1	AAI77874	Human silent SNP c
C 179	41.4	1.7	51	1	AAA77443	Human Alusubfamily	C 252	38.9	1.6	51	1	AAI77875	Human silent SNP c

253	38.8	1.6	51	1	AAA77229	Human clone c94397	C 326	32	1.3	41	1	ADL81463
c 254	38.8	1.6	51	1	AAI75651	Human silent SNP c	C 327	31.4	1.3	41	1	ABH49727
255	38.8	1.6	51	1	AAI79075	Human silent SNP c	C 328	31.4	1.3	41	1	ABV74811
256	38.8	1.6	51	1	AAI74819	Human silent SNP c	C 329	31.4	1.3	41	1	ABL40963
257	38.8	1.6	51	1	AAI79530	Human silent SNP c	C 330	31.4	1.3	41	1	ABL40964
258	38.8	1.6	51	1	AAI74884	Human silent SNP c	C 331	31.4	1.3	41	1	ABZ47125
c 259	38.8	1.6	51	1	AAI74965	Human silent SNP c	C 332	31.4	1.3	41	1	ABZ43249
c 260	38.8	1.6	51	1	ADK19818	Human mannosyl tra	C 333	31.4	1.3	41	1	ABZ49403
c 261	38.6	1.6	51	1	AAI75542	Human silent SNP c	C 334	31.2	1.3	41	1	AAI51683
c 262	38.4	1.6	40	1	AAV19044	Alu PCR primer 1.	C 335	31.2	1.3	41	1	AAI88864
c 263	38.4	1.6	40	1	AAI97659	Human MDM2 40mer p	C 336	31.2	1.3	41	1	ADCS9512
c 264	38.4	1.6	40	1	ABL59100	Nucleotide sequenc	C 337	31.2	1.3	41	1	ADCS9512
c 265	38.4	1.6	40	1	ABL60505	Human MDM2 mRNA fr	C 338	31.2	1.3	41	1	ABZ57501
c 266	38.4	1.6	50	1	AAI76503	Human silent SNP c	C 339	31	1.3	31	1	ABK66044
c 267	38.4	1.6	51	1	AAI73304	Human silent SNP c	C 340	31	1.3	33	1	AAZ89377
c 268	38.4	1.6	51	1	AAI76814	Human silent SNP c	C 341	31	1.3	40	1	ABZ48532
c 269	37.8	1.6	41	1	ABZ20667	Human g protein su	C 342	31	1.3	41	1	ABQ83633
c 270	37.8	1.6	41	1	ABZ43958	Human glutathione-	C 343	31	1.3	41	1	ABQ83634
c 271	37.8	1.6	41	1	ABZ44160	Human NDUFS5 gene	C 344	31	1.3	41	1	ABQ83634
c 272	37.8	1.6	41	1	ABZ49550	Human glutathione-	C 345	30.8	1.3	41	1	ABZ49550
c 273	37.8	1.6	41	1	ABZ49631	Human sulphotransf	C 346	29.8	1.3	33	1	ACC84461
c 274	37.8	1.6	41	1	ABZ43598	Human sulphotransf	C 347	29	1.2	29	1	AAI97662
c 275	37.8	1.6	41	1	ABZ50172	Human NDUFS5 gene	C 348	29	1.2	29	1	ABL60508
c 276	37.8	1.6	42	1	ADJ12523	Human BRCAL DNA ju	C 349	28.8	1.2	32	1	AAK91040
c 277	37.4	1.6	47	1	AAZ68649	Human map-related	C 350	28.8	1.2	32	1	AAK91040
c 278	36.2	1.5	41	1	ABA94091	Human tumour suppr	C 351	28.8	1.2	32	1	AAK90430
c 279	36.2	1.5	42	1	ADI12521	Human BRCAL DNA ju	C 352	28.8	1.2	32	1	ADJ15343
c 280	35.4	1.5	45	1	AAK91006	Human digestive sy	C 353	28.4	1.2	30	1	AAI47196
c 281	35.4	1.5	45	1	AAK86862	Human immune/haema	C 354	28.4	1.2	30	1	AAI47197
c 282	35.4	1.5	45	1	AAI02933	Human reproductive	C 355	28.4	1.2	32	1	ADE14248
c 283	35.4	1.5	45	1	AAI32041	Human liver associ	C 356	28.4	1.2	32	1	ADE14029
c 284	35.4	1.5	45	1	ABN90396	Human liver antige	C 357	28	1.2	28	1	AAI97658
c 285	35.4	1.5	45	1	ABZ74161	Secreted protein g	C 358	28	1.2	28	1	ABK65940
c 286	35.4	1.5	45	1	ABZ73706	Secreted protein g	C 359	28	1.2	28	1	ABK65940
c 287	35.4	1.5	45	1	ADA98416	Human secreted pro	C 360	28	1.2	28	1	ABK65939
c 288	35.4	1.5	45	1	ADA44446	Human secreted pro	C 361	28	1.2	28	1	ABK65939
c 289	35.4	1.5	45	1	ABZ67723	Human secreted pro	C 362	27.8	1.2	33	1	AAI11597
c 290	35.4	1.5	45	1	ABZ67302	Human secreted pro	C 363	27.8	1.2	33	1	AAI162688
c 291	35.4	1.5	45	1	ADJ15309	Human liver-relate	C 364	27.6	1.2	35	1	AAH91537
c 292	35.2	1.5	44	1	AAI76391	Human silent SNP c	C 365	27.4	1.2	31	1	AAQ73572
c 293	34.6	1.5	41	1	ABA94092	Human tumour suppr	C 366	27.4	1.2	32	1	AAQ73572
c 294	34.6	1.5	41	1	ABZ43599	Human sulphotransf	C 367	27	1.1	29	1	AAQ27389
c 295	34.6	1.5	41	1	ABZ49632	Human sulphotransf	C 368	27	1.1	29	1	AAA04371
c 296	34.6	1.5	41	1	ADL64133	Human single nucle	C 369	27	1.1	29	1	AAA04313
c 297	34.2	1.4	39	1	ACC84472	NTP peptide encodi	C 370	26.8	1.1	32	1	AAI4206
c 298	34	1.4	42	1	ACC84458	NTP peptide encodi	C 371	26	1.1	26	1	AAZ37740
c 299	33.6	1.4	41	1	AAK99206	Human-homo autoimm	C 372	26	1.1	26	1	AAA97660
c 300	33.6	1.4	41	1	AAK99207	Human-homo autoimm	C 373	26	1.1	26	1	AAA97660
c 301	33.6	1.4	41	1	ABZ45793	Human carbohydrate	C 374	26	1.1	26	1	AAI50949
c 302	33.6	1.4	41	1	ABZ46192	Human organic anio	C 375	26	1.1	26	1	AAI50949
c 303	33.6	1.4	41	1	ABZ48356	Human organic anio	C 376	26	1.1	26	1	AAI50949
c 304	33.6	1.4	44	1	AAI76390	Human silent SNP c	C 377	26	1.1	26	1	AAI50949
c 305	33.4	1.4	35	1	AAQ27391	Inter-Alu specific	C 378	26	1.1	26	1	ABL60506
c 306	33.4	1.4	41	1	AAI59551	Human proteolytic	C 379	26	1.1	29	1	ADD21705
c 307	33.4	1.4	41	1	AAI59550	Human proteolytic	C 380	25.8	1.1	29	1	AAA04303
c 308	33	1.4	33	1	ADP12341	Taqman probe set 2	C 381	25.4	1.1	30	1	AAI42705
c 309	33	1.4	41	1	ABZ50127	Human NDUFS1 gene	C 382	25.4	1.1	29	1	AAA04312
c 310	33	1.4	41	1	ABZ44117	Human NDUFS1 gene	C 383	25.4	1.1	29	1	AAA04312
c 311	33	1.4	41	1	ADP75520	Human ADAM19 gene	C 384	25.4	1.1	29	1	AAA04395
c 312	33	1.4	41	1	ADL64280	Human single nucle	C 385	25.2	1.1	29	1	AAA04505
c 313	32.8	1.4	41	1	ABA96570	Human tyrosinase 9	C 386	25.2	1.1	32	1	AAQ73570
c 314	32.8	1.4	41	1	ABA96571	Human tyrosinase 9	C 387	25.2	1.1	33	1	AAH79009
c 315	32.8	1.4	41	1	ADC59511	Polypeptide-respir	C 388	25	1.1	33	1	ABK50423
c 316	32.6	1.4	40	1	AAH91207	Human inflammatory	C 389	25	1.1	25	1	AAI37741
c 317	32.6	1.4	41	1	ABL60966	Human retinoblasto	C 390	25	1.1	25	1	AAI37741
c 318	32.4	1.4	41	1	ABZ97057	Human 2-hydroxy ac	C 391	25	1.1	25	1	AAI37741
c 319	32.4	1.4	41	1	ABA97056	Human 2-hydroxy ac	C 392	25	1.1	25	1	AAI37741
c 320	32.2	1.4	38	1	AAH91831	Human inflammatory	C 393	25	1.1	25	1	AAI37741
c 321	32	1.3	41	1	ABZ72304	Gene 216 SNP refer	C 394	25	1.1	25	1	ADB04776
c 322	32	1.3	41	1	ABZ49727	Human sulphotransf	C 395	25	1.1	25	1	ADB04776
c 323	32	1.3	41	1	ABZ43574	Human sulphotransf	C 396	25	1.1	25	1	ADB04781
c 324	32	1.3	41	1	ABX75157	Human gene 216 DNA	C 397	25	1.1	25	1	ADB04770
c 325	32	1.3	41	1	ADJ36885	Gene 216 single nu	C 398	25	1.1	25	1	ADB04773

Gene 216 single nu
Human DNA mismatch
Signalase 11.22 pr
Transcription regu
Transcription regu
Human ATP-binding
Human ATP-binding
Human UDP glycosyl
PC6 protease 9-9
Saccharophosphotra
Polypeptide-respir
Ser/thr protein ki
Standardized polyn
Human mdm-2 probe
Human oligopeptide
Human mper3-10.01
Human mper3-10.01
cAMP dependent kin
Human retinoblasto
Genetic analysis m
NTP peptide encodi
Human MDM2 hybridi
Human MDM2 mRNA hy
Human digestive sy
Human liver associ
Human liver antige
Human liver-relate
Human rheumatoid a
Human rheumatoid a
Optineurin promote
Optineurin promote
Human MDM2 gene ta
Human gene specifi
Human gene specifi
Human MDM2 mRNA fr
Taqman probe of th
Human breast or ov
Human reproductive
Human inflammatory
Enhancer element e
Inter-Alu specific
Polymorphic fragme
Polymorphic fragme
Polymorphic fragme
Optineurin promote
Human mdm2 real-ti
Human mdm2 forward
Human mdm2 PCR pri
Human marathon cDN
Human mdm2 reverse
Reverse PCR primer
Human MDM2 mRNA am
Human mdm2-specifi
Polymorphic fragme
Hdm2 cDNA amplifiy
Polymorphic fragme
Polymorphic fragme
Polymorphic fragme
Enhancer element e
Human signal pepti
Human transfer dow
Human mdm2 real-ti
Human mdm2 amplifi
SNP specific SNPR
Fluorescent labell
Human Alu sequence
Human MDM27 scannin
Human MDM27 scannin
Human MDM27 scannin
Human MDM27 scannin
Human MDM27 scannin

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C1838	20	0.8	20	1	AD865742	Human Y chromosome
C1839	20	0.8	20	1	ADM65739	NRY polymorphism d
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C1845	20	0.8	20	1	AD180086	Human transforming
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C1847	20	0.8	20	1	ADJ30045	Human dual specifi
C1848	20	0.8	20	1	ADJ59829	Oligonucleotide as
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C1858	20	0.8	20	1	ADO46429	Human oligonucleot

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c1860	20	0.8	20	1	ADP12093	Set 2 right PCR pr	1933	19.2	0.8	24	1	ABA01638	Human tyrosinase 1
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c1862	20	0.8	20	1	ADP11268	Set 1 right PCR pr	1935	19.2	0.8	24	1	ABV74685	Human SOX3 protein
c1863	20	0.8	20	1	ADN30395	Human Notch2 DNA a	c1936	19.2	0.8	24	1	AAI19678	RT-PCR primer #2 f
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c1865	20	0.8	22	1	AAF84350	Human CYP2C18i PCR	1938	19.2	0.8	24	1	ABA05003	Human tyrosine kin
c1866	20	0.8	22	1	AAI11629	Human CYP2B6 allele	1939	19.2	0.8	24	1	ABA95476	Human dihydroorota
c1867	20	0.8	25	1	ADB04761	Human MD27 scannin	1940	19.2	0.8	24	1	ADC48698	Human epilepsia as
c1868	20	0.8	26	1	ABL60500	Human MDM2 mRNA fr	1941	19.2	0.8	24	1	ADZ57061	Human excitatory amino a
c1869	19.8	0.8	23	1	AAH37414	SNP specific lower	1942	19.2	0.8	24	1	ADG83872	Human SLC6A14 forw
c1870	19.8	0.8	23	1	ABZ83516	Toxicologically re	1943	19.2	0.8	25	1	ADB04577	Human MD27 scannin
c1871	19.8	0.8	24	1	AAI71673	Human myosin heavy	1944	19.2	0.8	25	1	ADB04583	Human MD27 scannin
c1872	19.8	0.8	24	1	AAI00333	PCR primer #2, use	1945	19.2	0.8	25	1	ADB04677	Human MD27 scannin
c1873	19.8	0.8	24	1	AAD42696	Primer #2 used to	1946	19.2	0.8	25	1	ADB04586	Human MD27 scannin
c1874	19.8	0.8	24	1	ABL50916	Human dihydroxyro	1947	19.2	0.8	25	1	ADB04747	Human MD27 scannin
c1875	19.8	0.8	25	1	ABV74727	Human clathrin lig	1948	19	0.8	19	1	AAI94763	Human progesterone
c1876	19.8	0.8	25	1	ADB04581	Human MD27 scannin	1949	19	0.8	19	1	AAI84754	FISH primer for hu
c1877	19.8	0.8	25	1	ADB04735	Human MD27 scannin	1950	19	0.8	19	1	AAH38677	SNP specific upper
c1878	19.8	0.8	25	1	ADB04662	Human MD27 scannin	1951	19	0.8	19	1	AAH38221	SNP specific upper
c1880	19.8	0.8	25	1	ADB04580	Human MD27 scannin	c1952	19	0.8	19	1	ABL44474	Human chromosome 1
c1881	19.6	0.8	26	1	ABZ22656	Human PEPT1 PCR pr	c1953	19	0.8	19	1	ADK41249	Human chromosome 1
c1882	19.6	0.8	26	1	AAA39394	Alu repeat 3' end	c1954	19	0.8	19	1	ADK41375	Human chromosome 1
c1883	19.6	0.8	26	1	AAF62473	Human SRCX 2826468	1955	19	0.8	19	1	ADO23055	Human p53-binding
c1884	19.6	0.8	26	1	AAF64089	Primer #33. Homo	1956	19	0.8	19	1	ADO23052	Human p53-binding
c1885	19.6	0.8	26	1	AAH22716	Human secreted pro	1957	19	0.8	19	1	ADO23051	Human p53-binding
c1886	19.6	0.8	26	1	ABK61474	Human NOV3 Exon 11	1958	19	0.8	19	1	ADO23053	Human p53-binding
c1887	19.6	0.8	26	1	ABX97292	Human NOV-associat	1959	19	0.8	19	1	ADO22917	Human p53-binding
c1888	19.6	0.8	26	1	ADN62195	Human NOV20a RTQ-P	1960	19	0.8	19	1	ADO23054	Human p53-binding
c1889	19.4	0.8	21	1	AAV40598	Human TSC gene exo	1961	19	0.8	19	1	ADO80008	CENPC1 extend prim
c1890	19.4	0.8	21	1	AAH86419	PCR primer PDZK5.6	1962	19	0.8	19	1	ADO61537	Anti-MDM2 siRNA re
c1891	19.4	0.8	21	1	AAH38522	SNP specific lower	1963	19	0.8	19	1	ADO61535	Anti-MDM2 siRNA re
c1892	19.4	0.8	21	1	AAH40070	SNP specific lower	1964	19	0.8	19	1	ADO61536	Anti-MDM2 siRNA re
c1893	19.4	0.8	21	1	AAH24567	Human Alu sequence	1965	19	0.8	19	1	ADO61538	Anti-MDM2 siRNA re
c1894	19.4	0.8	21	1	ABQ74069	Microsatellite typ	c1966	19	0.8	20	1	ABS59253	Human CAS gene ant
c1895	19.4	0.8	21	1	ABS98158	Human multidrug re	c1967	19	0.8	20	1	ABL60514	Human MDM2 mRNA fr
c1896	19.4	0.8	21	1	ABS97183	Human CYP450L2 pr	c1968	19	0.8	20	1	ABL60513	Human MDM2 mRNA fr
c1897	19.4	0.8	21	1	ABS98107	Human multidrug re	c1969	19	0.8	20	1	ABL60512	Human MDM2 mRNA fr
c1898	19.4	0.8	21	1	ABS98163	Human multidrug re	c1970	19	0.8	20	1	ABL60511	Human MDM2 mRNA fr
c1899	19.4	0.8	21	1	ABS98105	Human multidrug re	c1971	19	0.8	20	1	ADL21777	Mouse mdm2 antisen
c1900	19.4	0.8	21	1	ADE14130	Optineurin promote	c1972	19	0.8	20	1	ADP47745	Human 5-HT7 recept
c1901	19.4	0.8	21	1	ADH59601	Non-nucleotide pro	c1973	19	0.8	20	1	ADM14508	Human mPGES-1 chim
c1902	19.4	0.8	21	1	ADH59613	Non-nucleotide pro	c1974	19	0.8	20	1	ADM15268	Human mPGES-1 chim
c1903	19.4	0.8	21	1	ADI23739	Human LPDLR PCR pr	c1975	19	0.8	22	1	AAH38422	SNP specific lower
c1904	19.4	0.8	21	1	ADM65580	Human Y chromosome	c1976	19	0.8	23	1	ADO47348	Human SORBS1 gene
c1905	19.4	0.8	22	1	ADO55495	HIV gene expressio	c1977	19	0.8	24	1	AAI66603	Human ubiquitin-li
c1906	19.4	0.8	22	1	AAI059910	Human biallelic po	c1978	19	0.8	25	1	AAF24672	PCR primer for exo
c1907	19.4	0.8	22	1	AAF23797	Preseniline-1 gene	1979	19	0.8	25	1	ADB04760	Human MD27 scannin
c1908	19.4	0.8	23	1	ADH13395	PCR primer for amp	c1980	18.8	0.8	22	1	AAQ82257	Chromosome 11 (loc
c1909	19.4	0.8	24	1	ABS55410	Human malignant ne	c1981	18.8	0.8	22	1	AAI71928	Primer detects mar
c1910	19.4	0.8	24	1	ABK14172	Human DNA mismatch	c1982	18.8	0.8	22	1	AAI71925	Primer detects mar
c1911	19.4	0.8	24	1	ABV76761	Insulin like growt	c1983	18.8	0.8	22	1	AAI72000	Primer detects mar
c1912	19.4	0.8	24	1	ABV76761	Ras GTP enzyme-act	c1984	18.8	0.8	22	1	AAI71997	Primer detects mar
c1913	19.4	0.8	24	1	ABL42193	PCR primer #2 for	1985	18.8	0.8	22	1	AAZ32938	Sequence tagged si
c1914	19.4	0.8	24	1	ABS55854	Human SOX3 protein	c1986	18.8	0.8	22	1	AAH38401	SNP specific upper
c1915	19.2	0.8	20	1	ABZ24886	High-mobility comp	1987	18.8	0.8	22	1	AAF62067	Reverse PCR primer
c1916	19.2	0.8	23	1	AAI63214	Primer Alu 5' used	1988	18.8	0.8	22	1	AAI66346	Human M30 protein
c1917	19.2	0.8	24	1	ADL72189	Alu-specific prime	c1989	18.8	0.8	22	1	ACA88980	Selection and ampl
c1918	19.2	0.8	24	1	AAV52725	Hepatocyte nuclear	1990	18.8	0.8	24	1	AAH77082	Human vesicular tr
c1919	19.2	0.8	24	1	AAZ27978	PCR primer for B18	c1991	18.8	0.8	24	1	AAH91382	Human inflammatory
c1920	19.2	0.8	24	1	AAZ27181	Reverse primer P2	1992	18.8	0.8	24	1	ABK49351	RNA polymerase II
c1921	19.2	0.8	24	1	AAH92846	Human ABC1 transcr	1993	18.8	0.8	24	1	ABA04737	Human alkylation D
c1922	19.2	0.8	24	1	AAI66532	SNP specific lower	1994	18.8	0.8	24	1	ABZ21179	Human transforme-
c1923	19.2	0.8	24	1	ABA82841	Human perin-molyb	1995	18.8	0.8	24	1	ABZ79587	Hydrogenase 9.46 r
c1924	19.2	0.8	24	1	ABL41332	Human protective D	c1996	18.8	0.8	24	1	AAL55813	RT-PCR primer 1 to
c1925	19.2	0.8	24	1	ABS56119	Human mitochondria	c1997	18.8	0.8	24	1	ADC56863	RT-PCR primer Seq
c1926	19.2	0.8	24	1	ABS56119	RT-PCR primer #2 f	1998	18.8	0.8	25	1	AAI96023	H7A HLA-C gene PCR
c1927	19.2	0.8	24	1	ABS56756	DNA topoisomerase	1999	18.8	0.8	25	1	AAI65600	Primer for microsa
c1928	19.2	0.8	24	1	ABK52730	Human Mch2 protein	2000	18.8	0.8	25	1	ADB04582	Human MD27 scannin
c1929	19.2	0.8	24	1	ABQ77952	Mitochondrial tran							
c1930	19.2	0.8	24	1	ABL41338	Human TFIIID subuni							
c1931	19.2	0.8	24	1	ABK89466	Human large protei							
	19.2	0.8	24	1	ABA94088	Human tumour suppr							

ALIGNMENTS


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XX 26-FEB-2004 (first entry)
XX AAK72850/c
XX AAK72850 standard; DNA; 99 BP.
XX
XX Human respiratory system associated genomic DNA seq id 720.
XX
XX antiinflammatory; antiallergic; antiasthmatic; cytostatic; gene therapy;
XX respiratory system antigen;
XX
Query Match 3.4%; Score 82.6; DB 1; Length 100;
Best Local Similarity 90.7%; Pred. No. 2.9;
Matches 88; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 2264 AGTAGAGACAGGGTTTCCCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATC 2323
Db 1 AGTAGAGATGGGGTTTCCCGTGTGGTCCAGGATGGTCTCGATCTCTGACCTGTGATC 60
QY 2324 CGCCACCTCGGCTCCCAAGTCTGGGATTACAGG 2360
Db 61 CTCCCGCTCGGCTCCAAAGGTGCTGGGATTACAGG 97
RESULT 13
AAK85166
ID AAK85166 standard; DNA; 96 BP.
XX
XX AAK85166;
XX
XX 07-NOV-2001 (first entry)
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39978.
XX
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
XX
Query Match 3.4%; Score 81.6; DB 1; Length 96;
Best Local Similarity 90.6%; Pred. No. 3.2;
Matches 87; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 2251 TTTTGTGACTTTTAGTAGAGACAGGGTTTCCACGTTGTAGCCAGGATGGTCTCGATCTCC 2310
Db 1 TTTTGTGATTTTAGTAGAGACAGGGTTTCCACATCTTGGCCAGGATGGTCTCGACTCC 60
QY 2311 TGACCTCGTATCCACCTGCTCGGCTCCCAAGT 2346
Db 61 TGACCTCGTATCCACCTGCTCGGCTCCCAAGT 96
RESULT 14
AAK90852/c
ID AAK90852 standard; DNA; 100 BP.
XX
XX AAK90852;
XX
XX 05-NOV-2001 (first entry)
XX Human digestive system antigen genomic sequence SEQ ID NO: 4428.
XX
XX Human; digestive system antigen; gene therapy; cancer; appendicitis;
XX ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
XX
Query Match 3.4%; Score 81.5; DB 1; Length 100;
Best Local Similarity 94.1%; Pred. No. 3.3;
Matches 95; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 2254 TTGTACTTTTAGTAGAGACAGGGTTTCCCGTGTAGCCAGGATGGTCTCGATCTCTGTA 2313
Db 100 TTGTATTTTAGTAGAGACGGGGTTTCA-CGTGTAGCCAGGATGGTCTCGATCTCTGTA 42
QY 2314 CCTCGTATCGGCCACCTCGGCTCCCAAGTCTGGGAT 2354
Db 41 CCTCATGATCGGCTGCTCGGCTCCCAAGTCTGGGAT 1
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RESULT 15
AAK72850/c
ID AAK72850 standard; DNA; 99 BP.
XX
XX AAK72850;
XX
XX 06-NOV-2001 (first entry)
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27662.
XX
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
XX
Query Match 3.4%; Score 81.4; DB 1; Length 99;
Best Local Similarity 88.9%; Pred. No. 3.3;
Matches 88; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 2265 GTAGAGACAGGGTTTCCCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATC 2324
Db 99 GTAGAGACGGGATTTCCACATGTTGCCAGGTTGGTCTTGAACCTCTGAACCTCGTGATC 40
QY 2325 GCCACCTCGGCTCCCAAGTCTGGGATTACAGGCAT 2363
Db 39 GCCCGCTTGGCTCCCAAGTCTGGGATTACAGGCGT 1
RESULT 16
AAC23951
ID AAC23951 standard; cDNA; 94 BP.
XX
XX AAC23951;
XX
XX 06-OCT-2000 (first entry)
XX Human secreted protein 5' EST, SEQ ID NO: 28026.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping; ss.
XX
Query Match 3.4%; Score 81.2; DB 1; Length 94;
Best Local Similarity 91.5%; Pred. No. 3.3;
Matches 86; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 2263 TAGTAGAGACAGGGTTTCCCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGAT 2322
Db 1 TAGTAGAGACGAGGTTTCCACGAAATTAGCCAGGATGGTCTCGATCTCTGACCTCGTGAT 60
QY 2323 CGCCACCTCGGCTCCCAAGTCTGGGATTA 2356
Db 61 CTGCCGCTTGGCTCCCAAGTCTGGGATTA 94
RESULT 17
AAC28711
ID AAC28711 standard; cDNA; 95 BP.
XX
XX AAC28711;
XX
XX 06-OCT-2000 (first entry)
XX Human secreted protein 5' EST, SEQ ID NO: 32786.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping; ss.
XX
Query Match 3.4%; Score 80.6; DB 1; Length 95;
Best Local Similarity 90.5%; Pred. No. 3.6;
Matches 86; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 2264 AGTAGAGACAGGGTTTCCCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATC 2323
Db 1 AGTAGAGACAGGGTTTCCCGTGTAGCCAGGATGGTCTCGATCTCTGATCTTGTGATC 60
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KW re-vascularisation; thrombosis; arteriosclerosis; mineral content;
Query Match 3.2%; Score 75.8; DB 1; Length 87;
Best Local Similarity 92.0%; Pred. No. 6;
Matches 80; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2280 CACCGTGTAGCCAGGATGCTCGATCTCTGACCTCGTGATCGGCCACCTCGGCCTC 2339
DB 87 CACCATGTTGGCCAGGCTGCTCGAACTCTGACCTCATGATCCGCCACCTCGGCCTC 28
QY 2340 CCAAAGTGTGGGATTACAGGCATGAG 2366
DB 27 CCAAAGTGTGGGATTACAGGTGAG 1
RESULT 24
ADJ31148/c
ID ADJ31148 standard; DNA; 87 BP.
XX AC ADJ31148;
XX DT 20-MAY-2004 (first entry)
XX DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3775.
XX DE Human musculoskeletal system; cytostatic; osteopathic; cancer; osteoporosis;
KW musculoskeletal system; cytostatic; cancer; osteoporosis;
KW gene therapy; vaccine; human; ds.
Query Match 3.2%; Score 75.8; DB 1; Length 87;
Best Local Similarity 92.0%; Pred. No. 6;
Matches 80; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2280 CACCGTGTAGCCAGGATGCTCGATCTCTGACCTCGTGATCGGCCACCTCGGCCTC 2339
DB 87 CACCATGTTGGCCAGGCTGCTCGAACTCTGACCTCATGATCCGCCACCTCGGCCTC 28
QY 2340 CCAAAGTGTGGGATTACAGGCATGAG 2366
DB 27 CCAAAGTGTGGGATTACAGGTGAG 1
RESULT 25
AAK79823/c
ID AAK79823 standard; DNA; 87 BP.
XX AC AAK79823;
XX DT 07-NOV-2001 (first entry)
XX DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34635.
XX DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
Query Match 3.1%; Score 74.2; DB 1; Length 87;
Best Local Similarity 90.8%; Pred. No. 7.2;
Matches 79; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 2280 CACCGTGTAGCCAGGATGCTCGATCTCTGACCTCGTGATCGGCCACCTCGGCCTC 2339
DB 87 CACCATGTTGGCCAGGCTGCTCGAACTCTGACCTCATGATCCGCCACCTCGGCCTC 28
QY 2340 CCAAAGTGTGGGATTACAGGCATGAG 2366
DB 27 CCAAAGTGTGGGATTACAGGCATGAG 1
RESULT 26
AAK35141/c
ID AAK35141 standard; DNA; 73 BP.
XX AC AAK35141;
XX XX

DT 01-JUL-1999 (first entry)
XX Nucleotide sequence SEQ ID 49.
XX DE MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin;
Query Match 3.1%; Score 73; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 665 AGGTACATCTGTGAGTGAGACAGGTGTCACTTGAAGTGGAGTGATCAAAAGACCT 724
DB 73 AGGTACATCTGTGAGTGAGACAGGTGTCACTTGAAGTGGAGTGATCAAAAGACCT 14
QY 725 TGTACAAGAGCTT 737
DB 13 TGTACAAGAGCTT 1
RESULT 27
AAD65023/c
ID AAD65023 standard; DNA; 73 BP.
XX AC AAD65023;
XX DT 11-MAR-2004 (first entry)
XX DE Human mouse double minute (MDM2) non-coding antisense oligonucleotide.
XX DE MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; antisense; ss.
Query Match 3.1%; Score 73; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 665 AGGTACATCTGTGAGTGAGACAGGTGTCACTTGAAGTGGAGTGATCAAAAGACCT 724
DB 73 AGGTACATCTGTGAGTGAGACAGGTGTCACTTGAAGTGGAGTGATCAAAAGACCT 14
QY 725 TGTACAAGAGCTT 737
DB 13 TGTACAAGAGCTT 1
RESULT 28
AAC13689/c
ID AAC13689 standard; cDNA; 76 BP.
XX AC AAC13689;
XX DT 06-OCT-2000 (first entry)
XX DE Human secreted protein 5' EST, SEQ ID NO: 17764.
XX DE Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
Query Match 3.1%; Score 72.8; DB 1; Length 76;
Best Local Similarity 97.4%; Pred. No. 8;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2285 TGTAGCCAGGATGCTCTCGATCTCTGACCTCGTGATCGGCCACCTCGGCCTCCCAA 2344
DB 76 TGTAGCCAGGATGCTCTCGATCTCTGACCTCGTGATCGGCCACCTCGGCCTCCCAA 1
QY 2345 GTGCTGGGATTACAGG 2360
DB 16 GTGCTGGGATTACAGG 1
RESULT 29

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AAK75687/c
ID AAK75687 standard; DNA; 87 BP.
XX
AC AAK75687;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30499.
XX
DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX
KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match 3.1%; Score 72.6; DB 1; Length 87;
Best Local Similarity 89.7%; Pred. No. 8.7;
Matches 78; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATATTGGCCAGGCTGGTCTCGAACTCTGACCTCGTGATCCGCCACCTCGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACAGGTGTGAG 1

RESULT 30
AAK76817
ID AAK76817 standard; DNA; 87 BP.
XX
AC AAK76817;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:31629.
XX
DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX
KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match 3.1%; Score 72.6; DB 1; Length 87;
Best Local Similarity 89.7%; Pred. No. 8.7;
Matches 78; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATATTGGCCAGGCTGGTCTCGAACTCTGACCTCGTGATCCGCCACCTCGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACAGGTGTGAG 1

RESULT 31
AAK82025/c
ID AAK82025 standard; DNA; 87 BP.
XX
AC AAK82025;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36837.
XX
DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX
KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match 3.1%; Score 72.6; DB 1; Length 87;
Best Local Similarity 89.7%; Pred. No. 8.7;
Matches 78; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATATTGGCCAGGCTGGTCTCGAACTCTGACCTCGTGATCCGCCACCTCGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
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Db 27 CCAAAGTCTGGGATTACAGGTGTGAG 1

RESULT 32
AAK75689/c
ID AAK75689 standard; DNA; 87 BP.
XX
AC AAK75689;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30501.
XX
DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX
KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match 3.1%; Score 72.6; DB 1; Length 87;
Best Local Similarity 89.7%; Pred. No. 8.7;
Matches 78; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATATTGGCCAGGCTGGTCTCGAACTCTGACCTCGTGATCCGCCACCTCGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACAGGTGTGAG 1

RESULT 33
AAK76646/c
ID AAK76646 standard; DNA; 87 BP.
XX
AC AAK76646;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:31458.
XX
DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX
KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match 3.1%; Score 72.6; DB 1; Length 87;
Best Local Similarity 89.7%; Pred. No. 8.7;
Matches 78; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATATTGGCCAGGCTGGTCTCGAACTCTGACCTCGTGATCCGCCACCTCGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACAGGTGTGAG 1

RESULT 34
AAK75688/c
ID AAK75688 standard; DNA; 87 BP.
XX
AC AAK75688;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30500.
XX
DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX
KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match 3.1%; Score 72.6; DB 1; Length 87;
Best Local Similarity 89.7%; Pred. No. 8.7;
Matches 78; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
```

QY 2280 CACCGTGTAGCCAGGATGCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATGTGGCCAGGCTGGTCTCGAACTCTGACCTCGTGATCCGGCTGCTTGGCCTC 28
QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACAGGTGTGAG 1

RESULT 35
AAI928528
ID AAS28528 standard; DNA; 87 BP.

XX AAS28528;

DT 07-NOV-2001 (first entry)

XX Genomic sequence #368 encoding for novel human respiratory antigen.

XX Human; respiratory antigen; respiratory disorder; throat disorder;
KW lung disorder; nose disorder; lung cancer; gene therapy; cytostatic;

Query Match 3.1%; Score 72.6; DB 1; Length 87;

Best Local Similarity 89.7%; Pred. No. 8.7; Indels 0; Gaps 0;
Matches 78; Conservative 0; Mismatches 9;

QY 2280 CACCGTGTAGCCAGGATGCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATGTGGCCAGGCTGGTCTCGAACTCTGACCTCGTGATCCGGCTGCTTGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366

Db 61 CCAAAGTCTGGGATTACAGGCGTGAG 87

RESULT 36

ADG41724

ID ADG41724 standard; DNA; 87 BP.

XX ADG41724;

DT 26-FEB-2004 (first entry)

XX Human respiratory system associated genomic DNA seq id 962.

XX antiinflammatory; antiallergic; antiasthmatic; cytostatic; gene therapy;
KW respiratory system antigen;

Query Match 3.1%; Score 72.6; DB 1; Length 87;

Best Local Similarity 89.7%; Pred. No. 8.7; Indels 0; Gaps 0;
Matches 78; Conservative 0; Mismatches 9;

QY 2280 CACCGTGTAGCCAGGATGCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATGTGGCCAGGCTGGTCTCGAACTCTGACCTCGTGATCCGGCTGCTTGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366

Db 61 CCAAAGTCTGGGATTACAGGCGTGAG 87

RESULT 37

AAC12517

ID AAC12517 standard; cDNA; 84 BP.

XX AAC12517;

DT 06-OCT-2000 (first entry)

XX Human secreted protein 5' EST, SEQ ID NO: 16592.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.

Query Match 3.0%; Score 71.4; DB 1; Length 84;
Best Local Similarity 92.6%; Pred. No. 9.8; Indels 0; Gaps 0;
Matches 75; Conservative 0; Mismatches 6;

QY 2248 AATTTTGTACTTTTAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATC 2307
Db 2 AATTTTGTATTTTAGTAGAGATGGGGTTTCACCATGTGTAGCCAGGATGGTCTCGATC 61

QY 2308 TCCTGACCTCGTGATCCGCC 2328

Db 62 TCCTGACCTCGTGATCCACCC 82

RESULT 38

AAC24033

ID AAC24033 standard; cDNA; 79 BP.

XX AAC24033;

DT 06-OCT-2000 (first entry)

XX Human secreted protein 5' EST, SEQ ID NO: 28108.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.

Query Match 3.0%; Score 71; DB 1; Length 79;

Best Local Similarity 93.7%; Pred. No. 10; Indels 0; Gaps 0;
Matches 74; Conservative 0; Mismatches 5;

QY 2252 TTTTGTACTTTTAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCCT 2311
Db 1 TTTTGTATTTTAGTAGAGACCGGGTTTCACCATGTTAACAGGATGGTCTCGATCTCCT 60

QY 2312 GACCTCGTATCCGCCAC 2330

Db 61 GACCTCGTATCCGCCCGC 79

RESULT 39

AAI99210

ID AAI99210 standard; DNA; 87 BP.

XX AAI99210;

DT 07-JAN-2002 (first entry)

XX Human excretory related polynucleotide SEQ ID NO 974.

XX Human; neutropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;

Query Match 3.0%; Score 71; DB 1; Length 87;

Best Local Similarity 88.5%; Pred. No. 10; Indels 0; Gaps 0;
Matches 77; Conservative 0; Mismatches 10;

QY 2280 CACCGTGTAGCCAGGATGCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATGTGGTCAGGCTGGTCTCAAACTCTGACTTCGTGATCTGCCACCTTGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366

Db 61 CCAAAGTCTGGGATTACAGGCGTGAG 87

RESULT 40

AAI99208

ID AAI99208 standard; DNA; 87 BP.

XX AAI99208;

DT 07-JAN-2002 (first entry)

```
XX Human excretory related polynucleotide SEQ ID NO 972.
DE
XX
KW Human; neutropic; neuroprotective; cytostatic; dermatological; virucide;
  immunosuppressive; antinflammatory; anti-HIV; antibacterial; vulnerary;

Query Match      3.0%; Score 71; DB 1; Length 87;
Best Local Similarity 88.5%; Pred. No. 10;
Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATGTGTGTCAGGCTGGTCTCAAACTCTGACTTGTGATCTGCCACCTTGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGGGATTACAGGCGTGAG 87

RESULT 41
AAK87263/c
ID AAK87263 standard; DNA; 87 BP.
XX
AC AAK87263;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human excretory related polynucleotide SEQ ID NO 975.
KW Human; neutropic; neuroprotective; cytostatic; dermatological; virucide;
  immunosuppressive; antinflammatory; anti-HIV; antibacterial; vulnerary;

Query Match      3.0%; Score 71; DB 1; Length 87;
Best Local Similarity 88.5%; Pred. No. 10;
Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATGTGTGTCAGGCTGGTCTCAAACTCTGACTTGTGATCTGCCACCTTGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGGGATTACAGGCGTGAG 87

RESULT 42
AAK87263/c
ID AAK87263 standard; DNA; 87 BP.
XX
AC AAK87263;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42075.
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
  cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match      3.0%; Score 71; DB 1; Length 87;
Best Local Similarity 88.5%; Pred. No. 10;
Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATGTGTGTCAGGCTGGTCTCAAACTCTGACTTGTGATCTGCCACCTTGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGGGATTACAGGCGTGAG 87

RESULT 43
AAK84994
ID AAK84994 standard; DNA; 87 BP.
XX
AC AAK84994;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39806.
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
  cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match      3.0%; Score 71; DB 1; Length 87;
Best Local Similarity 88.5%; Pred. No. 10;
Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATGTGTGTCAGGCTGGTCTCAAACTCTGACTTGTGATCTGCCACCTTGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGGGATTACAGGCGTGAG 87

RESULT 44
AAK87262/c
ID AAK87262 standard; DNA; 87 BP.
XX
AC AAK87262;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42074.
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
  cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match      3.0%; Score 71; DB 1; Length 87;
Best Local Similarity 88.5%; Pred. No. 10;
Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATGTGTGTCAGGCTGGTCTCAAACTCTGACTTGTGATCTGCCACCTTGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACAGGTTGTGAG 1

RESULT 45
AAK78040
ID AAK78040 standard; DNA; 87 BP.
XX
AC AAK78040;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32852.
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
  cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match      3.0%; Score 71; DB 1; Length 87;
Best Local Similarity 88.5%; Pred. No. 10;
Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATGTGTGTCAGGCTGGTCTCGAACTCTGACCTTGTGATCCGCCACCTCGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 1 CCAAAGTCTGGGATTACAGGTTGTGAG 1
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XX AAK84994 standard; DNA; 87 BP.
XX
AC AAK84994;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39806.
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
  cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match      3.0%; Score 71; DB 1; Length 87;
Best Local Similarity 88.5%; Pred. No. 10;
Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATGTGTGTCAGGCTGGTCTCAAACTCTGACTTGTGATCTGCCACCTTGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGGGATTACAGGCGTGAG 87

RESULT 44
AAK87262/c
ID AAK87262 standard; DNA; 87 BP.
XX
AC AAK87262;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42074.
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
  cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match      3.0%; Score 71; DB 1; Length 87;
Best Local Similarity 88.5%; Pred. No. 10;
Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATGTGTGTCAGGCTGGTCTCAAACTCTGACTTGTGATCTGCCACCTTGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACAGGTTGTGAG 1

RESULT 45
AAK78040
ID AAK78040 standard; DNA; 87 BP.
XX
AC AAK78040;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32852.
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
  cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match      3.0%; Score 71; DB 1; Length 87;
Best Local Similarity 88.5%; Pred. No. 10;
Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATGTGTGTCAGGCTGGTCTCGAACTCTGACCTTGTGATCCGCCACCTCGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 1 CCAAAGTCTGGGATTACAGGTTGTGAG 1
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Db      61 CCAAAGTGTGGGATTACAGGTGTGAG 87
RESULT 46
AAK84995
ID      AAK84995 standard; DNA; 87 BP.
XX
XX      AAK84995;
AC
XX      07-NOV-2001 (first entry)
DT
XX      Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39807.
DE
XX      Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX      cytostatic; gene therapy; vaccine; metastasis; ds.
KW
XX      Query Match      3.0%; Score 71; DB 1; Length 87;
XX      Best Local Similarity 88.5%; Pred. No. 10;
XX      Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY      2280 CACCGTGTAGCCAGGATGCTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db      1 CACCATGTGGTCAGGCTGGTCTCAAACTCTCTGATCTCGTGTGATCGCCACCTTGGCCTC 60
QY      2340 CCAAAGTGTGGGATTACAGGCATGAG 2366
Db      61 CCAAAGTGTGGGATTACAGGCATGAG 87
RESULT 47
AAK68262
ID      AAK68262 standard; DNA; 87 BP.
XX
XX      AAK68262;
AC
XX      06-NOV-2001 (first entry)
DT
XX      Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23074.
DE
XX      Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX      cytostatic; gene therapy; vaccine; metastasis; ds.
KW
XX      Query Match      3.0%; Score 71; DB 1; Length 87;
XX      Best Local Similarity 88.5%; Pred. No. 10;
XX      Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY      2280 CACCGTGTAGCCAGGATGCTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db      1 CACCATGTGGTCAGGCTGGTCTCAAACTCTCTGATCTCGTGTGATCGCCACCTTGGCCTC 60
QY      2340 CCAAAGTGTGGGATTACAGGCATGAG 2366
Db      61 CCAAAGTGTGGGATTACAGGCATGAG 87
RESULT 48
AAK84992
ID      AAK84992 standard; DNA; 87 BP.
XX
XX      AAK84992;
AC
XX      07-NOV-2001 (first entry)
DT
XX      Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39804.
DE
XX      Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX      cytostatic; gene therapy; vaccine; metastasis; ds.
KW
XX      Query Match      3.0%; Score 71; DB 1; Length 87;
XX      Best Local Similarity 88.5%; Pred. No. 10;
XX      Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY      2280 CACCGTGTAGCCAGGATGCTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
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Db      1 CACCATGTGGTCAGGCTGGTCTCAAACTCTCTGATCTCGTGTGATCGCCACCTTGGCCTC 60
QY      2340 CCAAAGTGTGGGATTACAGGCATGAG 2366
Db      61 CCAAAGTGTGGGATTACAGGCATGAG 87
RESULT 49
AAK68855
ID      AAK68855 standard; DNA; 87 BP.
XX
XX      AAK68855;
AC
XX      06-NOV-2001 (first entry)
DT
XX      Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23667.
DE
XX      Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX      cytostatic; gene therapy; vaccine; metastasis; ds.
KW
XX      Query Match      3.0%; Score 71; DB 1; Length 87;
XX      Best Local Similarity 88.5%; Pred. No. 10;
XX      Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY      2280 CACCGTGTAGCCAGGATGCTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db      1 CACCATGTGGTCAGGCTGGTCTCAAACTCTCTGATCTCGTGTGATCGCCACCTTGGCCTC 60
QY      2340 CCAAAGTGTGGGATTACAGGCATGAG 2366
Db      61 CCAAAGTGTGGGATTACAGGCATGAG 87
RESULT 50
AAK68854
ID      AAK68854 standard; DNA; 87 BP.
XX
XX      AAK68854;
AC
XX      06-NOV-2001 (first entry)
DT
XX      Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23666.
DE
XX      Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX      cytostatic; gene therapy; vaccine; metastasis; ds.
KW
XX      Query Match      3.0%; Score 71; DB 1; Length 87;
XX      Best Local Similarity 88.5%; Pred. No. 10;
XX      Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY      2280 CACCGTGTAGCCAGGATGCTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db      1 CACCATGTGGTCAGGCTGGTCTCAAACTCTCTGATCTCGTGTGATCGCCACCTTGGCCTC 60
QY      2340 CCAAAGTGTGGGATTACAGGCATGAG 2366
Db      61 CCAAAGTGTGGGATTACAGGCATGAG 87
RESULT 51
AAS28332
ID      AAS28332 standard; DNA; 87 BP.
XX
XX      AAS28332;
AC
XX      07-NOV-2001 (first entry)
DT
XX      Genomic sequence #172 encoding for novel human respiratory antigen.
DE
XX      Human; respiratory antigen; respiratory disorder; throat disorder;
XX      lung disorder; nose disorder; lung cancer; gene therapy; cytostatic;
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XX ADG41528;
XX AC
XX DT
XX 26-FEB-2004 (first entry)
XX Human respiratory system associated genomic DNA seq id 766.
XX
XX antiinflammatory; antiallergic; antiasthmatic; cytostatic; gene therapy;
XX respiratory system antigen;
KW

Query Match 3.0%; Score 71; DB 1; Length 87;
Best Local Similarity 88.5%; Pred. No. 10;
Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCAGGATGCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACATGTTGTCAGGTGCTCTCAACTCTGATCTTGATCCGCCCTCAGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGGGATTACAGCGTGAG 87

RESULT 58
ABZ67838/c
ID ABZ67838 standard; DNA; 87 BP.
XX
XX AC ABZ67838;
XX DT
XX 26-MAR-2003 (first entry)
XX Human secreted protein encoding genomic DNA SEQ ID NO 1361.
XX
XX Human; secreted protein; nootropic; neuroprotective; cytostatic;
XX virucide; dermatological; immunosuppressive; antiinflammatory; anti-HIV;
KW

Query Match 3.0%; Score 71; DB 1; Length 87;
Best Local Similarity 88.5%; Pred. No. 10;
Matches 77; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCAGGATGCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATGTTGTCAGGTGCTCTCAACTCTGATCTCGTGATCCGCCCTTGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACAGCGTGAG 1

RESULT 59
ABK45727
ID ABK45727 standard; cDNA; 84 BP.
XX
XX AC ABK45727;
XX DT
XX 05-JUN-2002 (first entry)
XX cDNA encoding colon tumour protein, SEQ ID NO 1278.
XX
XX Human; colon tumour; vaccine; colon cancer; immunogenic; immunotherapy;
KW gene; ss.

Query Match 3.0%; Score 70.8; DB 1; Length 84;
Best Local Similarity 91.5%; Pred. No. 11;
Matches 75; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2291 CCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCCTCGGCCTCCCAAAGTGCTG 2350
Db 1 CCAGATGGTCTGATCTCTGACCTCGTGATCTGCCGCTCGGCCTCCCAAAGTGCTG 60

QY 2351 GGATTACAGGCATGAGCCACG 2372
Db 61 GGATTACCGGTGTGAGCCACG 82
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RESULT 60
AAC11340
ID AAC11340 standard; cDNA; 92 BP.
XX
XX AC AAC11340;
XX DT
XX 06-OCT-2000 (first entry)
XX Human secreted protein 5' EST, SEQ ID NO: 15415.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.

Query Match 3.0%; Score 70.2; DB 1; Length 92;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 78; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2251 TTTTGTACTTTTAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCC 2310
Db 1 TTTTGTATTTTAGTAGAGACGGGGTTTCACCATGTTGTCAGGCTGGTCTTGAACCTCC 60

QY 2311 TGACCTCGTGATCCGCCACCTCGGCCTCCC 2341
Db 61 TGACCTTGTGATCCACCTCGCTTGGCCTCCC 91

RESULT 61
AAS36366
ID AAS36366 standard; DNA; 87 BP.
XX
XX AC AAS36366;
XX DT
XX 17-DEC-2001 (first entry)
XX Human cardiovascular system antigen genomic DNA SEQ ID NO 1866.
XX
XX Cardiovascular system antigen; human; mouse; rabbit; goat; horse; cat;
XX chicken; sheep; immunosuppressive; antiarthritic; vasotropic; dog;
KW

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCAGGATGCTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATGTTGTCAGGCTGATCTCGAACTCTGACCTCGTGATCCGCCCTTGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGGGATTACAGGATGAG 87

RESULT 62
AAK91304
ID AAK91304 standard; DNA; 87 BP.
XX
XX AC AAK91304;
XX DT
XX 05-NOV-2001 (first entry)
XX Human digestive system antigen genomic sequence SEQ ID NO: 4880.
XX
XX Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCAGGATGCTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATGTTGTCAGGCTGATCTCGAACTCTGACCTCGTGATCCGCCCTTGGCCTC 60
```

Db 1 CACCATCTTGGCCAGGCTGGTCTCAAACTCCTGACCTCGTGTATCCGCCCGCTTGGCCTC 60

QY 2340 CCAAGTCTGGGATTACAGGCATGAG 2366
|||||
Db 61 CCAAAAGTCTGAGATTACCGCGTGAG 87

RESULT 63
AAK91305
ID AAK91305 standard; DNA; 87 BP.
XX
AC AAK91305;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human digestive system antigen genomic sequence SEQ ID NO: 4881.
XX
KW Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
|||||
Db 1 CACCATCTTGGCCAGGCTGGTCTCAAACTCCTGACCTCGTGTATCCGCCCGCTTGGCCTC 60

QY 2340 CCAAAAGTCTGGGATTACAGGCATGAG 2366
|||||
Db 61 CCAAAAGTCTGAGATTACCGCGTGAG 87

RESULT 64
AAK91307
ID AAK91307 standard; DNA; 87 BP.
XX
AC AAK91307;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human digestive system antigen genomic sequence SEQ ID NO: 4883.
XX
KW Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
|||||
Db 1 CACCATCTTGGCCAGGCTGGTCTCAAACTCCTGACCTCGTGTATCCGCCCGCTTGGCCTC 60

QY 2340 CCAAAAGTCTGGGATTACAGGCATGAG 2366
|||||
Db 61 CCAAAAGTCTGAGATTACCGCGTGAG 87

RESULT 65
AAK86755
ID AAK86755 standard; DNA; 87 BP.
XX
AC AAK86755;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41567.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match 2.9%; Score 69.4; DB 1; Length 87;

Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
|||||
Db 1 CACCATCTTGGCCAGGCTGGTCTCGAACTCCTGACCTTGTGTATCCACCTGCTTGGCCTC 60

QY 2340 CCAAAAGTCTGGGATTACAGGCATGAG 2366
|||||
Db 61 CCAAAAGTCTGGGATTACAGGTGTGAG 87

RESULT 66
AAK75934/c
ID AAK75934 standard; DNA; 87 BP.
XX
AC AAK75934;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30746.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
|||||
Db 87 CACCATCTTGGTCCAGGCTGGTCTCCAACCTCCTGACCTCGTGATCCGCCCGCTTGGCCTC 28

QY 2340 CCAAAAGTCTGGGATTACAGGCATGAG 2366
|||||
Db 27 CCAAAAGTCTGGGATTATAGGTGTGAG 1

RESULT 67
AAK81974/c
ID AAK81974 standard; DNA; 87 BP.
XX
AC AAK81974;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36786.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
|||||
Db 87 CACCATCTTGGTCCAGGCTGGTCTCGAACTCCTGACCTTGTGTATCCGCCCGCTTGGCCTC 28

QY 2340 CCAAAAGTCTGGGATTACAGGCATGAG 2366
|||||
Db 27 CCAAAAGTCTGGGATTACAGGTGTGAG 1

RESULT 68
AAK81975/c
ID AAK81975 standard; DNA; 87 BP.
XX
AC AAK81975;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36787.

AC	AAK83799;
XX	
DT	07-NOV-2001 (first entry)
XX	
DE	Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38611.
XX	
DE	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW	cytostatic; gene therapy; vaccine; metastasis; ds.
KW	
	Query Match 2.9%; Score 69.4; DB 1; Length 87;
	Best Local Similarity 87.4%; Pred. No. 13;
	Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY	2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db	87 CACCATGTTGGCCAGCGGCTCTCAACTCTGACCTTGTGATCGCCCGCTTCGGCCTC 28
QY	2340 CCAAAGTGTGGGATTACAGGCATGAG 2366
Db	27 CCAAAGTGTGGGATTACAGGCATGAG 1
RESULT 72	
AAK86753	
ID	AAK86753 standard; DNA; 87 BP.
XX	
AC	AAK86753;
XX	
DT	07-NOV-2001 (first entry)
XX	
DE	Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41565.
XX	
DE	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW	cytostatic; gene therapy; vaccine; metastasis; ds.
KW	
	Query Match 2.9%; Score 69.4; DB 1; Length 87;
	Best Local Similarity 87.4%; Pred. No. 13;
	Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY	2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db	1 CACCATGTTGGCCAGCGGCTCTCGAACTCTGACCTTGTGATCCACCTCGCTTCGGCCTC 60
QY	2340 CCAAAGTGTGGGATTACAGGCATGAG 2366
Db	61 CCAAAGTGTGGGATTACAGGCATGAG 87
RESULT 73	
AAK36467/C	
ID	AAK36467 standard; DNA; 87 BP.
XX	
AC	AAK36467;
XX	
DT	08-JAN-2002 (first entry)
XX	
DE	Human musculoskeletal system related polynucleotide SEQ ID NO 2832.
XX	
DE	Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW	antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW	
	Query Match 2.9%; Score 69.4; DB 1; Length 87;
	Best Local Similarity 87.4%; Pred. No. 13;
	Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY	2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db	87 CACCATGTTGGCCAGCGTGTCTAGAACTCTGACCTCGTGATCCGCCCGCTTCGGCCTC 28
QY	2340 CCAAAGTGTGGGATTACAGGCATGAG 2366
Db	27 CCAAAGTGTGGGATTACAGGCATGAG 1

RESULT 74
AAL36466/c
ID AAL36466 standard; DNA; 87 BP.
XX
AC AAL36466;
XX
DT 08-JAN-2002 (first entry)
XX
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2831.
XX
DE Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
XX
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW
Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
DB 87 CACCATGTGGCCAGGCTTGTCTAGAACTCTGACCTCGTGATCCGCCCGCTTCGGCCTC 28
QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
DB 27 CCAAAGTCTGGGATTACAGGTGTGAG 1
RESULT 75
AAL36464/c
ID AAL36464 standard; DNA; 87 BP.
XX
AC AAL36464;
XX
DT 08-JAN-2002 (first entry)
XX
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2829.
XX
DE Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
XX
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW
Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
DB 87 CACCATGTGGCCAGGCTTGTCTAGAACTCTGACCTCGTGATCCGCCCGCTTCGGCCTC 28
QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
DB 27 CCAAAGTCTGGGATTACAGGTGTGAG 1
RESULT 76
AAL02848
ID AAL02848 standard; DNA; 87 BP.
XX
AC AAL02848;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen DNA SEQ ID NO: 5536.
XX
DE Human; reproductive system related antigen; reproductive system disorder;
XX
KW cancer; gene therapy; ds.
Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
DB 1 CACCATGTGGCCAGGCTTGTCTCAAACTCTGACCTCGTGATCCGCCACTTTGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
DB 61 CCAAAGTCTGGGATTACAGCGTAAAG 87
RESULT 77
AAL02849
ID AAL02849 standard; DNA; 87 BP.
XX
AC AAL02849;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen DNA SEQ ID NO: 5537.
XX
DE Human; reproductive system related antigen; reproductive system disorder;
XX
KW cancer; gene therapy; ds.
Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
DB 1 CACCATGTGGCCAGGCTTGTCTCAAACTCTGACCTCGTGATCCGCCACTTTGGCCTC 60
QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
DB 61 CCAAAGTCTGGGATTACAGCGTAAAG 87
RESULT 78
AAL07338/c
ID AAL07338 standard; DNA; 87 BP.
XX
AC AAL07338;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen DNA SEQ ID NO: 10026.
XX
DE Human; reproductive system related antigen; reproductive system disorder;
XX
KW cancer; gene therapy; ds.
Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
DB 87 CACCATGTGGCCAGGCTTGTCTCGAACTCTGACCTCGTGATCCGCCACTTTGGCCTC 28
QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
DB 27 CCAAAGTCTGGGATTACAGATGTGAG 1
RESULT 79
AAS32132
ID AAS32132 standard; DNA; 87 BP.
XX
AC AAS32132;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human liver associated genomic DNA #306.
XX
DE Liver associated protein; human; mouse; rabbit; goat; horse; cat; dog;
XX
KW chicken; sheep; immunosuppressive; antiarthritic; vasotropic;
KW
Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;

```
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATCTTGGCCAGGCTGGTCTCAAACTCTGACCTCGTGATCCGCCCGCCTTGGCCTC 60
QY 2340 CCAAAGTGTGGGATTTACAGGCATGAG 2366
Db 61 CCAAAGTGTGAGATTACCGGCGTGAG 87

RESULT 80
AAS32134
ID AAS32134 standard; DNA; 87 BP.
XX
AC AAS32134;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human liver associated genomic DNA #308.
XX
KW Liver associated protein; human; mouse; rabbit; goat; horse; cat; dog;
KW chicken; sheep; immunosuppressive; antiarthritic; vasotropic;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATCTTGGCCAGGCTGGTCTCAAACTCTGACCTCGTGATCCGCCCGCCTTGGCCTC 60
QY 2340 CCAAAGTGTGGGATTTACAGGCATGAG 2366
Db 61 CCAAAGTGTGAGATTACCGGCGTGAG 87

RESULT 81
AAS32131
ID AAS32131 standard; DNA; 87 BP.
XX
AC AAS32131;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human liver associated genomic DNA #305.
XX
KW Liver associated protein; human; mouse; rabbit; goat; horse; cat; dog;
KW chicken; sheep; immunosuppressive; antiarthritic; vasotropic;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATCTTGGCCAGGCTGGTCTCAAACTCTGACCTCGTGATCCGCCCGCCTTGGCCTC 60
QY 2340 CCAAAGTGTGGGATTTACAGGCATGAG 2366
Db 61 CCAAAGTGTGAGATTACCGGCGTGAG 87

RESULT 82
AEN90487
ID AEN90487 standard; DNA; 87 BP.
XX
AC AEN90487;
XX
DT 24-JUL-2002 (first entry)
XX
DE Human liver antigen HFVID08 genomic sequence, SEQ ID NO:608.
XX
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```
KW Human; liver antigen; liver disorder; hepatic disorder; infection;
KW hepatitis; viral; parasitic; bacterial; fungal; inflammatory condition;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATCTTGGCCAGGCTGGTCTCAAACTCTGACCTCGTGATCCGCCCGCCTTGGCCTC 60
QY 2340 CCAAAGTGTGGGATTTACAGGCATGAG 2366
Db 61 CCAAAGTGTGAGATTACCGGCGTGAG 87

RESULT 83
AEN90489
ID AEN90489 standard; DNA; 87 BP.
XX
AC AEN90489;
XX
DT 24-JUL-2002 (first entry)
XX
DE Human liver antigen HFVID08 genomic sequence, SEQ ID NO:610.
XX
KW Human; liver antigen; liver disorder; hepatic disorder; infection;
KW hepatitis; viral; parasitic; bacterial; fungal; inflammatory condition;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATCTTGGCCAGGCTGGTCTCAAACTCTGACCTCGTGATCCGCCCGCCTTGGCCTC 60
QY 2340 CCAAAGTGTGGGATTTACAGGCATGAG 2366
Db 61 CCAAAGTGTGAGATTACCGGCGTGAG 87

RESULT 84
AEN90486
ID AEN90486 standard; DNA; 87 BP.
XX
AC AEN90486;
XX
DT 24-JUL-2002 (first entry)
XX
DE Human liver antigen HFVID08 genomic sequence, SEQ ID NO:607.
XX
KW Human; liver antigen; liver disorder; hepatic disorder; infection;
KW hepatitis; viral; parasitic; bacterial; fungal; inflammatory condition;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATCTTGGCCAGGCTGGTCTCAAACTCTGACCTCGTGATCCGCCCGCCTTGGCCTC 60
QY 2340 CCAAAGTGTGGGATTTACAGGCATGAG 2366
Db 61 CCAAAGTGTGAGATTACCGGCGTGAG 87

RESULT 85
ABX59454/c
ID ABX59454 standard; cDNA; 87 BP.
XX
AC ABX59454;
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XX 26-FEB-2003 (first entry)
DT
XX cDNA encoding novel human musculoskeletal system antigen #1798.
DE
XX
XX Gene; ss; musculoskeletal system antigen; cancer; metastasis;
KW re-vascularisation; thrombosis; arteriosclerosis; mineral content;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATGTTGCCAGGCTTGTCTAGAACTCTGACCTCGTGATCCGCCCGCTTCGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACAGGTGTGAG 1

RESULT 86
ABX59455/c
ID ABX59455 standard; cDNA; 87 BP.
XX
AC ABX59455;
XX
DT 26-FEB-2003 (first entry)
XX
DE cDNA encoding novel human musculoskeletal system antigen #1799.
XX
KW Gene; ss; musculoskeletal system antigen; cancer; metastasis;
KW re-vascularisation; thrombosis; arteriosclerosis; mineral content;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATGTTGCCAGGCTTGTCTAGAACTCTGACCTCGTGATCCGCCCGCTTCGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACAGGTGTGAG 1

RESULT 87
ABX59452/c
ID ABX59452 standard; cDNA; 87 BP.
XX
AC ABX59452;
XX
DT 26-FEB-2003 (first entry)
XX
DE cDNA encoding novel human musculoskeletal system antigen #1796.
XX
KW Gene; ss; musculoskeletal system antigen; cancer; metastasis;
KW re-vascularisation; thrombosis; arteriosclerosis; mineral content;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATGTTGCCAGGCTTGTCTAGAACTCTGACCTCGTGATCCGCCCGCTTCGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACAGGTGTGAG 1

RESULT 88
ADE47060
ID ADE47060 standard; DNA; 87 BP.
XX
AC ADE47060;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human cardiovascular system related genomic DNA #626.
XX
KW Human; cardiovascular system related polypeptide; cancer;
KW proliferative disorder; foetal abnormality; developmental abnormality;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATGTTGGTCAGGCTGATCTCGAACTCTGACCTCGTGATCCGCCCGCTTCGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGGGATTACAGGAGTGAG 87

RESULT 89
ADJ15402
ID ADJ15402 standard; DNA; 87 BP.
XX
AC ADJ15402;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human liver-related genomic DNA - SEQ ID 610.
XX
KW liver; virucide; fungicide; antibacterial; antiparasitic; hepatotropic;
KW antiinflammatory; cytostatic; litholytic; antirheumatic; antiarthritic;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATCTTGGCCAGGCTGGTCTCAAACTCTGACCTCGTGATCCGCCCGCTTCGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGAGATTACCGGCGTGAG 87

RESULT 90
ADJ15399
ID ADJ15399 standard; DNA; 87 BP.
XX
AC ADJ15399;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human liver-related genomic DNA - SEQ ID 607.
XX
KW liver; virucide; fungicide; antibacterial; antiparasitic; hepatotropic;
KW antiinflammatory; cytostatic; litholytic; antirheumatic; antiarthritic;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATCTTGGCCAGGCTGGTCTCAAACTCTGACCTCGTGATCCGCCCGCTTCGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGAGATTACCGGCGTGAG 87

XX 26-FEB-2003 (first entry)
DT
XX cDNA encoding novel human musculoskeletal system antigen #1798.
DE
XX
XX Gene; ss; musculoskeletal system antigen; cancer; metastasis;
KW re-vascularisation; thrombosis; arteriosclerosis; mineral content;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATGTTGCCAGGCTTGTCTAGAACTCTGACCTCGTGATCCGCCCGCTTCGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACAGGTGTGAG 1

RESULT 86
ABX59455/c
ID ABX59455 standard; cDNA; 87 BP.
XX
AC ABX59455;
XX
DT 26-FEB-2003 (first entry)
XX
DE cDNA encoding novel human musculoskeletal system antigen #1799.
XX
KW Gene; ss; musculoskeletal system antigen; cancer; metastasis;
KW re-vascularisation; thrombosis; arteriosclerosis; mineral content;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATGTTGCCAGGCTTGTCTAGAACTCTGACCTCGTGATCCGCCCGCTTCGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACAGGTGTGAG 1

RESULT 87
ABX59452/c
ID ABX59452 standard; cDNA; 87 BP.
XX
AC ABX59452;
XX
DT 26-FEB-2003 (first entry)
XX
DE cDNA encoding novel human musculoskeletal system antigen #1796.
XX
KW Gene; ss; musculoskeletal system antigen; cancer; metastasis;
KW re-vascularisation; thrombosis; arteriosclerosis; mineral content;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATGTTGCCAGGCTTGTCTAGAACTCTGACCTCGTGATCCGCCCGCTTCGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACAGGTGTGAG 1

RESULT 88
ADE47060
ID ADE47060 standard; DNA; 87 BP.
XX
AC ADE47060;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human cardiovascular system related genomic DNA #626.
XX
KW Human; cardiovascular system related polypeptide; cancer;
KW proliferative disorder; foetal abnormality; developmental abnormality;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATGTTGGTCAGGCTGATCTCGAACTCTGACCTCGTGATCCGCCCGCTTCGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGGGATTACAGGAGTGAG 87

RESULT 89
ADJ15402
ID ADJ15402 standard; DNA; 87 BP.
XX
AC ADJ15402;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human liver-related genomic DNA - SEQ ID 610.
XX
KW liver; virucide; fungicide; antibacterial; antiparasitic; hepatotropic;
KW antiinflammatory; cytostatic; litholytic; antirheumatic; antiarthritic;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATCTTGGCCAGGCTGGTCTCAAACTCTGACCTCGTGATCCGCCCGCTTCGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGAGATTACCGGCGTGAG 87

RESULT 90
ADJ15399
ID ADJ15399 standard; DNA; 87 BP.
XX
AC ADJ15399;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human liver-related genomic DNA - SEQ ID 607.
XX
KW liver; virucide; fungicide; antibacterial; antiparasitic; hepatotropic;
KW antiinflammatory; cytostatic; litholytic; antirheumatic; antiarthritic;

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATCTTGGCCAGGCTGGTCTCAAACTCTGACCTCGTGATCCGCCCGCTTCGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGAGATTACCGGCGTGAG 87

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QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGGGATTACAGGCATGAG 87

RESULT 91
ADJ15400
ID ADJ15400 standard; DNA; 87 BP.
XX AC ADJ15400;
XX XX
XX 20-MAY-2004 (first entry)
XX DE Human liver-related genomic DNA - SEQ ID 608.
XX DE liver; virucide; fungicide; antibacterial; antiparasitic; hepatotropic;
XX KW antiinflammatory; cytostatic; litholytic; antirheumatic; antiarthritic;
XX KW

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTTAGCCAGGATGCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATGTTGCCAGGCTTGTCTAGAACTCTGACCTCGTGATCCGCCACCTCGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CCAAAGTCTGGGATTACAGGCATGAG 87

RESULT 92
ADJ30205/c
ID ADJ30205 standard; DNA; 87 BP.
XX AC ADJ30205;
XX XX
XX 20-MAY-2004 (first entry)
XX DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2832.
XX DE musculoskeletal system; cytostatic; osteopathic; cancer; osteoporosis;
XX KW gene therapy; vaccine; human; ds.

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTTAGCCAGGATGCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATGTTGCCAGGCTTGTCTAGAACTCTGACCTCGTGATCCGCCACCTCGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACAGGCATGAG 1

RESULT 93
ADJ30202/c
ID ADJ30202 standard; DNA; 87 BP.
XX AC ADJ30202;
XX XX
XX 20-MAY-2004 (first entry)
XX DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2829.
XX DE musculoskeletal system; cytostatic; osteopathic; cancer; osteoporosis;
XX KW gene therapy; vaccine; human; ds.

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
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QY 2280 CACCGTTAGCCAGGATGCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATGTTGCCAGGCTTGTCTAGAACTCTGACCTCGTGATCCGCCACCTCGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACAGGCATGAG 1

RESULT 94
ADJ30204/c
ID ADJ30204 standard; DNA; 87 BP.
XX AC ADJ30204;
XX XX
XX 20-MAY-2004 (first entry)
XX DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2831.
XX DE musculoskeletal system; cytostatic; osteopathic; cancer; osteoporosis;
XX KW gene therapy; vaccine; human; ds.

Query Match 2.9%; Score 69.4; DB 1; Length 87;
Best Local Similarity 87.4%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2280 CACCGTTAGCCAGGATGCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATGTTGCCAGGCTTGTCTAGAACTCTGACCTCGTGATCCGCCACCTCGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACAGGCATGAG 1

RESULT 95
AAK83861
ID AAK83861 standard; DNA; 90 BP.
XX AC AAK83861;
XX XX
XX 07-NOV-2001 (first entry)
XX DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38673.
XX DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match 2.9%; Score 68.3; DB 1; Length 90;
Best Local Similarity 91.2%; Pred. No. 14;
Matches 83; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 2233 CCACCACACCTGGCTAAATTTTGTACTTTTGTAGTAGAGACAGGGTTTCCCGTGTAGCC 2292
Db 1 CCACCACACCTGGCTAA-TTTTGTATTTTGTAGTAGAGACAGGGTTTCCACCATGTTGGCC 59

QY 2293 AGGATGCTCGATCTCTGACCTCGTGATC 2323
Db 60 AGGCTGCTCTCGAACTCTCTGACCTCGTGATC 90

RESULT 96
AAK85686/c
ID AAK85686 standard; DNA; 90 BP.
XX AC AAK85686;
XX XX
XX 07-NOV-2001 (first entry)
XX DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40498.
XX DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
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KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match      2.9%; Score 68.3; DB 1; Length 90;
Best Local Similarity 91.2%; Pred. No. 14;
Matches 83; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 2233 CCACCACACCTGGCTAAATTTTGTGACCTTTAGTAGACAGAGGTTTCCACGGTTAGCC 2292
Db 90 CCACCACACCTGGCTAA- TTTTGTGATTTTGTGGAGACGGGTTTCCACATGTTGGCC 32

QY 2283 AGGATGCTCGATCTCCTGACCTCGTGATC 2323
Db 31 AGGCTGGTCTCGAACTCTGACCTCGTGATC 1

RESULT 97
AAK90874
ID AAK90874 standard; DNA; 87 BP.
XX
AC AAK90874;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human digestive system antigen genomic sequence SEQ ID NO: 4450.
XX
KW Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;

Query Match      2.9%; Score 67.8; DB 1; Length 87;
Best Local Similarity 86.2%; Pred. No. 15;
Matches 75; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 1 CACCATGTTGGTCAGGCTGGTCTTGAACCTCGTACCTCGTGATCCGCCCGCTTGGCCTC 60

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 61 CTGAAGTCTGGGATTACAGGTGTGAG 87

RESULT 98
ABA15851/c
ID ABA15851 standard; DNA; 87 BP.
XX
AC ABA15851;
XX
DT 23-JAN-2002 (first entry)
XX
DE Human nervous system related polynucleotide SEQ ID NO 8182.
XX
KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;

Query Match      2.9%; Score 67.8; DB 1; Length 87;
Best Local Similarity 86.2%; Pred. No. 15;
Matches 75; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATATTGGCAGGCTGGTCTCAAACTCTGACCTCGTGATCCACCGCCTTGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACATGATGAG 1

RESULT 99
ABA15852/c
ID ABA15852 standard; DNA; 87 BP.
XX
AC ABA15852;
XX
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DT 23-JAN-2002 (first entry)
XX
DE Human nervous system related polynucleotide SEQ ID NO 8183.
XX
KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;

Query Match      2.9%; Score 67.8; DB 1; Length 87;
Best Local Similarity 86.2%; Pred. No. 15;
Matches 75; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATATTGGCCAGGCTGGTCTCAAACTCTGACCTCGTGATCCACCGCCTTGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAAGTCTGGGATTACATGATGAG 1

RESULT 100
AAK65876/c
ID AAK65876 standard; DNA; 87 BP.
XX
AC AAK65876;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20688.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match      2.8%; Score 66.2; DB 1; Length 87;
Best Local Similarity 85.1%; Pred. No. 18;
Matches 74; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATGTTGGCCAGGCTGGTCTCAAACTCTGACCTCATATAATCCGCCCGCTTGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAATGCTGGGATTACAGGTGTGAG 1

RESULT 101
AAK65878/c
ID AAK65878 standard; DNA; 87 BP.
XX
AC AAK65878;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20690.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match      2.8%; Score 66.2; DB 1; Length 87;
Best Local Similarity 85.1%; Pred. No. 18;
Matches 74; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCTC 2339
Db 87 CACCATGTTGGCCAGGCTGGTCTCAAACTCTGACCTCATATAATCCGCCCGCTTGGCCTC 28

QY 2340 CCAAAGTCTGGGATTACAGGCATGAG 2366
Db 27 CCAAATGCTGGGATTACAGGTGTGAG 1

RESULT 102
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AAK76883
ID AAK76883 standard; DNA; 82 BP.
XX
AC AAK76883;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:31695.
XX
DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
KW
Query Match 2.8%; Score 66; DB 1; Length 82;
Best Local Similarity 87.8%; Pred. No. 18;
Matches 72; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 2263 TAGTAGAGACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTCGTAT 2322
Db 1 TAATAGACACAGGGTTTACCATGTTGGCCAGGATGGTCTGTGATCTCTTGACCTTGTGAT 60
QY 2323 CCGCCCACTCTGGCTCCCAA 2344
Db 61 CTGCCCGCTTGGCTCCCAA 82
RESULT 103
AD112544/c
ID AD112544 standard; DNA; 80 BP.
XX
AC AD112544;
XX
DT 22-APR-2004 (first entry)
XX
DE Mutant human BRCA1 genomic DNA resulting from deletion 3 SeqID 27.
XX
KW db; cancer; human; tumour suppressor;
KW breast cancer susceptibility gene 1; BRCA1; repetitive Alu;
Query Match 2.7%; Score 64.4; DB 1; Length 80;
Best Local Similarity 91.9%; Pred. No. 21;
Matches 68; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2298 GGTCTCGATCTCTGACCTCGTATCGCCACCTCGGCTCCCAAAGTCTGGGATTAC 2357
Db 80 GGTCTCGAATCTCTGACCTGTGATCGCCGCTCGGCTCCCAAAGTCTGGGATTAC 21
QY 2358 AGGATGAGCCACC 2371
Db 20 AGGCGTAAGCCACC 7
RESULT 104
AAC11941
ID AAC11941 standard; cDNA; 81 BP.
XX
AC AAC11941;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 16016.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
Query Match 2.6%; Score 62.2; DB 1; Length 81;
Best Local Similarity 84.8%; Pred. No. 28;
Matches 67; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
QY 2253 TTTGTACTTTTAGTAGACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCCTG 2312
Db 2 TATTNNNTTAAAGTAGACAGGGTTTTCATCGTGTGGCCAGGATGRTCTCTCAAACTCCTG 61
QY 2313 ACCTCGTGTATCCGCCACC 2331

Db 62 ACCTCGTGTATCCGCCACC 80
RESULT 105
ABN39842
ID ABN39842 standard; DNA; 60 BP.
XX
AC ABN39842;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:12590.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
Query Match 2.5%; Score 60; DB 1; Length 60;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 98 TGACCGAGATCTCTGCTTTCGACCCAGGACCGTCCCTCCCGGATTAGTCGTA 157
Db 1 TGACCGAGATCTCTGCTTTCGACCCAGGACCGTCCCTCCCGGATTAGTCGTA 60
RESULT 106
ABZ09613/c
ID ABZ09613 standard; DNA; 68 BP.
XX
AC ABZ09613;
XX
DT 16-JAN-2003 (first entry)
XX
DE Human oligonucleotide SEQ ID 773.
XX
KW Human; tumour suppressor; virucide; cytostatic; nootropic;
KW neuroprotective; neuroleptic; gene therapy; tumour suppression;
Query Match 2.5%; Score 60; DB 1; Length 68;
Best Local Similarity 92.6%; Pred. No. 33;
Matches 63; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2256 GTACTTTTAGTAGACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCCTGACC 2315
Db 68 GTATTTTAGTAGACAGGGTTTACCATGTTAGTAGATGGTCTCGATTTCTCTGACC 9
QY 2316 TCGTGATC 2323
Db 8 TCGTGATC 1
RESULT 107
ABZ79066/c
ID ABZ79066 standard; DNA; 68 BP.
XX
AC ABZ79066;
XX
DT 24-APR-2003 (first entry)
XX
DE Tumour suppression-related sequence, SEQ ID 773.
XX
KW Cytostatic; virucide; apoptotic; gene therapy; tumour suppression;
KW tumour reversion; apoptosis; virus resistance; viral infection; tumour;
Query Match 2.5%; Score 60; DB 1; Length 68;
Best Local Similarity 92.6%; Pred. No. 33;
Matches 63; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2256 GTACTTTTAGTAGACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCCTGACC 2315
Db 68 GTATTTTAGTAGACAGGGTTTACCATGTTAGTAGATGGTCTCGATTTCTCTGACC 9

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QY 2316 TCGTGATC 2323
|||
Db 8 TCGTGATC 1

RESULT 108
ID ABZ09678/c
XX ABZ09678 standard; DNA; 68 BP.
XX ABZ09678;
AC ABZ09678;
DT 16-JAN-2003 (first entry)
XX Human oligonucleotide SEQ ID 838.
DE Human; tumour suppressor; virucide; cytostatic; nootropic;
KW neuroprotective; neuroleptic; gene therapy; tumour suppression;

Query Match 2.5%; Score 58.4; DB 1; Length 68;
Best Local Similarity 91.2%; Pred. No. 40;
Matches 62; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2256 GTACTTTTAGTAGACAGAGGGTTTCACCGTTAGCCAGGATGCTTCGATCTCCTGACC 2315
|||
Db 68 GTATTTTATAGAGGTGGGTTTCACCAATGTTAGCCAGGATGCTCTCAATCTCCTGACC 9

QY 2316 TCGTGATC 2323
|||
Db 8 TCGTGATC 1

RESULT 109
ID ABZ79131/c
XX ABZ79131 standard; DNA; 68 BP.
XX ABZ79131;
AC ABZ79131;
DT 24-APR-2003 (first entry)
XX Tumour suppression-related sequence, SEQ ID 838.
DE Cytostatic; virucide; apoptotic; gene therapy; tumour suppression;
KW tumour reversion; apoptosis; virus resistance; viral infection; tumour;

Query Match 2.5%; Score 58.4; DB 1; Length 68;
Best Local Similarity 91.2%; Pred. No. 40;
Matches 62; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2256 GTACTTTTAGTAGACAGAGGGTTTCACCGTTAGCCAGGATGCTTCGATCTCCTGACC 2315
|||
Db 68 GTATTTTATAGAGGTGGGTTTCACCAATGTTAGCCAGGATGCTCTCAATCTCCTGACC 9

QY 2316 TCGTGATC 2323
|||
Db 8 TCGTGATC 1

RESULT 110
ID ABZ09289
XX ABZ09289 standard; DNA; 68 BP.
XX ABZ09289;
AC ABZ09289;
DT 16-JAN-2003 (first entry)
XX Human oligonucleotide SEQ ID 449.
DE Human; tumour suppressor; virucide; cytostatic; nootropic;
KW neuroprotective; neuroleptic; gene therapy; tumour suppression;

Query Match 2.4%; Score 56.8; DB 1; Length 68;
Best Local Similarity 85.3%; Pred. No. 48;
Matches 58; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2256 GTACTTTTAGTAGACAGAGGGTTTCACCGTTAGCCAGGATGCTTCGATCTCCTGACC 2315
|||
Db 1 GTATTTTATAGAGGTGGGTTTCACCRGTGGTCAGGCTGGTCTCGAACTCTGACC 60

QY 2316 TCGTGATC 2323
|||
Db 61 TYGTGATC 68

RESULT 111
ID ABZ78742
XX ABZ78742 standard; DNA; 68 BP.
XX ABZ78742;
AC ABZ78742;
DT 24-APR-2003 (first entry)
XX Tumour suppression-related sequence, SEQ ID 449.
DE Cytostatic; virucide; apoptotic; gene therapy; tumour suppression;
KW tumour reversion; apoptosis; virus resistance; viral infection; tumour;

Query Match 2.4%; Score 56.8; DB 1; Length 68;
Best Local Similarity 85.3%; Pred. No. 48;
Matches 58; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2256 GTACTTTTAGTAGACAGAGGGTTTCACCGTTAGCCAGGATGCTTCGATCTCCTGACC 2315
|||
Db 1 GTATTTTATAGAGGTGGGTTTCACCRGTGGTCAGGCTGGTCTCGAACTCTGACC 60

QY 2316 TCGTGATC 2323
|||
Db 61 TYGTGATC 68

RESULT 112
ID AAS57672
XX AAS57672 standard; cDNA; 69 BP.
XX AAS57672;
AC AAS57672;
DT 13-FEB-2002 (first entry)
XX cDNA #348 encoding portion of a human colon tumour protein.
DE Human; colon tumour protein; colon cancer; gene therapy; cytostatic; ss.

Query Match 2.4%; Score 56.2; DB 1; Length 69;
Best Local Similarity 88.4%; Pred. No. 52;
Matches 61; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2291 CCAGGATGGTCTCGATCTCGTACCTCGATCGGCCACCTCGGCTCCCAAGTCTG 2350
|||
Db 1 CCAGCGCGGTCTCGAACTCCAGACCTCATGATCCCGGCTGGCTCCCAAGTCTG 60

QY 2351 GGATTACAG 2359
|||
Db 61 GGATTACAG 69

RESULT 113
ID AAC12925
XX AAC12925 standard; cDNA; 65 BP.
XX AAC12925;
AC AAC12925;
DT 06-OCT-2000 (first entry)
XX Human secreted protein 5' EST, SEQ ID NO: 17000.
DE Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
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KW gene therapy; chromosome mapping; ss.
Query Match 2.3%; Score 54.4; DB 1; Length 65;
Best Local Similarity 90.6%; Pred. No. 62;
Matches 58; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2270 GACAGGGTTTACCGTGTAGCCAGGATGTCGATCTCTGACCTCGTGATCCGCCCA 2329
    |||||
Db 1 GACGGGGTTTCTCGTGTAGCCAGGATGTCGATCTCTGACCTTGTAAATCCGCCCA 60

QY 2330 CCTC 2333
    |||
Db 61 CCGC 64

RESULT 114
ABZ09729/c
ID ABZ09729 standard; DNA; 60 BP.
XX
AC ABZ09729;
XX
DT 16-JAN-2003 (first entry)
DE Human oligonucleotide SEQ ID 889.
XX
KW Human; tumour suppressor; virucide; cytostatic; nootropic;
KW neuroprotective; neuroleptic; gene therapy; tumour suppression;
Query Match 2.2%; Score 52; DB 1; Length 60;
Best Local Similarity 91.7%; Pred. No. 79;
Matches 55; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2264 AGTAGAGATGGGGTTTCACTGTGTAGCCAGGATGTCCTCACTCTCTGACCTCGTGATC 1
    |||||
Db 60 AGTAGAGATGGGGTTTCACTGTGTAGCCAGGATGTCCTCACTCTCTGACCTCGTGATC 1

RESULT 115
ABZ79182/c
ID ABZ79182 standard; DNA; 60 BP.
XX
AC ABZ79182;
XX
DT 24-APR-2003 (first entry)
DE Tumour suppression-related sequence, SEQ ID 889.
XX
KW Cytostatic; virucide; apoptotic; gene therapy; tumour suppression;
KW tumour reversion; apoptosis; virus resistance; viral infection; tumour;
Query Match 2.2%; Score 52; DB 1; Length 60;
Best Local Similarity 91.7%; Pred. No. 79;
Matches 55; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2264 AGTAGAGATGGGGTTTCACTGTGTAGCCAGGATGTCCTGATCTCTGACCTCGTGATC 2323
    |||||
Db 60 AGTAGAGATGGGGTTTCACTGTGTAGCCAGGATGTCCTGATCTCTGACCTCGTGATC 1

RESULT 116
ADI12543/c
ID ADI12543 standard; DNA; 60 BP.
XX
AC ADI12543;
XX
DT 22-APR-2004 (first entry)
DE Mutant human BRCA1 genomic DNA resulting from deletion 3 SeqID 26.
XX
KW ds; cancer; human; tumour suppressor;
KW breast cancer susceptibility gene 1; BRCA1; repetitive Alu;
Query Match 2.2%; Score 52; DB 1; Length 60;

Best Local Similarity 91.7%; Pred. No. 79;
Matches 55; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2308 TCTGTACCTCGTGATCCGCCACCTCGGCTCCCAAAGTGTGGGATTACAGGCATCAGC 2367
    |||||
Db 60 TCTGTACCTTGTGATCTGCCCGCTCCCAAAGTGTGGGATTACAGGCGTAAGC 1

RESULT 117
AAK91064
ID AAK91064 standard; DNA; 66 BP.
XX
AC AAK91064;
XX
DT 05-NOV-2001 (first entry)
DE Human digestive system antigen genomic sequence SEQ ID NO: 4640.
XX
KW Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
Query Match 2.2%; Score 51.6; DB 1; Length 66;
Best Local Similarity 86.4%; Pred. No. 86;
Matches 57; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2251 TTTTGTACTTTTAGTAGAGACAGGGTTTTCACCGTGTAGCCAGGATGGTCTCGATCTCC 2310
    |||||
Db 1 TTTTGTATTTTAGTAGAGACGGGGTTTTCACCATATTGACCAGGCTGGTCTCAAACTCC 60

QY 2311 TGACCT 2316
    |||||
Db 61 TGACCT 66

RESULT 118
AAS32099
ID AAS32099 standard; DNA; 66 BP.
XX
AC AAS32099;
XX
DT 04-DEC-2001 (first entry)
DE Human liver associated genomic DNA #273.
XX
KW Liver associated protein; human; mouse; rabbit; goat; horse; cat; dog;
KW chicken; sheep; immunosuppressive; antiarthritic; vasotropic;
Query Match 2.2%; Score 51.6; DB 1; Length 66;
Best Local Similarity 86.4%; Pred. No. 86;
Matches 57; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2251 TTTTGTACTTTTAGTAGAGACAGGGTTTTCACCGTGTAGCCAGGATGGTCTCGATCTCC 2310
    |||||
Db 1 TTTTGTATTTTAGTAGAGACGGGGTTTTCACCATATTGACCAGGCTGGTCTCAAACTCC 60

QY 2311 TGACCT 2316
    |||||
Db 61 TGACCT 66

RESULT 119
ABN90454
ID ABN90454 standard; DNA; 66 BP.
XX
AC ABN90454;
XX
DT 24-JUL-2002 (first entry)
DE Human liver antigen HLD4V38 genomic sequence, SEQ ID NO:575.
XX
KW Human; liver antigen; liver disorder; hepatic disorder; infection;
KW hepatitis; viral; parasitic; bacterial; fungal; inflammatory condition;
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Query Match      2.2%; Score 51.6; DB 1; Length 66;
Best Local Similarity 86.4%; Pred. No. 86;
Matches 57; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2251 TTTTGTACTTTTAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCC 2310
      |||||
Db 1 TTTTGTATTTTAGTAGAGACAGGGTTTCACCATATTGACCAAGCTGGTCTCAAACTCC 60

QY 2311 TGACCT 2316
      |||||
Db 61 TGACCT 66

RESULT 120
ADJ15367
ID ADJ15367 standard; DNA; 66 BP.
XX
AC ADJ15367;
DT 20-MAY-2004 (first entry)
DE Human liver-related genomic DNA - SEQ ID 575.
XX
KW liver; virucide; fungicide; antibacterial; antiparasitic; hepatotropic;
antiinflammatory; cytostatic; litholytic; antirheumatic; antiarthritic;

Query Match      2.2%; Score 51.6; DB 1; Length 66;
Best Local Similarity 86.4%; Pred. No. 86;
Matches 57; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2251 TTTTGTACTTTTAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCC 2310
      |||||
Db 1 TTTTGTATTTTAGTAGAGACAGGGTTTCACCATATTGACCAAGCTGGTCTCAAACTCC 60

QY 2311 TGACCT 2316
      |||||
Db 61 TGACCT 66

RESULT 121
AAC11032/c
ID AAC11032 standard; cDNA; 68 BP.
XX
AC AAC11032;
DT 06-OCT-2000 (first entry)
DE Human secreted protein 5' EST, SEQ ID NO: 15107.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
gene therapy; chromosome mapping; ss.

Query Match      2.2%; Score 51; DB 1; Length 68;
Best Local Similarity 85.1%; Pred. No. 93;
Matches 57; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2251 TTTTGTACTTTTAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCC 2310
      |||||
Db 67 TTTTGTATTTTAGTAGAGACAGGGTTTCACCATATTGTCACAGGCTGGTCTCGAACTCC 8

QY 2311 TGACCTC 2317
      |||||
Db 7 TGACCCC 1

RESULT 122
AAC15723
ID AAC15723 standard; cDNA; 64 BP.
XX
AC AAC15723;
DT 06-OCT-2000 (first entry)
DE
XX
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DE Human secreted protein 5' EST, SEQ ID NO: 19798.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
gene therapy; chromosome mapping; ss.

Query Match      2.1%; Score 50.2; DB 1; Length 64;
Best Local Similarity 87.3%; Pred. No. 99;
Matches 55; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2255 TGTACTTTTAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCCGAC 2314
      |||||
Db 2 TGTATTTTAGTAGAGACAGGGTTTCGCCATGTTGTCGGGCTGGTCTCGAACTCTCTGAC 61

QY 2315 CTC 2317
      |||
Db 62 CTC 64

RESULT 123
ABZ04758
ID ABZ04758 standard; DNA; 50 BP.
XX
AC ABZ04758;
DT 09-JAN-2003 (first entry)
DE Human leukocyte gene expression profiling probe SEQ ID NO 4749.
XX
KW T7; leukocyte; gene expression profiling; allograft rejection;
atherosclerosis; congestive heart failure; systemic lupus erythematosus;

Query Match      2.1%; Score 50; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1747 GACAACCAATTCAAATGATTGTGCTAACTATTATTTCCCTAGTTGACCTGT 1796
      |||||
Db 1 GACAACCAATTCAAATGATTGTGCTAACTATTATTTCCCTAGTTGACCTGT 50

RESULT 124
ADP10274
ID ADP10274 standard; DNA; 50 BP.
XX
AC ADP10274;
DT 12-AUG-2004 (first entry)
DE 50-mer oligonucleotide marker probe of the invention #283.
XX
KW transplant rejection; immune system; rheumatoid arthritis; lupus;
inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.

Query Match      2.1%; Score 50; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1747 GACAACCAATTCAAATGATTGTGCTAACTATTATTTCCCTAGTTGACCTGT 1796
      |||||
Db 1 GACAACCAATTCAAATGATTGTGCTAACTATTATTTCCCTAGTTGACCTGT 50

RESULT 125
AAI69056
ID AAI69056 standard; DNA; 63 BP.
XX
AC AAI69056;
DT 29-JAN-2002 (first entry)
DE Activated T-cell derived DNA fragment #192.
XX
KW Activated T-cell; immunosuppressive; immunostimulant; antiinflammatory;
```

KW cytostatic; gene therapy; vaccine; allergen; transplamt rejection;
Query Match 2.1%; Score 50; DB 1; Length 63;
Best Local Similarity 91.4%; Pred. No. 1e+02;
Matches 53; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2250 TTTTTCGATCTTTAGTAGAGACAGGGTTTACCGTGTAGCCAGGATGCTCTCGATC 2307
|||||
DB 6 TTTTTCGAATTTTAGTAGATACGGGGTTTACCGTGTAGCCCTGGATGCTCTCGATC 63
|||||
RESULT 126
AAJ32116/c
ID AAL32116 standard; DNA; 51 BP.
XX
AC AAL32116;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #5324.
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
Query Match 2.1%; Score 49.4; DB 1; Length 51;
Best Local Similarity 98.0%; Pred. No. 99;
Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2292 CAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTCCCA 2342
|||||
DB 51 CAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTCCCA 1
|||||
RESULT 127
AAJ77488
ID AAA77488 standard; cDNA; 51 BP.
XX
AC AAA77488;
XX
DT 16-NOV-2000 (first entry)
XX
DE Human Alu subfamily SB gene polymorphic site, SEQ ID NO:1171.
KW Human; single nucleotide polymorphism; SNP; detection; identification;
KW gene therapy; ss.
Query Match 2.0%; Score 48.4; DB 1; Length 51;
Best Local Similarity 98.0%; Pred. No. 1.1e+02;
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2301 CTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTCCCAAAGTCTG 2350
|||||
DB 2 CTCGATCTCTGACCTCGTGATCCGCCACCTTGGCTCTCCCAAAGTCTG 51
|||||
RESULT 128
AAJ77877
ID AAI77877 standard; DNA; 51 BP.
XX
AC AAI77877;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:4818.
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 2.0%; Score 47.8; DB 1; Length 51;
Best Local Similarity 96.1%; Pred. No. 1.2e+02;
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2292 CAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTCCCA 2342
|||||

|||||
DB 1 CAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCCTCAGCCTCCCA 51
|||||
RESULT 129
AAJ79838/c
ID AAI79838 standard; DNA; 51 BP.
XX
AC AAI79838;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human nonconservative amino acid changing SNP nucleic acid SEQ:6779.
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 2.0%; Score 47.8; DB 1; Length 51;
Best Local Similarity 96.1%; Pred. No. 1.2e+02;
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2318 GTGATCCGCCACCTCGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCC 2368
|||||
DB 51 GTGATCCGCCACCTCGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCC 1
|||||
RESULT 130
AAJ79700/c
ID AAI79700 standard; DNA; 51 BP.
XX
AC AAI79700;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human conservative amino acid changing SNP nucleic acid SEQ:6641.
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 2.0%; Score 47.8; DB 1; Length 51;
Best Local Similarity 96.1%; Pred. No. 1.2e+02;
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2319 TGATCCGCCACCTCGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCC 2369
|||||
DB 51 TGATCCGCCACCTCGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCC 1
|||||
RESULT 131
AAH89466/c
ID AAH89466 standard; DNA; 51 BP.
XX
AC AAH89466;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 247.
KW Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.
Query Match 2.0%; Score 47.8; DB 1; Length 51;
Best Local Similarity 96.1%; Pred. No. 1.2e+02;
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2300 TCTGATCTCTGACCTCGTGATCCGCCACCTCGGCCTCCCAAAGTCTG 2350
|||||
DB 51 TCTGATCTCTGACCTCGTGATCCGCCACCTCGGCCTCCCAAAGTCTG 1
|||||
RESULT 132
AAK86585
ID AAK86585 standard; DNA; 63 BP.
|||||

```
XX AAK86585;
AC
XX 07-NOV-2001 (first entry)
DT
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41397.
DE
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match      2.0%; Score 47.6; DB 1; Length 63;
Best Local Similarity 85.5%; Pred. No. 1.3e+02;
Matches 53; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2256 GTACTTTTAGTAGACAGAGGGTTTCACCGTGTAGCCAGGATGTCGATCTCCTGACC 2315
Db 1 GTATTTTATAGTAGAGATGGTGTTCACCCCTGTTGGTCAGGCTGCTCGAAGTCTCCTGACC 60

QY 2316 TC 2317
Db 61 TC 62

RESULT 133
AAK85681/c
ID AAK85681 standard; DNA; 63 BP.
XX
AC AAK85681;
XX
XX 07-NOV-2001 (first entry)
DT
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40493.
DE
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match      2.0%; Score 47.6; DB 1; Length 63;
Best Local Similarity 85.5%; Pred. No. 1.3e+02;
Matches 53; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2256 GTACTTTTAGTAGACAGAGGGTTTCACCGTGTAGCCAGGATGTCGATCTCCTGACC 2315
Db 63 GTATTTTATAGTAGAGATGGTGTTCACCCCTGTTGGTCAGGCTGCTCGAAGTCTCCTGACC 4

QY 2316 TC 2317
Db 3 TC 2

RESULT 134
ABZ09432
ID ABZ09432 standard; DNA; 52 BP.
XX
AC ABZ09432;
XX
XX 16-JAN-2003 (first entry)
DT
XX Human oligonucleotide SEQ ID 592.
DE
XX Human; tumour suppressor; virucide; cytostatic; neutropic;
KW neuroprotective; neuroleptic; gene therapy; tumour suppression;

Query Match      2.0%; Score 47.2; DB 1; Length 52;
Best Local Similarity 94.2%; Pred. No. 1.3e+02;
Matches 49; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2256 GTACTTTTAGTAGACAGAGGGTTTCACCGTGTAGCCAGGATGTCGATCTCCTGATC 2307
Db 1 GCATTTTATAGTAGACAGAGGGTTTCACCATGTTAGCCAGGATGGTCTCGATC 52

RESULT 135
ABZ78885
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ID ABZ78885 standard; DNA; 52 BP.
XX
AC ABZ78885;
XX
XX 24-APR-2003 (first entry)
DT
XX Tumour suppression-related sequence, SEQ ID 592.
DE
XX Cytostatic; virucide; apoptotic; gene therapy; tumour suppression;
KW tumour reversion; apoptosis; virus resistance; viral infection; tumour;

Query Match      2.0%; Score 47.2; DB 1; Length 52;
Best Local Similarity 94.2%; Pred. No. 1.3e+02;
Matches 49; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2256 GTACTTTTAGTAGACAGAGGGTTTCACCGTGTAGCCAGGATGTCGATCTCCTGATC 2307
Db 1 GCATTTTATAGTAGACAGAGGGTTTCACCATGTTAGCCAGGATGGTCTCGATC 52

RESULT 136
AAZ69526
ID AAZ69526 standard; DNA; 47 BP.
XX
AC AAZ69526;
XX
XX 10-SEP-2001 (first entry)
DT
XX Human map-related biallelic marker SEQ ID NO:3882.
DE
XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;

Query Match      2.0%; Score 47; DB 1; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2271 ACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTC 2317
Db 1 ACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTC 47

RESULT 137
AAA77489
ID AAA77489 standard; cDNA; 51 BP.
XX
AC AAA77489;
XX
XX 16-NOV-2000 (first entry)
DT
XX Human Alu subfamily SB gene polymorphic site, SEQ ID NO:1172.
DE
XX Human; single nucleotide polymorphism; SNP; detection; identification;
KW gene therapy; ss.

Query Match      2.0%; Score 46.8; DB 1; Length 51;
Best Local Similarity 96.0%; Pred. No. 1.3e+02;
Matches 48; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2301 CTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCCTCCCAAAGTGTG 2350
Db 2 CTCGATCTCTGACCTCGTGATCCACCACCTTGGCTCCCAAAGTGTG 51

RESULT 138
ABK45620/c
ID ABK45620 standard; cDNA; 59 BP.
XX
AC ABK45620;
XX
XX 05-JUN-2002 (first entry)
DT
XX cDNA encoding colon tumour protein, SEQ ID NO 1171.
DE
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AAH40328/c
ID AAH40328 standard; DNA; 51 BP.
XX
AC AAH40328;
XX
DT 14-AUG-2001 (first entry)
XX
DE Human SNP flanking oligonucleotide SEQ ID 3124.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 1.9%; Score 46.2; DB 1; Length 51;
Best Local Similarity 94.1%; Pred. No. 1.4e+02;
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2304 GATCTCTGACCTCGTGATCCGCCACCTCGGCTCCCAAAGTGTGGAT 2354
DB 51 GATCTCTGACCTCGTGATCCGCCACCTCGGCTCCCAAAGTGTGGAT 1

RESULT 146
ABL00161
ID ABL00161 standard; DNA; 51 BP.
XX
AC ABL00161;
XX
DT 05-MAR-2002 (first entry)
XX
DE Human silent noncoding SNP oligonucleotide SEQ ID NO:152.
XX
KW Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
KW immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;

Query Match 1.9%; Score 46.2; DB 1; Length 51;
Best Local Similarity 94.1%; Pred. No. 1.4e+02;
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2258 ACTTTAGTAGACAGGGTTTACCGTGTGTAGCCAGATGGTCTCGATCT 2308
DB 1 ATTTTGTAGAGACGGGTTTCACTGTGTGTAGCCAGATGGTCTCGATCT 51

RESULT 147
AAH38992
ID AAH38992 standard; DNA; 51 BP.
XX
AC AAH38992;
XX
DT 14-AUG-2001 (first entry)
XX
DE Human SNP flanking oligonucleotide SEQ ID 1788.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 1.9%; Score 45.8; DB 1; Length 51;
Best Local Similarity 92.2%; Pred. No. 1.5e+02;
Matches 47; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2300 TCTGATCTCTGACCTGTGATCCGCCACCTCGGCTCCCAAAGTGTG 2350
DB 1 TCTGATCTCTGACCTGTGATCCGCCACCTCGGCTCCCAAAGTGTG 51

RESULT 148
AAC29627/c
ID AAC29627 standard; cDNA; 57 BP.
XX
AC AAC29627;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 33702.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.

Query Match 1.9%; Score 45.8; DB 1; Length 57;
Best Local Similarity 87.7%; Pred. No. 1.6e+02;
Matches 50; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2252 TTTTGTACTTTTAGTAGACAGGGTTTACCGTGTGTAGCCAGATGGTCTCGATCT 2308
DB 57 TTTTGTACTTTTAGTAGACAGGGTTTACCGTGTGTAGCCAGATGGTCTCGACT 1

RESULT 149
AAK83961/c
ID AAK83961 standard; DNA; 57 BP.
XX
AC AAK83961;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38773.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match 1.9%; Score 45.6; DB 1; Length 57;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 48; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2320 GATCCGCCACCTCGGCTCCCAAAGTGTGGATTACAGGCATGAGCCACC 2371
DB 57 GATCTGCTCCTCAGCCTCCCAAAGTGTGGATTACAGGCATGAGCCACC 6

RESULT 150
AAI77324
ID AAI77324 standard; DNA; 51 BP.
XX
AC AAI77324;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:4265.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match 1.9%; Score 45.2; DB 1; Length 51;
Best Local Similarity 94.0%; Pred. No. 1.6e+02;
Matches 47; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2323 CCGCCACCTCGGCTCCCAAAGTGTGGATTACAGGCATGAGCCACC 2372
DB 1 CTTCCGCTCCTCGGCTCCCAAAGTGTGGATTACAGGCATGAGCCACC 50

RESULT 151
AAI79589
ID AAI79589 standard; DNA; 51 BP.
XX
AC AAI79589;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:6530.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match 1.9%; Score 45.2; DB 1; Length 51;
Best Local Similarity 94.0%; Pred. No. 1.6e+02;

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XX Human Alueubfamily SQ gene polymorphic site, SEQ ID NO:1125.
DE
XX
XX Human; single nucleotide polymorphism; SNP; detection; identification;
KW gene therapy; ss.

Query Match      1.8%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 2e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2252 TTTTGTACTTTTAGTAGACAGCGGTTTCACCGTGTAGCCAGGATGGTCT 2302
DB 1 TTTTGTATTTTAGTAGACAGCGGTTTCACCATGTTGGCCAGGCTGGTCT 51

RESULT 159
AAI76988/c
ID AAI76988 standard; cDNA; 51 BP.
XX
AC AAI76988;
XX
DT 16-NOV-2000 (first entry)
XX
DE Human clone cg42924993 polymorphic site, SEQ ID NO:671.
XX
KW Human; single nucleotide polymorphism; SNP; detection; identification;
KW gene therapy; ss.

Query Match      1.8%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 2e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2252 TTTTGTACTTTTAGTAGACAGCGGTTTCACCGTGTAGCCAGGATGGTCT 2302
DB 51 TTTTGTATTTTAGTAGACAGCGGTTTCACCATGTTGGCCAGGCTGGTCT 1

RESULT 160
AAI76185/c
ID AAI76185 standard; DNA; 51 BP.
XX
AC AAI76185;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:3126.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.8%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 2e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2255 TGTACTTTTAGTAGACAGCGGTTTCACCGTGTAGCCAGGATGGTCTCGA 2305
DB 51 TGTATTTTAGTAGACAGCGGTTTCACCATGTTGGCCAGGCTGGTCTCGA 1

RESULT 161
AAI76192/c
ID AAI76192 standard; DNA; 51 BP.
XX
AC AAI76192;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:3133.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.8%; Score 43; DB 1; Length 51;
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Best Local Similarity 90.2%; Pred. No. 2e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2262 TTAGTAGACAGCGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCTG 2312
DB 51 TTAGTAGACAGCGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCTG 1

RESULT 162
AAI79867/c
ID AAI79867 standard; DNA; 51 BP.
XX
AC AAI79867;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human nonconservative amino acid changing SNP nucleic acid SEQ:6808.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.8%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 2e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2264 AGTAGACAGCGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCTGAC 2314
DB 51 AGTAGACAGCGGCTTCACCGTGTAGCCAGGATGGTCTCAAACTCTCTGAC 1

RESULT 163
AAI79689
ID AAI79689 standard; DNA; 51 BP.
XX
AC AAI79689;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human conservative amino acid changing SNP nucleic acid SEQ:6630.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.8%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 2e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2300 TCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCTCCCAAAGTCTG 2350
DB 1 TCTGAACTCTCTGACCTCAAGATCCGCTCGGCTCCCAAAGTCTG 51

RESULT 164
AAH90176/c
ID AAH90176 standard; cDNA; 51 BP.
XX
AC AAH90176;
XX
DT 08-OCT-2001 (first entry)
XX
DE Human clone cg42869755 SNP site, SEQ ID NO:56.
XX
KW Human; single nucleotide polymorphism; SNP; chromosome 1; detection;
KW identification; gene therapy; genetic disorder; ss.

Query Match      1.8%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 2e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2308 TCTGACCTCGTGATCCGCCACCTCGGCTCCCAAAGTCTGGGATTACA 2358
DB 51 TACTGACCTCGTGATCCACCTGCCAGGCTCCCAAAGTCTGGGATTACA 1
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RESULT 165
AAH89484/c
ID AAH89484 standard; DNA; 51 BP.
XX
AC AAH89484;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 265.
XX
KW Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.

Query Match 1.8%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 2e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2261 TTTAGTAGACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCCT 2311
Db 51 TTTAGTAGACAGGGTTTACCATGTTGCCAGGCTGGTCTCAAACTCCT 1

RESULT 166
AAH89506
ID AAH89506 standard; DNA; 51 BP.
XX
AC AAH89506;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 287.
XX
KW Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.

Query Match 1.8%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 2e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2264 AGTAGACACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCCTGAC 2314
Db 1 AGTAGACACAGGGTTTACCATGTTAGCCAGGCTGGTCTCAAACTCCTGAC 51

RESULT 167
AAH89303
ID AAH89303 standard; DNA; 51 BP.
XX
AC AAH89303;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 84.
XX
KW Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.

Query Match 1.8%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 2e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2252 TTTTGTACTTTTAGTAGACAGGGTTTACCGTGTAGCCAGGATGGTCT 2302
Db 1 TTTTGTATTTTAGTAGACAGGGGCTTCCGTGTATTCAGATGGTCT 51

RESULT 168
ADK19860
ID ADK19860 standard; DNA; 51 BP.
XX
AC ADK19860;
XX

DT 06-MAY-2004 (first entry)
XX
DE Human mannosyl transferase-related SNP region DNA SeqID62.
XX
KW human; mannosyl transferase; antimanic; antidepressant; gene therapy;
KW fusion protein; chromosome 9 fusion protein; chromosome 11 translocation;

Query Match 1.8%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 2e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2089 TTATTTTGTGAGACCGAGTCTTGCTCTGTACCCAGGCTGGAGTGCAGT 2139
Db 1 TTTTGTATTTTGAGACAGAGTCTTATCTGTGCTCCAGGCTGGAGTGCAGT 51

RESULT 169
AAK65537
ID AAK65537 standard; DNA; 49 BP.
XX
AC AAK65537;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20349.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.

Query Match 1.8%; Score 42.6; DB 1; Length 49;
Best Local Similarity 91.8%; Pred. No. 2.1e+02;
Matches 45; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2267 AGAGACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCCTGACC 2315
Db 1 AGAGACGGGGTTTACCATTTTATAGCCAGGATGGTCTCGATATCTCCTGACC 49

RESULT 170
AAI62905/c
ID AAI62905 standard; DNA; 49 BP.
XX
AC AAI62905;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human genomic DNA SEQ ID NO 233.
XX
KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnetary;

Query Match 1.8%; Score 42.6; DB 1; Length 49;
Best Local Similarity 91.8%; Pred. No. 2.1e+02;
Matches 45; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2267 AGAGACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCCTGACC 2315
Db 49 AGAGACGGGGTTTACCATTTTATAGCCAGGATGGTCTCGATATCTCCTGACC 1

RESULT 171
AAI79513
ID AAI79513 standard; DNA; 51 BP.
XX
AC AAI79513;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:6454.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

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Query Match      1.8%; Score 42.2; DB 1; Length 51;
Best Local Similarity 93.6%; Pred. No. 2.2e+02;
Matches 44; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2271 ACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTC 2317
    |||||
Db 1 ACAGGGTTTACCGTGTAGCCAGGATGGTCTTGAACCTCTCTGACCTC 47

RESULT 172
ADG84273/c
ID ADG84273 standard; DNA; 50 BP.
XX
AC ADG84273;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human TMD0621 promoter DNA sequence SeqID211.
XX
KW tissue specific gene; tissue specific gene cluster;
KW lq22 immune gene complex; bone marrow specific gene;

Query Match      1.8%; Score 42; DB 1; Length 50;
Best Local Similarity 90.0%; Pred. No. 2.3e+02;
Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2319 TGATCCGCCACCTCGGCTCCCAAAGTGTGGGATTACAGGATGAGCC 2368
    |||||
Db 50 TGATCCACCTCGCTCGGCTCCCAAAGTGTGGGATTATAGCGGTGAGCC 1

RESULT 173
AAI75515
ID AAI75515 standard; DNA; 51 BP.
XX
AC AAI75515;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:2456.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.8%; Score 42; DB 1; Length 51;
Best Local Similarity 90.0%; Pred. No. 2.3e+02;
Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2268 GAGACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTC 2317
    |||||
Db 1 GAGACAGGGTTTACCATGTTGACACAGCTGGTCTCGAAGTCTCTGACCTC 50

RESULT 174
AAI73069/c
ID AAI73069 standard; DNA; 51 BP.
XX
AC AAI73069;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:10.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.8%; Score 42; DB 1; Length 51;
Best Local Similarity 90.0%; Pred. No. 2.3e+02;
Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2089 TTAATTTTTTGGACACGAGTCTGTCTGTATACCGAGGTGGAGTGCAG 2138
    |||||
Db 50 TTAATTTTTTGGACACGAGTCTGTCTGTATACCGAGGTGGAGTGCAG 1
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RESULT 175
AAI79770
ID AAI79770 standard; DNA; 51 BP.
XX
AC AAI79770;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human nonconservative amino acid changing SNP nucleic acid SEQ:6711.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.8%; Score 42; DB 1; Length 51;
Best Local Similarity 90.0%; Pred. No. 2.3e+02;
Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2246 CTAATTTTTTGTACTTTTAGTAGACAGCGGTTTCACCGTGTAGCCAGG 2295
    |||||
Db 1 CTAATTTTTTGTATTTTAGTAGACAGCGGGTTTCGCCATGTGTGCCCAGG 50

RESULT 176
AAI79646/c
ID AAI79646 standard; DNA; 51 BP.
XX
AC AAI79646;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:6587.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.8%; Score 41.6; DB 1; Length 51;
Best Local Similarity 91.7%; Pred. No. 2.4e+02;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2241 CCTGGCTAATTTTGTACTTTTAGTAGACAGCGGTTTCACCGTGT 2288
    |||||
Db 48 CCTGGCTAATTTTATATTTTAGTAGACAGCGGGTTTCACCAIGTT 1

RESULT 177
AAI73533/c
ID AAI73533 standard; DNA; 51 BP.
XX
AC AAI73533;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:474.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.8%; Score 41.6; DB 1; Length 51;
Best Local Similarity 91.7%; Pred. No. 2.4e+02;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2324 CGCCACCTCGGCTCCCAAAGTGTGGGATTACAGGATGAGCCACC 2371
    |||||
Db 51 CGCCCGCTCGGCTCCCAAAGTGTGGGATTACAGGCTTGAGTCACC 4

RESULT 178
AAC22417
ID AAC22417 standard; cDNA; 52 BP.
XX
AC AAC22417;
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```
XX 06-OCT-2000 (first entry)
XX Human secreted protein 5' EST, SEQ ID NO: 26492.
DE Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
KW

Query Match      1.8%; Score 41.6; DB 1; Length 52;
Best Local Similarity 86.5%; Pred. No. 2.4e+02;
Matches 45; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2255 TGTACTTTTGTAGACAGCGGTTTCACCGTGTAGCCAGGATGGTCTCGAT 2306
Db 1 TGTATTTTGBAGACAGCGGTTTCGCCATGTTGGCCAGGATGGTCTCGAT 52

RESULT 179
AAI77443
ID AAA77443 standard; cDNA; 51 BP.
XX
AC AAA77443;
XX
DT 16-NOV-2000 (first entry)
XX Human Alusubfamily SQ gene polymorphic site, SEQ ID NO:1126.
DE
DE Human; single nucleotide polymorphism; SNP; detection; identification;
KW gene therapy; ss.
KW

Query Match      1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2252 TTTTGTACTTTTGTAGACAGCGGTTTCACCGTGTAGCCAGGATGGTCT 2302
Db 1 TTTTGTATTTTGTAGACAGCGGCTTCACCATGTTGGCCAGGCTGGTCT 51

RESULT 180
AAI76989/c
ID AAA76989 standard; cDNA; 51 BP.
XX
AC AAA76989;
XX
DT 16-NOV-2000 (first entry)
XX Human clone cg42924993 polymorphic site, SEQ ID NO:672.
DE
DE Human; single nucleotide polymorphism; SNP; detection; identification;
KW gene therapy; ss.
KW

Query Match      1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2252 TTTTGTACTTTTGTAGACAGCGGTTTCACCGTGTAGCCAGGATGGTCT 2302
Db 51 TTTTGTATTTTGTAGACAGCGGCTTCACCATGTTGGCCAGGCTGGTCT 1

RESULT 181
AAI77230
ID AAA77230 standard; cDNA; 51 BP.
XX
AC AAA77230;
XX
DT 16-NOV-2000 (first entry)
XX Human clone cg43972482 polymorphic site, SEQ ID NO:913.
DE
DE Human; single nucleotide polymorphism; SNP; chromosome 8; detection;
KW identification; gene therapy; ss.
KW
```

```
Query Match      1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2262 TTAGTAGACAGCGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCCTG 2312
Db 1 TTAGTAGACAGCGGTTTCACCATGTTGGTCAGGCTGGTCTCGAATCCTG 51

RESULT 182
AAI73071/c
ID AAI73071 standard; DNA; 51 BP.
XX
AC AAI73071;
XX
DT 09-NOV-2001 (first entry)
XX Human silent SNP containing nucleic acid SEQ:12.
DE
DE Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW

Query Match      1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2087 TATTATTTTGTAGACCGAGTCTTGTCTGTACCCAGGCTGGAGTGCA 2137
Db 51 TTTTCTTTTGTAGACAGAGTCTTACTCTGTGCCCGGCTGGAGTGCA 1

RESULT 183
AAI76193/c
ID AAI76193 standard; DNA; 51 BP.
XX
AC AAI76193;
XX
DT 09-NOV-2001 (first entry)
XX Human silent SNP containing nucleic acid SEQ:3134.
DE
DE Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW

Query Match      1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2262 TTAGTAGACAGCGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCCTG 2312
Db 51 TTAGTAGACAGCGGTTTCACCATGCTGCCAGGCTGGTCTCGAATCCTG 1

RESULT 184
AAI79866/c
ID AAI79866 standard; DNA; 51 BP.
XX
AC AAI79866;
XX
DT 09-NOV-2001 (first entry)
XX Human nonconservative amino acid changing SNP nucleic acid SEQ:6807.
DE
DE Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW

Query Match      1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2264 AGTAGACAGCGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCCTGAC 2314
Db 1 AGTAGACAGCGGTTTCACCATGTTGGTCAGGCTGGTCTCGAATCCTG 51
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Db 51 ACTAGAGACGGGCTTACCGTGTGCTGGCCAGGATGGTCTCAAACTCCTGAC 1

RESULT 185
AAI74978/c
ID AAI74978 standard; DNA; 51 BP.
XX
XX
AC AAI74978;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:1919.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2262 TTAGTAGACAGAGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCCTG 2312
Db 51 TTAGTAGACAGAGGTTTTCATCATGTTGGCCAGGCTGCTTGAACCTCCTG 1

RESULT 186
AAI74450/c
ID AAI74450 standard; DNA; 51 BP.
XX
XX
AC AAI74450;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:1391.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2320 GATCGCCCACTCGGCTCCCAAAGTGTGGGATTACAGGCATGAGCCAC 2370
Db 51 GATCCTCTGCTAGCCTCCCAAAGTGTGGGATTACAGGCATGAGCCAC 1

RESULT 187
AAI75457/c
ID AAI75457 standard; DNA; 51 BP.
XX
XX
AC AAI75457;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:2398.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2292 CAGGATGCTCTCGATCTCTCGATCTCGATCCGCCACCTCGGCTCCCA 2342
Db 51 CAGGCTGTCTCAAACTCTCATCTGTCATCCGCCGCCCTCGGCTCCCA 1

RESULT 188
AAI76650/c
ID AAI76650 standard; DNA; 51 BP.
XX
XX
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AC AAI76650;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:3591.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2225 GTCATCTGCCACACACACCTGGCTAAATTTTGTACTTTTAGTAGAGACAGG 2275
Db 51 GGCACCTGCCACCATGCTGGCTAAATTTTGTATTATTTTAGTAGAGACAGG 1

RESULT 189
AAI75653/c
ID AAI75653 standard; DNA; 51 BP.
XX
XX
AC AAI75653;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:2594.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2242 CTGGCTAAATTTTGTACTTTTAGTAGAGACAGGTTTACCGTGTAGCC 2292
Db 51 CTGGCTGATTTTGTATTATTTTAGTAGAGACAGGTTTCCCATGTTGGCC 1

RESULT 190
AAI76184/c
ID AAI76184 standard; DNA; 51 BP.
XX
XX
AC AAI76184;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:3125.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2255 TGTACTTTTAGTAGAGACAGGTTTTCACCGTGTAGCCAGGATGCTCGA 2305
Db 51 TGTATTTTAGTAGAGACAGGTTTACCATGTTGGCCAGGCTGCTCGA 1

RESULT 191
AAI79688
ID AAI79688 standard; DNA; 51 BP.
XX
XX
AC AAI79688;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human conservative amino acid changing SNP nucleic acid SEQ:6629.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
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KW protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2300 TCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCTCCCAAAGTGCTG 2350
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1 TCTCGAACTCTGACCTCAAGATCCACCTGCTCGGCTCCCAAAGTGCTG 51

RESULT 192
AAH90585/c
ID AAH90585 standard; cDNA; 51 BP.
XX
AC AAH90585;
XX
DT 08-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO:465.
XX
KW Human; single nucleotide polymorphism; SNP; detection; identification;
KW gene therapy; genetic disorder; ss.

Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2319 TGATCCGCCACCTCGGCTCCCAAAGTGCTGGATTACAGGATGAGCCA 2369
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 51 TGATCCACTCGCTCGGCTCCCAAAGTGCTGGATTATAGGCGTGAGCCA 1

RESULT 193
AAH90175/c
ID AAH90175 standard; cDNA; 51 BP.
XX
AC AAH90175;
XX
DT 08-OCT-2001 (first entry)
XX
DE Human clone c942869755 SNP site, SEQ ID NO:55.
XX
KW Human; single nucleotide polymorphism; SNP; chromosome 1; detection;
KW identification; gene therapy; genetic disorder; ss.

Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2308 TCTGACCTCGTGATCCGCCACCTCGGCTCCCAAAGTGCTGGATTACA 2358
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 51 TACTGACCTCGTGATCCACTGCGATGCGCTCCCAAAGTGCTGGATTACA 1

RESULT 194
AAH89507
ID AAH89507 standard; DNA; 51 BP.
XX
AC AAH89507;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 288.
XX
KW Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.

Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2264 AGTAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCTGAC 2314
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Db 1 AGTAGACGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCTGAC 51

RESULT 195
AAH89485/c
ID AAH89485 standard; DNA; 51 BP.
XX
AC AAH89485;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 266.
XX
KW Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.

Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2261 TTAGTAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCT 2311
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 51 TTAGTAGACAGGGTTTCACCATATGGCCAGGCTGGTCTCAAACTCTCT 1

RESULT 196
AAH89308/c
ID AAH89308 standard; DNA; 51 BP.
XX
AC AAH89308;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 89.
XX
KW Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.

Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2279 TCACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCGCCCA 2329
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 51 TCATCATGTTGCCAGGATGGTCTGATTTCTGACCTCGTGATCGCCCA 1

RESULT 197
AAH89304
ID AAH89304 standard; DNA; 51 BP.
XX
AC AAH89304;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 85.
XX
KW Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.

Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2245 GCTAATTTTGTACTTTTAGTAGACAGGAGTTTCACCGTGTAGCCAGG 2295
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1 GCTAATTTTGTATTTTATAGAGCGGGATTACCATGTTGCGCAGG 51

RESULT 198
AAH89519/c
ID AAH89519 standard; DNA; 51 BP.
```

```
XX AAB89519;
AC
XX
DT 01-OCT-2001 (first entry)
DE
XX Human coding sequence polymorphic site SEQ ID NO: 300.
XX
XX Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.
KW
Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2318 GTGATCCGCCACCTCGCCCTCCCAAGTGTCTGGATTACAGGATGAGCC 2368
Db 51 GTGATCCATCCGCTTGGCTCCCAAGTGTCTGGATTACAGGCGGGAGCC 1

RESULT 199
ABL00076/c
ID ABL00076 standard; DNA; 51 BP.
XX
XX ABL00076;
AC
XX
DT 05-MAR-2002 (first entry)
DE
XX Human silent noncoding SNP oligonucleotide SEQ ID NO:67.
XX
XX Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
KW immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
KW
Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2218 GCTACACTCATCTGCCACACACCTGGCTAAATTTTGTACTTTTAGTAG 2268
Db 51 GACTACAGGATGGCCACACCGCTGGCTAAATTTTGTATTTTTAGTAG 1

RESULT 200
ADK19850
ID ADK19850 standard; DNA; 51 BP.
XX
XX ADK19850;
AC
XX
DT 06-MAY-2004 (first entry)
DE
XX Human mannosyl transferase-related SNP region DNA SeqID52.
XX
XX human; mannosyl transferase; antimanic; antidepressant; gene therapy;
KW fusion protein; chromosome 9 fusion protein; chromosome 11 translocation;
KW
Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 2.4e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2270 GACAGGGTTTCACCGTTTACCCAGGATGGTCTCGATCTCTGACCTCGTG 2320
Db 1 GACAGGGTTTCACCATGTTGGCCAGCCTGGTCTCGAACTCTGACCTCATG 51

RESULT 201
AAZ66299/c
ID AAZ66299 standard; DNA; 47 BP.
XX
XX AAZ66299;
AC
XX
DT 10-SEP-2001 (first entry)
DE
XX Human map-related biallelic marker SEQ ID NO:646.
XX
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```
XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX
Query Match 1.7%; Score 41.2; DB 1; Length 47;
Best Local Similarity 93.5%; Pred. No. 2.4e+02;
Matches 43; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2261 TTTAGTAGACACAGGGTTTCACCGTGTTCAGCCAGGATGGTCTCGAT 2306
Db 47 TTTAGTAGACACGGGGTTTCACCTCTGTTCAGCCAGGATGGTCTCGAT 2

RESULT 202
AAF89248/c
ID AAF89248 standard; DNA; 47 BP.
XX
XX AAF89248;
AC
XX
DT 10-DEC-2001 (first entry)
DE
XX Sample member clustering method related human polymorphic site #48.
XX
XX Cluster; hierarchical clustering algorithm; population based study;
KW clinical trial; DNA fingerprint; genetic profile analysis; PCR primer;
KW
Query Match 1.7%; Score 41.2; DB 1; Length 47;
Best Local Similarity 93.5%; Pred. No. 2.4e+02;
Matches 43; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2261 TTTAGTAGACACAGGGTTTCACCGTGTTCAGCCAGGATGGTCTCGAT 2306
Db 47 TTTAGTAGACACGGGGTTTCACCTCTGTTCAGCCAGGATGGTCTCGAT 2

RESULT 203
AAL31459
ID AAL31459 standard; DNA; 51 BP.
XX
XX AAL31459;
AC
XX
DT 24-JAN-2002 (first entry)
DE
XX Human SNP oligonucleotide #4667.
XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KW
Query Match 1.7%; Score 41.2; DB 1; Length 51;
Best Local Similarity 93.5%; Pred. No. 2.5e+02;
Matches 43; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2326 CCCACCTCGCCCTCCCAAGTGTCTGGGATTACAGGATGAGCCACC 2371
Db 1 CCGCGCTTGGCTCCCAAGTGTCTGAGATTACAGGATGAGCCACC 46

RESULT 204
AAI79699/c
ID AAI79699 standard; DNA; 51 BP.
XX
XX AAI79699;
AC
XX
DT 09-NOV-2001 (first entry)
DE
XX Human conservative amino acid changing SNP nucleic acid SEQ:6640.
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW
Query Match 1.7%; Score 41.2; DB 1; Length 51;
Best Local Similarity 93.5%; Pred. No. 2.5e+02;
Matches 43; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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XX Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.

Query Match      1.7%; Score 40.4; DB 1; Length 50;
Best Local Similarity 88.0%; Pred. No. 2.7e+02;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2294 CGATGGTCTCGATCTCTGACCTGTGATCCGCCACCTCGGCTCCCAA 2343
DB 50 CGATGGTCTCGATCTCTTACCTCATGATCCACCGCTTGGCTCCCAA 1

RESULT 212
AAI77228
ID AAA77228 standard; cDNA; 51 BP.
XX
AC AAA77228;
XX
DT 16-NOV-2000 (first entry)
XX
DE Human clone c943971764 polymorphic site, SEQ ID NO:911.
XX
KW Human; single nucleotide polymorphism; SNP; chromosome 15; detection;
KW identification; gene therapy; ss.

Query Match      1.7%; Score 40.4; DB 1; Length 51;
Best Local Similarity 97.6%; Pred. No. 2.7e+02;
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2330 CCTCGGCTCCCAAAGTCTGGATTACAGGATGAGCCACC 2371
DB 1 CCTGAGCTCCCAAAGTCTGGATTACAGGATGAGCCACC 42

RESULT 213
ADC16930/c
ID ADC16930 standard; DNA; 51 BP.
XX
AC ADC16930;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human single nucleotide polymorphism (SNP) region Seq ID32.
XX
KW sequence polymorphism analysis; human identity; human relatedness;
KW single nucleotide polymorphism; SNP; genetic disease; cytostatic;

Query Match      1.7%; Score 40.4; DB 1; Length 51;
Best Local Similarity 88.0%; Pred. No. 2.7e+02;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2268 GAGACAGGGTTTACCCGTGTTAGCCAGGATGGTCTCGATCTCTGACCTC 2317
DB 51 GAGACGGGGTTTACCATAATTGGCGGGATGGTCTCGAACTCTGACCTC 2

RESULT 214
AAI79771
ID AAI79771 standard; DNA; 51 BP.
XX
AC AAI79771;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human nonconservative amino acid changing SNP nucleic acid SEQ:6712.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.7%; Score 40.4; DB 1; Length 51;
Best Local Similarity 88.0%; Pred. No. 2.7e+02;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 2246 CTAATTTTGTACTTTTAGTAGACAGAGGGTTTACCGTGTGTAGCCAGG 2295
DB 1 CTAATTTTGTATTTTATTAGTAGAGGGGGGTTTTCGCCATGTTGGCCAGG 50

RESULT 215
AAI75514
ID AAI75514 standard; DNA; 51 BP.
XX
AC AAI75514;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:2455.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.7%; Score 40.4; DB 1; Length 51;
Best Local Similarity 88.0%; Pred. No. 2.7e+02;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2268 GAGACAGGGTTTCCACCGTGTTAGCCAGGATGGTCTCGATCTCTGACCTC 2317
DB 1 GAGACAGGGTTTCCACCATGTTGACCGGGCTGGTCTCGAACTCTCTGACCTC 50

RESULT 216
AAI73068/c
ID AAI73068 standard; DNA; 51 BP.
XX
AC AAI73068;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:9.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.7%; Score 40.4; DB 1; Length 51;
Best Local Similarity 88.0%; Pred. No. 2.7e+02;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2089 TTATTTTGTAGACCGAGTCTTGTCTGTGTACCCAGGCTGGAGTGCAG 2138
DB 50 TTCTTTTGTAGACAGAGTCTCACTCTGTCTGCCCGGCTGGAGTGCAG 1

RESULT 217
ADB73481/c
ID ADB73481 standard; DNA; 48 BP.
XX
AC ADB73481;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human breakpoint region MLL #1.
XX
KW Human; ds; MLL; cancer; AP-4; CDK-6; SEPTIN6; ALL;
KW acute lymphoblastic leukaemia; AML; acute myeloid leukaemia;

Query Match      1.7%; Score 40; DB 1; Length 48;
Best Local Similarity 89.6%; Pred. No. 2.8e+02;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2263 TAGTAGACAGCGGTTTCCCGTGTGTAGCCAGGATGGTCTCGATCTCC 2310
DB 48 TAGTAGAGATGGGGTTTTCATGTTGTAGCGAGGATGGTCTCAATCTCC 1

RESULT 218

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AAI79647/C
ID  AAI79647 standard; DNA; 51 BP.
XX
AC  AAI79647;
XX
DT  09-NOV-2001 (first entry)
XX
DE  Human silent SNP containing nucleic acid SEQ:6588.
XX
KW  Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW  protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.7%; Score 40; DB 1; Length 51;
Best Local Similarity 89.6%; Pred. No. 2.8e+02;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  2241 CCTGGCTAAATTTTGTACTTTTAGTAGACACAGGGTTTCACCGTGT 2288
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  48 CCTGGCTAAATTTTATATTTTCAGTAGACACGGGTTTCACCATGTT 1

RESULT 219
AAI73305
ID  AAI73305 standard; DNA; 51 BP.
XX
AC  AAI73305;
XX
DT  09-NOV-2001 (first entry)
XX
DE  Human silent SNP containing nucleic acid SEQ:246.
XX
KW  Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW  protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.7%; Score 40; DB 1; Length 51;
Best Local Similarity 89.6%; Pred. No. 2.8e+02;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  2318 GTGATCGGCCACCTCGGCCTCCAAAGTCTGGGATTACAGGCATGA 2365
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  4 GTGATCTCTCGCTCGGCCTCCAAAGTCTGGGATTACAGATATGA 51

RESULT 220
AAH39524
ID  AAH39524 standard; DNA; 51 BP.
XX
AC  AAH39524;
XX
DT  14-AUG-2001 (first entry)
XX
DE  Human SNP flanking oligonucleotide SEQ ID 2320.
XX
KW  Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW  SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match      1.7%; Score 40; DB 1; Length 51;
Best Local Similarity 89.6%; Pred. No. 2.8e+02;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  2260 TTTTAGTAGACAGAGGTTTCACCGTGTAGCCAGGATGCTCTCGATC 2307
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  2 TTTTAGTAGAGATGGGGTTTCACCGTGTAGCCAGGCTGCTCTWGATC 49

RESULT 221
ABZ09598
ID  ABZ09598 standard; DNA; 51 BP.
XX
AC  ABZ09598;
XX
DT  16-JAN-2003 (first entry)
XX
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DE  Human oligonucleotide SEQ ID 758.
XX
KW  Human; tumour suppressor; virucide; cytostatic; nootropic;
KW  neuroprotective; neuroleptic; gene therapy; tumour suppression;

Query Match      1.7%; Score 40; DB 1; Length 51;
Best Local Similarity 89.6%; Pred. No. 2.8e+02;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  2260 TTTTAGTAGACAGAGGTTTCACCGTGTAGCCAGGATGCTCTCGATC 2307
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  4 TTTTAGTAGAGATGGGGTTTCACATGTTGGCCAGGATGCTCTCGATC 51

RESULT 222
ABZ79051
ID  ABZ79051 standard; DNA; 51 BP.
XX
AC  ABZ79051;
XX
DT  24-APR-2003 (first entry)
XX
DE  Tumour suppression-related sequence, SEQ ID 758.
XX
KW  Cytostatic; virucide; apoptotic; gene therapy; tumour suppression;
KW  tumour reversion; apoptosis; virus resistance; viral infection; tumour;

Query Match      1.7%; Score 40; DB 1; Length 51;
Best Local Similarity 89.6%; Pred. No. 2.8e+02;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  2260 TTTTAGTAGACAGAGGTTTCACCGTGTAGCCAGGATGCTCTCGATC 2307
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  4 TTTTAGTAGAGATGGGGTTTCACATGTTGGCCAGGATGCTCTCGATC 51

RESULT 223
AAA77231
ID  AAA77231 standard; cDNA; 51 BP.
XX
AC  AAA77231;
XX
DT  16-NOV-2000 (first entry)
XX
DE  Human clone cg43972482 polymorphic site, SEQ ID NO:914.
XX
KW  Human; single nucleotide polymorphism; SNP; chromosome 8; detection;
KW  identification; gene therapy; ss.

Query Match      1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY  2262 TTAGTAGACAGAGGTTTCACCGTGTAGCCAGGATGCTCTCGATCCTG 2312
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  1 TTAGTAGACAGCGGGTTTCACCATGCTGTGCTCAGGCTGGTCTCGAACTCTG 51

RESULT 224
AAC14922/c
ID  AAC14922 standard; cDNA; 51 BP.
XX
AC  AAC14922;
XX
DT  06-OCT-2000 (first entry)
XX
DE  Human secreted protein 5' EST, SEQ ID NO: 18997.
XX
KW  Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW  gene therapy; chromosome mapping; ss.

Query Match      1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
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Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2086 TTATATATTTTTTTGAGACCCAGCTCTGCTCTGTTACCCAGGCTGGAGTGC 2136
DB 51 TTTTATTTTTTTTGGAGATGGAGTCTCACTCTGTGTGCCAGGCTGGAGTGC 1

RESULT 225
AAI74451/c
ID AAI74451 standard; DNA; 51 BP.
XX
AC AAI74451;
XX
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:1392.
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2320 GATCGCCACCTCGGCTCCCAAGTCTGGGATTACAGGSCATGAGCCAC 2370
DB 51 GATCCTCTGCTCAGCCTCCCAATTGCTGGGATTACAGGSCATGAGCCAC 1

RESULT 226
AAI75652/c
ID AAI75652 standard; DNA; 51 BP.
XX
AC AAI75652;
XX
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:2593.
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2242 CTGGCTAATTTTTTGTACTTTTAGTAGAGACAGGGTTTCACCGTGTAGCC 2292
DB 51 CTGGCTGATTTTTTGTATTTTATTAGTGGAGACGGGGTTTCGCCATGTTGGCC 1

RESULT 227
AAI75456/c
ID AAI75456 standard; DNA; 51 BP.
XX
AC AAI75456;
XX
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:2397.
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2292 CAGGATGCTCGATCTCGTCACTCTGATCCGCCACCTCGGCTCCCA 2342
DB 51 CAGGCTGCTCTCAAACTCTGATCTTGTATCCGCCCGCTCGGCTCCCA 1
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RESULT 228
AAI77410/c
ID AAI77410 standard; DNA; 51 BP.
XX
AC AAI77410;
XX
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:4351.
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2202 CTCCCAATTTAGCTTGGCTTACAGTCTATCTGCCACACACCTGGCTAATTT 2252
DB 51 CTCCCAATTTAGCTTGGACTTACAGGCACAGGCCACACCTGGCTAATTT 1

RESULT 229
AAI75454/c
ID AAI75454 standard; DNA; 51 BP.
XX
AC AAI75454;
XX
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:2395.
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2294 GGATGCTCGATCTCTGACCTCGTGCATCCGCCACCTCGGCTCCCA 2344
DB 51 GGCTGCTCTCAAACTCTGATCTTGTATCCGCCCGCTCGGCTCCCA 1

RESULT 230
AAI77409/c
ID AAI77409 standard; DNA; 51 BP.
XX
AC AAI77409;
XX
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:4350.
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2320 GATCCGCCACCTCGGCTCCCAAGTCTGGGATTACAGGSCATGAGCCAC 2370
DB 51 GATCCTCTGCTTGGCTCCCAAGTCTGGGATTATAGGSCATGAGCCGC 1

RESULT 231
AAI74979/c
ID AAI74979 standard; DNA; 51 BP.
XX
AC AAI74979;
XX
DT 09-NOV-2001 (first entry)
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XX DE Human silent SNP containing nucleic acid SEQ:1920.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW
Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2362 TTAGTACAGACAGGGTTTACCGGTTAGCCAGGATGCTCGATCTCCCTG 2312
DB 51 TTAGTACAGACAGGGTTTATCATGCTGCGCAGGCTGGTCTTGAACCTCTG 1

RESULT 232
AAH90586/c
ID AAI73070 standard; DNA; 51 BP.
XX
AC AAI73070;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:11.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW
Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2087 TATTATTTTTTTGAGACCGAGTCTTGCTCTGTGTACCCAGGCTGGAGTGCA 2137
DB 51 TTTCCTTTTTTTGAGACAGAGTCTCACTCTGTGCGCCAGGCTGGAGTGCA 1

RESULT 233
AAH90586/c
ID AAH90586 standard; cDNA; 51 BP.
XX
AC AAH90586;
XX
DT 08-OCT-2001 (first entry)
XX
DE Human clone cg43080072 SNP site, SEQ ID NO:466.
XX
KW Human; single nucleotide polymorphism; SNP; detection; identification;
KW gene therapy; genetic disorder; ss.

Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2319 TGATCCGCCACCTCGCGCTCCCAAAGTGTGGGATTACAGGCATGAGCCA 2369
DB 51 TGATCCACTCGCTTCGCGCTCCCAAAGTGTGGGATTATAGGCTGAGCCA 1

RESULT 234
AAH89305
ID AAH89305 standard; DNA; 51 BP.
XX
AC AAH89305;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 86.
XX
KW Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.

Query Match 1.7%; Score 39.8; DB 1; Length 51;

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Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2245 GCTAATTTTTTTGTACTTTTAGTAGACAGACAGGGTTTCACCGTGTAGCCAGG 2295
DB 1 GCTAATTTTTTTGTATTATTTTAATAGAAACGGGGATTACCATGTGGCCAGG 51

RESULT 235
AAH89317/c
ID AAH89317 standard; DNA; 51 BP.
XX
AC AAH89317;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 98.
XX
KW Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.

Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2214 CTTGGCCTACAGTCACTCTGCCACACACACCTGGCTAATTTTTTGTACTTTTA 2264
DB 51 CTGGGACTACAGCATATGCCACCACGCTGGCTAATTTTTTATATTTTA 1

RESULT 236
AAH89553/c
ID AAH89553 standard; DNA; 51 BP.
XX
AC AAH89553;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 334.
XX
KW Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.

Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2267 AGAGACAGGGTTTCACCGTGTAGCCAGGATGCTCGATCTCCTGACCTC 2317
DB 51 AGAGACGGGGTTTTCACCATTTTGGCCAGGCTGCTTGAACCTCCTGACCTC 1

RESULT 237
AAH89518/c
ID AAH89518 standard; DNA; 51 BP.
XX
AC AAH89518;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 299.
XX
KW Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.

Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2318 GTGATCCGCCACCTCGGCTCCCAAAGTGTGGGATTACAGCATGAGCC 2368
DB 51 GTGATCCATCCGCTTGGGCTCCCAAGTGTGGGATTACAGCGGAGCC 1

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RESULT 238
AAH89309/c
ID AAH89309 standard; DNA; 51 BP.
XX
AC AAH89309;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 90.
XX
DE Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.

Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2279 TCACCGTCTTAGCCAGGATGCTCGATCTCTGACCTCGTGATCCGCCCA 2329
DB 51 TCATCATGTTGCCAGGATGCTCTTAATTTCTGACCTCGTGATCCGCCCA 1

RESULT 239
AAH89566/c
ID AAH89566 standard; DNA; 51 BP.
XX
AC AAH89566;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 347.
XX
DE Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.

Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2218 GCCTACAGTCATCGCCACCAACACCTGGCTAAATTTTGTACTTTTAGTAG 2268
DB 51 GACTACAGGCATATGCCACCATGCTGCTAAATTTTATATTTTAGTAG 1

RESULT 240
ABL00112/c
ID ABL00112 standard; DNA; 51 BP.
XX
AC ABL00112;
XX
DT 05-MAR-2002 (first entry)
XX
DE Human silent noncoding SNP oligonucleotide SEQ ID NO:103.
XX
DE Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
KW immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;

Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.9e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2254 TTGTAATTTTATAGTAGAGACAGGGTTTCCCGTGTATCCAGGATGGTCTCG 2304
DB 51 TTGTAATTTTATAGTAGAGATGGGGTTGCACCATGTTGGCCAGGCTGGTCTCG 1

RESULT 241
AAI79698/c
ID AAI79698 standard; DNA; 51 BP.
XX
AC AAI79698;
XX

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DT 09-NOV-2001 (first entry)
XX
DE Human conservative amino acid changing SNP nucleic acid SEQ.6639.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match 1.7%; Score 39.6; DB 1; Length 51;
Best Local Similarity 91.3%; Pred. No. 3e+02;
Matches 42; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2096 TTTTGAGACGAGTCTTGCTCTTACCCAGGCTGGAGTGCAGTGG 2141
DB 51 TTTAGAGACAGAGTCTTGCTCTTGTCCCGAGGCTGGAGTACAGTGG 6

RESULT 242
ABZ20666/c
ID ABZ20666 standard; DNA; 41 BP.
XX
AC ABZ20666;
XX
DT 03-MAR-2003 (first entry)
XX
DE Human G protein subunit 9-02 coding sequence probe #1.
XX
DE Human; G protein subunit 9.02; cancer; constipation; diarrhoea; cough;
KW cardiac asthma; colic; psychic disease; probe;

Query Match 1.7%; Score 39.4; DB 1; Length 41;
Best Local Similarity 97.6%; Pred. No. 2.8e+02;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2322 TCCGCCACCTCGGCCTCCCAAAGTCTGGGATTACAGGCA 2362
DB 41 TCCACCCACCTCGGCCTCCCAAAGTCTGGGATTACAGGCA 1

RESULT 243
ABZ49551/c
ID ABZ49551 standard; DNA; 41 BP.
XX
AC ABZ49551;
XX
DT 26-JUN-2003 (first entry)
XX
DE Human glutathione-S-transferase MGST2 gene polymorphic site, #6334.
XX
DE Human; drug metabolising enzyme; gene; drug metabolism; chromosome 4;
KW polymorphic site; drug evaluation; drug screening; genotyping;

Query Match 1.7%; Score 39.4; DB 1; Length 41;
Best Local Similarity 97.6%; Pred. No. 2.8e+02;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2298 GGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCT 2338
DB 41 GGTCTCGATCTCTGACCTCATGATCCGCCACCTCGGCCT 1

RESULT 244
ABZ43959/c
ID ABZ43959 standard; DNA; 41 BP.
XX
AC ABZ43959;
XX
DT 26-JUN-2003 (first entry)
XX
DE Human glutathione-S-transferase MGST2 gene polymorphic site, #743.
XX
DE Human; drug metabolising enzyme; gene; drug metabolism; chromosome 4;
KW polymorphic site; drug evaluation; drug screening; genotyping;

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Query Match      1.7%; Score 39.4; DB 1; Length 41;
Best Local Similarity 97.6%; Pred. No. 2.8e+02;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2298 GGTCTCGATCTCTGACCTCGTGATCGGCCACCTCGGCCT 2338
      |||||
Db 41 GGTCTCGATCTCTGACCTCGTGATCGGCCACCTCGGCCT 1

RESULT 245
AAI79580/c
ID AAI79580 standard; DNA; 51 BP.
XX
AC AAI79580;
XX
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:6521.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.7%; Score 39.4; DB 1; Length 51;
Best Local Similarity 97.6%; Pred. No. 3e+02;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 GTGATCGGCCACCTCGGCCTCCCAAAGTCTGGGATTACA 2358
      |||||
Db 41 GTGATCGGCCCGCTCGGCCTCCCAAAGTCTGGGATTACA 1

RESULT 246
AAH89818
ID AAH89818 standard; DNA; 51 BP.
XX
AC AAH89818;
XX
DT 01-OCT-2001 (first entry)
DE Human coding sequence polymorphic site SEQ ID NO: 599.
XX
KW Human; single nucleotide polymorphism; SNP; paternity test;
forensic test; aberrant protein expression; ds.

Query Match      1.7%; Score 39.4; DB 1; Length 51;
Best Local Similarity 97.8%; Pred. No. 3e+02;
Matches 43; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2232 GCCACACACCTCGCTAAATTTTGTACTTTTGTAGTAGACAGGGTTTC 2280
      |||||
Db 3 GCCACACACCCAGCTAAATTTTGTATTATTTTAAATAGACGGGGATTC 51

RESULT 247
ADI12541/c
ID ADI12541 standard; DNA; 44 BP.
XX
AC ADI12541;
XX
DT 22-APR-2004 (first entry)
DE Mutant human BRCA1 genomic DNA resulting from deletion 3 SeqID 24.
XX
KW ds; cancer; human; tumour suppressor;
breast cancer susceptibility gene 1; BRCA1; repetitive Alu;

Query Match      1.7%; Score 39.2; DB 1; Length 44;
Best Local Similarity 93.2%; Pred. No. 2.9e+02;
Matches 41; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2316 TCGTGATCGGCCACCTCGGCCTCCCAAAGTCTGGGATTACAG 2359
      |||||
Db 44 TTGTGATCTGCCCGCTCGGCCTCCCAAAGTCTGGGATTACAG 1

Query Match      1.7%; Score 39.2; DB 1; Length 51;
Best Local Similarity 93.2%; Pred. No. 3.1e+02;
Matches 41; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2329 ACCTCGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACCG 2372
      |||||
Db 1 ACCTGGCCTCCCAAAGTCTGGGACTACAGGCATGAGCCACCG 44

RESULT 248
AAI78301
ID AAI78301 standard; DNA; 51 BP.
XX
AC AAI78301;
XX
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:5242.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.7%; Score 39.2; DB 1; Length 51;
Best Local Similarity 93.2%; Pred. No. 3.1e+02;
Matches 41; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2329 ACCTCGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACCG 2372
      |||||
Db 1 ACCTGGCCTCCCAAAGTCTGGGACTACAGGCATGAGCCACCG 44

RESULT 249
ADI12532
ID ADI12532 standard; DNA; 49 BP.
XX
AC ADI12532;
XX
DT 22-APR-2004 (first entry)
DE Mutant human BRCA1 genomic DNA resulting from deletion 1 SeqID 15.
XX
KW ds; cancer; human; tumour suppressor;
breast cancer susceptibility gene 1; BRCA1; repetitive Alu;

Query Match      1.6%; Score 39; DB 1; Length 49;
Best Local Similarity 89.4%; Pred. No. 3.1e+02;
Matches 42; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2326 CCCACCTCGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACCG 2372
      |||||
Db 1 CCCGTCTCGGCCTCCCAAAGTCTGGGATTACAGGTGTGAGCCATCG 47

RESULT 250
AAI78038/c
ID AAI78038 standard; DNA; 51 BP.
XX
AC AAI78038;
XX
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:4979.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match      1.6%; Score 39; DB 1; Length 51;
Best Local Similarity 89.4%; Pred. No. 3.2e+02;
Matches 42; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2326 CCCACCTCGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACCG 2372
      |||||
Db 50 CCTGCCTCAGCCTCCCAAAGTCTAGGATTACAGGCATGAGCCACTG 4

RESULT 251
AAI77874
ID AAI77874 standard; DNA; 51 BP.
XX
AC AAI77874;
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XX 09-NOV-2001 (first entry)
DT Human silent SNP containing nucleic acid SEQ:4815.
DE
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match 1.6%; Score 38.9; DB 1; Length 51;
Best Local Similarity 96.2%; Pred. No. 3.2e+02;
Matches 50; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2248 AATTTTGTACTTTTGTAGACAGAGGTTTACCGTGTAGCCAGGATGG 2299
Db 1 AATTTTGTATTTTGTAGACAC-GGGTTTACCGTGTAGCCAGGATGG 51

RESULT 252
AAI77875
ID AAI77875 standard; DNA; 51 BP.
XX
XX AAI77875;
AC
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:4816.
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match 1.6%; Score 38.9; DB 1; Length 51;
Best Local Similarity 96.2%; Pred. No. 3.2e+02;
Matches 50; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2248 AATTTTGTACTTTTGTAGACAGAGGTTTACCGTGTAGCCAGGATGG 2299
Db 1 AATTTTGTATTTTGTAGACAC-GGTTTACCGTGTAGCCAGGATGG 51

RESULT 253
AAI77229
ID AAA77229 standard; cDNA; 51 BP.
XX
XX AAA77229;
AC
DT 16-NOV-2000 (first entry)
DE Human clone cg43971764 polymorphic site, SEQ ID NO:912.
XX
XX Human; single nucleotide polymorphism; SNP; chromosome 15; detection;
KW identification; gene therapy; ss.

Query Match 1.6%; Score 38.8; DB 1; Length 51;
Best Local Similarity 95.2%; Pred. No. 3.2e+02;
Matches 40; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2330 CCTGGCCTCCCAAGTCTGGGATTACAGCATAGCCACC 2371
Db 1 CCTCAGCCTCCCAAGTCTGGGATCAGCATAGCCACC 42

RESULT 254
AAI75651/c
ID AAI75651 standard; DNA; 51 BP.
XX
XX AAI75651;
AC
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:2592.
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

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Query Match 1.6%; Score 38.8; DB 1; Length 51;
Best Local Similarity 86.0%; Pred. No. 3.2e+02;
Matches 43; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2249 ATTTTGTACTTTTGTAGACAGAGGTTTACCGTGTAGCCAGGATG 2298
Db 50 ATTTTGTATTTTGTAGTGAGACAGGTTTCGCCATGTGTCGGCGGCTG 1

RESULT 255
AAI79075
ID AAI79075 standard; DNA; 51 BP.
XX
XX AAI79075;
AC
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:6016.
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match 1.6%; Score 38.8; DB 1; Length 51;
Best Local Similarity 86.0%; Pred. No. 3.2e+02;
Matches 43; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2089 TTATTTTGTAGACCGAGTCTGTCTGTACCCAGGCTGGAGTGCAG 2138
Db 2 TTATTTTGTAAACAGGCTCTCGCTCTGCTGCCAGGCTGGAGTGCAG 51

RESULT 256
AAI74819
ID AAI74819 standard; DNA; 51 BP.
XX
XX AAI74819;
AC
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:1760.
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match 1.6%; Score 38.8; DB 1; Length 51;
Best Local Similarity 86.0%; Pred. No. 3.2e+02;
Matches 43; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2089 TTATTTTGTAGACCGAGTCTGTCTGTACCCAGGCTGGAGTGCAG 2138
Db 2 TTATTTTGTAAACAGGCTCTCGCTCTGCTGCCAGGCTGGAGTGCAG 51

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RESULT 257
AAI79530
ID AAI79530 standard; DNA; 51 BP.
XX
XX AAI79530;
AC
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:6471.
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match 1.6%; Score 38.8; DB 1; Length 51;
Best Local Similarity 86.0%; Pred. No. 3.2e+02;
Matches 43; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2220 CTACAGTCATCTGCCACACACCTGCTGAATTTTGTACTTTTAGTAGA 2269
Db 1 CTACAGTCATCTGCCACACACCTGCTGAATTTTGTACTTTTAGTAGA 2269

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Db 2 CTACAGCACGCGCCACCACCGCGGCTAAATTTTGTATTTTAGTAGA 51

RESULT 258

AAI74884
ID AAI74884 standard; DNA; 51 BP.

XX AC AAI74884;

XX DT 09-NOV-2001 (first entry)

XX DE Human silent SNP containing nucleic acid SEQ:1825.

XX KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match 1.6%; Score 38.8; DB 1; Length 51;

Best Local Similarity 86.0%; Pred. No. 3.2e+02; Mismatches 7; Indels 0; Gaps 0;

QY 2256 GTACTTTTAGTAGACAGCGTTTACCGTGTAGCCAGGATGCTCTCGA 2305

Db 1 GTATTTTCAGTAGACAGCGGTTTACCAATGTTGGCCAGGCTGCTCTCGA 50

RESULT 259

AAI74965/c
ID AAI74965 standard; DNA; 51 BP.

XX AC AAI74965;

XX DT 09-NOV-2001 (first entry)

XX DE Human silent SNP containing nucleic acid SEQ:1906.

XX KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match 1.6%; Score 38.8; DB 1; Length 51;

Best Local Similarity 86.0%; Pred. No. 3.2e+02; Mismatches 7; Indels 0; Gaps 0;

QY 2268 GAGACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTC 2317

Db 51 GAGACAGGGTTTCACTATGTTGGTAGGCTGGTCTCGAATCTCTGATCTC 2

RESULT 260

ADK19818/c
ID ADK19818 standard; DNA; 51 BP.

XX AC ADK19818;

XX DT 06-MAY-2004 (first entry)

XX DE Human mannosyl transferase-related SNP region DNA SeqID20.

XX KW human; mannosyl transferase; antimanic; antidepressant; gene therapy;
KW fusion protein; chromosome 9 fusion protein; chromosome 11 translocation;

Query Match 1.6%; Score 38.8; DB 1; Length 51;

Best Local Similarity 86.0%; Pred. No. 3.2e+02; Mismatches 7; Indels 0; Gaps 0;

QY 2311 TGACCTCGTATCGCCACCTCGGCTCCCAAAGTCTGGGATTACAGG 2360

Db 50 TGACCTCGTATCGCTCTCGACCTCCCAAAGTACCGGGATTACAGG 1

RESULT 261

AAI75542
ID AAI75542 standard; DNA; 51 BP.

XX

AC AAI75542;
XX DT 09-NOV-2001 (first entry)
XX DE Human silent SNP containing nucleic acid SEQ:2483.
XX KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match 1.6%; Score 38.6; DB 1; Length 51;
Best Local Similarity 91.1%; Pred. No. 3.3e+02; Mismatches 4; Indels 0; Gaps 0;

QY 2318 GTGATCCGCCACCTCGGCTCCCAAAGTCTGGGATTACAGCA 2362

Db 7 GCGATCCTCCAAACCCGCGCTCCCAAAGTCTGGGATTACAGCA 51

RESULT 262

AAV19044/c
ID AAV19044 standard; DNA; 40 BP.

XX AC AAV19044;

XX DT 28-JUL-1998 (first entry)

XX DE Alu PCR primer 1.

XX KW PCR; primer; amplification; Alu repeat sequence; vector;
KW circular yeast artificial chromosome; YAC; ss.

Query Match 1.6%; Score 38.4; DB 1; Length 40;

Best Local Similarity 97.5%; Pred. No. 3.1e+02; Mismatches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2332 TCGGCTCCCAAAGTCTGGGATTACAGCATGAGCCACC 2371

Db 40 TCGGCTCCCAAAGTCTGGGATTACAGCGTGAGCCACC 1

RESULT 263

AAA97659
ID AAA97659 standard; DNA; 40 BP.

XX AC AAA97659;

XX DT 15-FEB-2001 (first entry)

XX DE Human MDM2 40mer PCR template.

XX KW Pseudocyclic oligonucleotide; functional segment; protective segment;
KW nucleic acid detection; mRNA cleavage; antisense therapy; PCO;

Query Match 1.6%; Score 38.4; DB 1; Length 40;

Best Local Similarity 97.5%; Pred. No. 3.1e+02; Mismatches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 659 GGACTCAGGTACATCTGTGAGTGAGAACACAGGTGTACCTT 698

Db 1 GGACCCAGGTACATCTGTGAGTGAGAACACAGGTGTACCTT 40

RESULT 264

ABL59100/c
ID ABL59100 standard; DNA; 40 BP.

XX AC ABL59100;

XX DT 27-SEP-2002 (first entry)

XX DE Nucleotide sequence of an Alu PCR primer.

XX KW Yeast artificial chromosome; YAC; inter-Alu PCR;

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KW transformation-associated recombination; PCR; primer; ss.

Query Match 1.6%; Score 38.4; DB 1; Length 40;
Best Local Similarity 97.5%; Pred. No. 3.1e+02;
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2332 TCGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACC 2371
DB 40 TCGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACC 1

RESULT 265
ABL60505
ID ABL60505 standard; DNA; 40 BP.
XX ABL60505;
AC ABL60505;
XX
DT 12-AUG-2002 (first entry)
DE Human MDM2 mRNA fragment complementary oligo 17.
XX
KW Pseudo-cyclic oligonucleotide; PCO; gene expression; protein kinase A;
KW nucleic acid detection; ribozyme inhibition; gene transcription; MDM2;

Query Match 1.6%; Score 38.4; DB 1; Length 40;
Best Local Similarity 97.5%; Pred. No. 3.1e+02;
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 659 GGACTCAGGTACATCTGTGAGTGAGAACAGGTGTCACTT 698
DB 1 GGACCCAGGTACATCTGTGAGTGAGAACAGGTGTCACTT 40

RESULT 266
AAI76503
ID AAI76503 standard; DNA; 50 BP.
XX AAI76503;
AC AAI76503;
XX
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:3444.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match 1.6%; Score 38.4; DB 1; Length 50;
Best Local Similarity 87.5%; Pred. No. 3.4e+02;
Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2241 CTGGCTAATTTTGTACTTTTGTAGTAGACACAGGTTTACCGTGT 2288
DB 3 CCCAGCTAATTTTGTATTTTGTAGTAGATGAGTGTACCGTGT 50

RESULT 267
AAI73304
ID AAI73304 standard; DNA; 51 BP.
XX AAI73304;
AC AAI73304;
XX
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:245.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match 1.6%; Score 38.4; DB 1; Length 51;
Best Local Similarity 87.5%; Pred. No. 3.4e+02;
Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2318 GTGATCCGCCACCTCGGCCCTCCCAAGTGTGGGATTACAGGCATGA 2365
DB 4 GTGATCTCTGCTCGGCCCTCTCAAGTGTGGGATTACAGATATGA 51

Db 4 GTGATCTCTGCTCGGCCCTCTCAAGTGTGGGATTACAGATATGA 51

RESULT 268
AAI76814
ID AAI76814 standard; DNA; 51 BP.
XX AAI76814;
AC AAI76814;
XX
DT 09-NOV-2001 (first entry)
DE Human silent SNP containing nucleic acid SEQ:3755.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;

Query Match 1.6%; Score 38.4; DB 1; Length 51;
Best Local Similarity 87.5%; Pred. No. 3.4e+02;
Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGACAGGTTTTCACCGTGTAGCCAGGATGTTCTCGATC 2307
DB 4 TTTTAGTAGACAGGTTTTCGCCATGTTCGCCAGGCTGTTCTTGAC 51

RESULT 269
ABZ20667/C
ID ABZ20667 standard; DNA; 41 BP.
XX ABZ20667;
AC ABZ20667;
XX
DT 03-MAR-2003 (first entry)
DE Human G protein subunit 9-02 coding sequence probe #2.
XX
KW Human; G protein subunit 9.02; cancer; constipation; diarrhoea; cough;
KW cardiac asthma; colic; psychic disease; probe;

Query Match 1.6%; Score 37.8; DB 1; Length 41;
Best Local Similarity 95.1%; Pred. No. 3.3e+02;
Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2322 TCCGCCACCTCGGCCCTCCCAAGTGTCTGGGATTACAGGCA 2362
DB 41 TCCACCCACCTCGGCCCTCCCGAAGTGTCTGGGATTACAGGCA 1

RESULT 270
ABZ43958
ID ABZ43958 standard; DNA; 41 BP.
XX ABZ43958;
AC ABZ43958;
XX
DT 26-JUN-2003 (first entry)
DE Human glutathione-S-transferase MGST2 gene polymorphic site, #742.
XX
KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 4;
KW polymorphic site; drug evaluation; drug screening; genotyping;

Query Match 1.6%; Score 37.8; DB 1; Length 41;
Best Local Similarity 95.1%; Pred. No. 3.3e+02;
Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2314 CCTCGATCCGCCACCTCGGCCCTCCCAAGTGTCTGGGAT 2354
DB 1 CCTCGATTTTGGCCACCTCGGCCCTCCCAAGTGTCTGGGAT 41

RESULT 271
ABZ44160
ID ABZ44160 standard; DNA; 41 BP.
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XX ABZ44160;
 AC
 XX
 DT 26-JUN-2003 (first entry)
 XX
 DE Human NDUFS5 gene polymorphic site, #944.
 XX
 KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 1;
 KW polymorphic site; drug evaluation; drug screening; genotyping;
 Query Match 1.6%; Score 37.8; DB 1; Length 41;
 Best Local Similarity 95.1%; Pred. No. 3.3e+02;
 Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2264 AGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGCTCTCG 2304
 DB 1 AGTAGAGACGGGGTTTCACCGTGTAGCCAGCATGCTCTCG 41
 RESULT 272
 ABZ49550
 ID ABZ49550 standard; DNA; 41 BP.
 XX
 AC ABZ49550;
 XX
 DT 26-JUN-2003 (first entry)
 XX
 DE Human glutathione-S-transferase MGST2 gene polymorphic site, #6333.
 XX
 KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 4;
 KW polymorphic site; drug evaluation; drug screening; genotyping;
 Query Match 1.6%; Score 37.8; DB 1; Length 41;
 Best Local Similarity 95.1%; Pred. No. 3.3e+02;
 Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2314 CCTCGTATCCGCCACCTCGGCTCCCAAAGTCTGGGAT 2354
 DB 1 CCTCGTATTTGCCACCTCGGCTCCCAAAGTCTGGGAT 41
 RESULT 273
 ABZ49631/c
 ID ABZ49631 standard; DNA; 41 BP.
 XX
 AC ABZ49631;
 XX
 DT 26-JUN-2003 (first entry)
 XX
 DE Human sulphotransferase SULT1C1 gene polymorphic site, #6413.
 XX
 KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 2;
 KW polymorphic site; drug evaluation; drug screening; genotyping;
 Query Match 1.6%; Score 37.8; DB 1; Length 41;
 Best Local Similarity 95.1%; Pred. No. 3.3e+02;
 Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2328 CACCTCGGCTCCCAAAGTCTGGGATTACAGGCATGAGCC 2368
 DB 41 CGCCTCGGCTCCCAAAGTCTGGGATTACAGGCATGAGCC 1
 RESULT 274
 ABZ43598/c
 ID ABZ43598 standard; DNA; 41 BP.
 XX
 AC ABZ43598;
 XX
 DT 26-JUN-2003 (first entry)
 XX
 DE Human sulphotransferase SULT1C1 gene polymorphic site, #382.
 XX

KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 2;
 KW polymorphic site; drug evaluation; drug screening; genotyping;
 Query Match 1.6%; Score 37.8; DB 1; Length 41;
 Best Local Similarity 95.1%; Pred. No. 3.3e+02;
 Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2328 CACCTCGGCTCCCAAAGTCTGGGATTACAGGCATGAGCC 2368
 DB 41 CGCCTCGGCTCCCAAAGTCTGGGATTACAGGCATGAGCC 1
 RESULT 275
 ABZ50172
 ID ABZ50172 standard; DNA; 41 BP.
 XX
 AC ABZ50172;
 XX
 DT 26-JUN-2003 (first entry)
 XX
 DE Human NDUFS5 gene polymorphic site, #6954.
 XX
 KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 1;
 KW polymorphic site; drug evaluation; drug screening; genotyping;
 Query Match 1.6%; Score 37.8; DB 1; Length 41;
 Best Local Similarity 95.1%; Pred. No. 3.3e+02;
 Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2264 AGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGCTCTCG 2304
 DB 1 AGTAGAGACGGGGTTTCACCGTGTAGCCAGCATGCTCTCG 41
 RESULT 276
 AD112523/c
 ID AD112523 standard; DNA; 42 BP.
 XX
 AC AD112523;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Human BRCA1 DNA junction sequence comprising large deletion SegID 3.
 KW ds; cancer; human; tumour suppressor;
 KW breast cancer susceptibility Gene 1; BRCA1; repetitive Alu;
 Query Match 1.6%; Score 37.8; DB 1; Length 42;
 Best Local Similarity 95.1%; Pred. No. 3.4e+02;
 Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2318 GTGATCGCCACCTCGGCTCCCAAAGTCTGGGATTACA 2358
 DB 41 GTGATCGCCCGCTCGGCTCCCAAAGTCTGGGATTACA 1
 RESULT 277
 AAZ68649
 ID AAZ68649 standard; DNA; 47 BP.
 XX
 AC AAZ68649;
 XX
 DT 10-SEP-2001 (first entry)
 XX
 DE Human map-related biallelic marker SEQ ID NO:2999.
 XX
 KW Human genome; biallelic marker; high density disequilibrium map;
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
 Query Match 1.6%; Score 37.4; DB 1; Length 47;
 Best Local Similarity 87.2%; Pred. No. 3.7e+02;
 Matches 41; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

AAK86862/C

ADJ15309/c
ID ADJ15309 standard; DNA; 45 BP.
XX
AC ADJ15309;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human liver-related genomic DNA - SEQ ID 517.
XX
KW liver; virucide; fungicide; antibacterial; antiparasitic; hepatotropic;
KW antinflammatory; cytostatic; litholytic; antirheumatic; antiarthritic;
Query Match 1.5%; Score 35.4; DB 1; Length 45;
Best Local Similarity 86.7%; Pred. No. 4.5e+02;
Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2087 TATTATTTTTCGAGACCGAGTCTTCTCTGTGTACCCAGGCTGG 2131
Db 45 TTTTTCGAGACCGAGTCTCTCTGTGTACCCAGGCTGG 1
RESULT 292
AAI76391
ID AAI76391 standard; DNA; 44 BP.
XX
AC AAI76391;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:3332.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
Query Match 1.5%; Score 35.2; DB 1; Length 44;
Best Local Similarity 92.5%; Pred. No. 4.5e+02;
Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2316 TCGTGATCCGCCACCTCGGCTCCCAAGTGTGGATT 2355
Db 5 TCATGATCCGCCCGCTCGGCTCTCAAGTGTGGATT 44
RESULT 293
ABA94092/c
ID ABA94092 standard; DNA; 41 BP.
XX
AC ABA94092;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human tumour suppressor factor 11.77 probe 2 SEQ ID NO:9.
XX
KW Human; tumour suppressor factor 11.77; cytostatic; haemostatic; virucide;
KW immunomodulatory; antiinflammatory; gene therapy; malignant tumour;
Query Match 1.5%; Score 34.6; DB 1; Length 41;
Best Local Similarity 90.2%; Pred. No. 4.7e+02;
Matches 37; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2322 TCCGCCACCTCGGCTCCCAAGTGTGGATTACAGGCA 2362
Db 41 TCCGCCGCTTGTGGCTCCCGAAGTGTGGATTACAGGCA 1
RESULT 294
ABZ43599/c
ID ABZ43599 standard; DNA; 41 BP.
XX
AC ABZ43599;
XX
DT 26-JUN-2003 (first entry)
XX

DE Human sulphotransferase SUL1C1 gene polymorphic site, #383.
XX
KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 2;
KW polymorphic site; drug evaluation; drug screening; genotyping;
Query Match 1.5%; Score 34.6; DB 1; Length 41;
Best Local Similarity 90.2%; Pred. No. 4.7e+02;
Matches 37; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2307 CTCCTGACCTCGTGATCCGCCACCTCGGCTCCCAAAGTG 2347
Db 41 CTCCTGACTTTGTGATCCACCGCTCGGCTCCCAAAGTG 1
RESULT 295
ABZ49632/c
ID ABZ49632 standard; DNA; 41 BP.
XX
AC ABZ49632;
XX
DT 26-JUN-2003 (first entry)
XX
DE Human sulphotransferase SUL1C1 gene polymorphic site, #6414.
XX
KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 2;
KW polymorphic site; drug evaluation; drug screening; genotyping;
Query Match 1.5%; Score 34.6; DB 1; Length 41;
Best Local Similarity 90.2%; Pred. No. 4.7e+02;
Matches 37; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2307 CTCCTGACCTCGTGATCCGCCACCTCGGCTCCCAAAGTG 2347
Db 41 CTCCTGACTTTGTGATCCACCGCTCGGCTCCCAAAGTG 1
RESULT 296
ADL64133/c
ID ADL64133 standard; DNA; 41 BP.
XX
AC ADL64133;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human single nucleotide polymorphism (SNP) #56.
XX
KW ss; human; single nucleotide polymorphism; SNP;
KW C1 S subcomponent protein; C1S; alanyl aminopeptidase protein; ANPEP;
Query Match 1.5%; Score 34.6; DB 1; Length 41;
Best Local Similarity 90.2%; Pred. No. 4.7e+02;
Matches 37; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2298 GGTCTCGATCTCTGTACCTCGTGATCCGCCACCTCGGCT 2338
Db 41 GGTCTTGAACTCTTAACCTCGTGATCCACCCACCTCGGCT 1
RESULT 297
ACC84472
ID ACC84472 standard; DNA; 39 BP.
XX
AC ACC84472;
XX
DT 28-AUG-2003 (first entry)
XX
DE NTP peptide encoding sequence #19.
XX
KW Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;
KW neural thread protein; NTP; tumour; ds.
Query Match 1.4%; Score 34.2; DB 1; Length 39;
Best Local Similarity 92.3%; Pred. No. 4.9e+02;

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Matches 36; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2326 CCCACCTCGGCTCCCAAGTCTGGGATTACAGGCATG 2364
DB 1 CCTGCTCGGCTCCCAAGTCTGGGATTACAGGCATG 39

RESULT 298
ACC84458
ID ACC84458 standard; DNA; 42 BP.
XX
AC ACC84458;
XX
DT 28-AUG-2003 (first entry)
XX
DE NTP peptide encoding sequence #5.
XX
KW Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;
KW neural thread protein; NTP; tumour; ds.

Query Match 1.4%; Score 34; DB 1; Length 42;
Best Local Similarity 88.1%; Pred. No. 5.1e+02;
Matches 37; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2322 TCCGCCACCTCGGCTCCCAAGTCTGGGATTACAGGCAT 2363
DB 1 TCCACCTGCTCAGCCTCCCAAGTCTGGGATTACAGGCAT 42

RESULT 299
AAK99206/C
ID AAK99206 standard; DNA; 41 BP.
XX
AC AAK99206;
XX
DT 27-MAY-2002 (first entry)
XX
DE Human-homo autoimmune disease-associated protein 10 probe #1.
KW Human; cytostatic; haemostatic; virucide; immunomodulator; haemopathy;
KW antiinflammatory; homo autoimmune disease-associated protein 10;

Query Match 1.4%; Score 33.6; DB 1; Length 41;
Best Local Similarity 90.0%; Pred. No. 5.3e+02;
Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2278 TTCACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTC 2317
DB 41 TTACCTTGTGGCCAGGATGGTCTCGATCTCTGATCTC 2

RESULT 300
AAK99207/C
ID AAK99207 standard; DNA; 41 BP.
XX
AC AAK99207;
XX
DT 27-MAY-2002 (first entry)
XX
DE Human-homo autoimmune disease-associated protein 10 probe #2.
KW Human; cytostatic; haemostatic; virucide; immunomodulator; haemopathy;
KW antiinflammatory; homo autoimmune disease-associated protein 10;

Query Match 1.4%; Score 33.6; DB 1; Length 41;
Best Local Similarity 90.0%; Pred. No. 5.3e+02;
Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2278 TTCACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTC 2317
DB 41 TTACCTTGTGGCCAGGATGGTCTCGATCTCTGATCTC 2
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RESULT 301
ABZ45793/C
ID ABZ45793 standard; DNA; 41 BP.
XX
AC ABZ45793;
XX
DT 26-JUN-2003 (first entry)
XX
DE Human carbohydrate sulphotransferase CHST3 gene polymorphic site, #2577.
KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 10;
KW polymorphic site; drug evaluation; drug screening; genotyping;

Query Match 1.4%; Score 33.6; DB 1; Length 41;
Best Local Similarity 90.0%; Pred. No. 5.3e+02;
Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2326 CCCACCTCGGCTCCCAAGTCTGGGATTACAGGCATGA 2365
DB 40 CCCACCTCGGCTCCCAACTGCTGGGATTACAGGTATGA 1

RESULT 302
ABZ46192
ID ABZ46192 standard; DNA; 41 BP.
XX
AC ABZ46192;
XX
DT 26-JUN-2003 (first entry)
XX
DE Human organic anion transporter OATP8 gene polymorphic site, #2976.
KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 12;
KW polymorphic site; drug evaluation; drug screening; genotyping;

Query Match 1.4%; Score 33.6; DB 1; Length 41;
Best Local Similarity 90.0%; Pred. No. 5.3e+02;
Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2092 TTTTITTTGAGACCGAGTCTGCTCTGTACCAGGCTGG 2131
DB 1 TTTTITTTGAGATGGAGTCTGCTCTGTGCCAGGCTGG 40

RESULT 303
ABZ48356
ID ABZ48356 standard; DNA; 41 BP.
XX
AC ABZ48356;
XX
DT 26-JUN-2003 (first entry)
XX
DE Human organic anion transporter OATP8 gene polymorphic site, #5139.
KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 12;
KW polymorphic site; drug evaluation; drug screening; genotyping;

Query Match 1.4%; Score 33.6; DB 1; Length 41;
Best Local Similarity 90.0%; Pred. No. 5.3e+02;
Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2092 TTTTITTTGAGACCGAGTCTGCTCTGTACCAGGCTGG 2131
DB 1 TTTTITTTGAGATGGAGTCTGCTCTGTGCCAGGCTGG 40

RESULT 304
AAI76390
ID AAI76390 standard; DNA; 44 BP.
XX
AC AAI76390;
XX
DT 09-NOV-2001 (first entry)
```

XX Human silent SNP containing nucleic acid SEQ:3331.
 DE XX
 KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
 protein therapy; vaccine; probe; diagnostic assay; detection;
 Query Match 1.4%; Score 33.6; DB 1; Length 44;
 Best Local Similarity 90.0%; Pred. No. 5.4e+02;
 Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2316 TCGTGATCCGCCACCTCGGCTCCCAAGTGTGGATT 2355
 Db 5 TCATGATCCGCCCTCGGCTCTCAAGTGTGGATT 44

RESULT 305
 AAQ27391
 ID AAQ27391 standard; DNA; 35 BP.
 XX
 AC AAQ27391;
 XX
 DT 25-MAR-2003 (revised)
 DE 27-JAN-1993 (first entry)
 XX
 DE Inter-Alu specific primer PDJ33.
 KW Polymerase chain reaction; PCR; repetitive element; ss.

Query Match 1.4%; Score 33.4; DB 1; Length 35;
 Best Local Similarity 97.1%; Pred. No. 5.1e+02;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2335 GCCTCCCAAGTGTGGATTACAGGATGAGCCA 2369
 Db 1 GCCTCCCAAGTGTGGATTACAGGCGTGAGCCA 35

RESULT 306
 AAS15951/C
 ID AAS15951 standard; DNA; 41 BP.
 XX
 AC AAS15951;
 XX
 DT 14-FEB-2002 (first entry)
 DE Human proteolytic enzyme regulatory protein 11, probe #2.
 KW Human; proteolytic enzyme regulatory protein 11; cytostatic; virucidal;
 immunomodulatory; antiinflammatory; haemostatic; cancer; haemopathy;
 Query Match 1.4%; Score 33.4; DB 1; Length 41;
 Best Local Similarity 97.1%; Pred. No. 5.4e+02;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2107 AGTCTTGCTCTGTACCCAGGCTGGAGTGCAGTGG 2141
 Db 40 AGTCTTGCTCTGTGCCAGGCTGGAGTGCAGTGG 6

RESULT 307
 AAS15950/C
 ID AAS15950 standard; DNA; 41 BP.
 XX
 AC AAS15950;
 XX
 DT 14-FEB-2002 (first entry)
 DE Human proteolytic enzyme regulatory protein 11, probe #1.
 KW Human; proteolytic enzyme regulatory protein 11; cytostatic; virucidal;
 immunomodulatory; antiinflammatory; haemostatic; cancer; haemopathy;
 Query Match 1.4%; Score 33.4; DB 1; Length 41;

Best Local Similarity 97.1%; Pred. No. 5.4e+02;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2107 AGTCTTGCTCTGTACCCAGGCTGGAGTGCAGTGG 2141
 Db 40 AGTCTTGCTCTGTGCCAGGCTGGAGTGCAGTGG 6

RESULT 308
 ADP12341/C
 ID ADP12341 standard; DNA; 33 BP.
 XX
 AC ADP12341;
 XX
 DT 12-AUG-2004 (first entry)
 DE XX
 DE Tagman probe set 2 #199.
 XX
 KW transplant rejection; immune system; rheumatoid arthritis; lupus;
 inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss; probe.
 Query Match 1.4%; Score 33; DB 1; Length 33;
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1559 GGNAGAAACCCAGACAAAGAGAGAGTGTGGA 1591
 Db 33 GGAAGAAACCCAGACAAAGAGAGAGTGTGGA 1

RESULT 309
 ABZ50127/C
 ID ABZ50127 standard; DNA; 41 BP.
 XX
 AC ABZ50127;
 XX
 DT 26-JUN-2003 (first entry)
 DE Human NDUFS1 gene polymorphic site, #6909.
 KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 2;
 polymorphic site; drug evaluation; drug screening; genotyping;
 Query Match 1.4%; Score 33; DB 1; Length 41;
 Best Local Similarity 87.8%; Pred. No. 5.6e+02;
 Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 2252 TTTTGTAATTTTAGTAGACAGCGGGTTTCCCGTGTAGCC 2292
 Db 41 TTTTGTAATTTTAGTAGACAGCGGGTTTCCCGTGTAGCC 1

RESULT 310
 ABZ44117/C
 ID ABZ44117 standard; DNA; 41 BP.
 XX
 AC ABZ44117;
 XX
 DT 26-JUN-2003 (first entry)
 DE Human NDUFS1 gene polymorphic site, #901.
 KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 2;
 polymorphic site; drug evaluation; drug screening; genotyping;
 Query Match 1.4%; Score 33; DB 1; Length 41;
 Best Local Similarity 87.8%; Pred. No. 5.6e+02;
 Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 2252 TTTTGTAATTTTAGTAGACAGCGGGTTTCCCGTGTAGCC 2292
 Db 41 TTTTGTAATTTTAGTAGACAGCGGGTTTCCCGTGTAGCC 1

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RESULT 311
ADP75520/c
ID ADP75520 standard; DNA; 41 BP.
XX
XX
AC ADP75520;
XX
DT 12-AUG-2004 (first entry)
DE Human ADAM19 gene, sequence surrounding SNP 16.
XX
DE Human; ds; ADAM19; Endophilin 1; Endophilin 2; NRG2; ADAMTS2;
XX a disintegrin and metalloprotease; neuroregulin 2; SNP;
KW
KW
Query Match 1.4%; Score 33; DB 1; Length 41;
Best Local Similarity 87.8%; Pred. No. 5.6e+02;
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2327 CCACCTGGCTCCCAAGTGTGGGATTACAGGCATGAGC 2367
Db 41 CCGCCTTGCCCAACCAAGTGTGGGATTACAGGCATGAGC 1

RESULT 312
ADL64280/c
ID ADL64280 standard; DNA; 41 BP.
XX
XX
AC ADL64280;
XX
DT 20-MAY-2004 (first entry)
DE Human single nucleotide polymorphism (SNP) #203.
XX
DE ss; human; single nucleotide polymorphism; SNP;
XX C1 S subcomponent protein; CIS; alanyl aminopeptidase protein; ANPEP;
KW
KW
Query Match 1.4%; Score 33; DB 1; Length 41;
Best Local Similarity 87.8%; Pred. No. 5.6e+02;
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2298 GGTCTCGATCTCCTGACCTGTCATCGCCACCTCGGCT 2338
Db 41 GGTCTTGAACCTCTTAACCTCATGATCACCACCTCGGCT 1

RESULT 313
ABA96570
ID ABA96570 standard; DNA; 41 BP.
XX
XX
AC ABA96570;
XX
DT 19-MAR-2002 (first entry)
DE Human tyrosinase 9 probe, SEQ ID NO:8.
XX
DE Human; tyrosinase 9; recombinant production; malignant tumour; cancer;
KW blood disease; HIV infection; gene therapy; human immunodeficiency virus;
KW
KW
Query Match 1.4%; Score 32.8; DB 1; Length 41;
Best Local Similarity 94.4%; Pred. No. 5.7e+02;
Matches 34; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2106 GAGTCTTGCTCTGTACCCAGGCTGGAGTGCAGTGG 2141
Db 3 GAGTCTTACTCTGTCTACCCAGGCTGGAGTGCAGTGG 38

RESULT 314
ABA96571
ID ABA96571 standard; DNA; 41 BP.
XX
XX
AC ABA96571;
XX

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DT 19-MAR-2002 (first entry)
XX
XX
DE Human tyrosinase 9 probe, SEQ ID NO:9.
XX
XX
KW Human; tyrosinase 9; recombinant production; malignant tumour; cancer;
KW blood disease; HIV infection; gene therapy; human immunodeficiency virus;
KW
KW
Query Match 1.4%; Score 32.8; DB 1; Length 41;
Best Local Similarity 94.4%; Pred. No. 5.7e+02;
Matches 34; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2106 GAGTCTTGCTCTGTACCCAGGCTGGAGTGCAGTGG 2141
Db 3 GAGTCTTACTCTGTCTACCCAGGCTGGAGTGCAGTGG 38

RESULT 315
ADC59511
ID ADC59511 standard; DNA; 41 BP.
XX
XX
AC ADC59511;
XX
DT 18-DEC-2003 (first entry)
XX
DE Polypeptide-respiratory chain dehydrogenase-11.55 specific probe, #1.
XX
XX
KW Polypeptide-respiratory chain dehydrogenase-11.55; cancer;
KW malignant tumour; haemopathy; human immunodeficiency virus infection;
KW
KW
Query Match 1.4%; Score 32.8; DB 1; Length 41;
Best Local Similarity 94.4%; Pred. No. 5.7e+02;
Matches 34; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2106 GAGTCTTGCTCTGTACCCAGGCTGGAGTGCAGTGG 2141
Db 3 GAGTCTTACTCTGTCTACCCAGGCTGGAGTGCAGTGG 38

RESULT 316
AAH91207/c
ID AAH91207 standard; DNA; 40 BP.
XX
XX
AC AAH91207;
XX
DT 09-OCT-2001 (first entry)
XX
DE Human inflammatory bowel disease associated polymorphic site #282.
XX
XX
KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
KW
KW
Query Match 1.4%; Score 32.6; DB 1; Length 40;
Best Local Similarity 87.5%; Pred. No. 5.8e+02;
Matches 35; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2277 TTTACCGTGTAGCAGGATGGTCTCGATCTCCTGACCT 2316
Db 40 TTTACCATGTAGTACGAGCTGTCTCNAACTCCTGACCT 1

RESULT 317
ABL60966/c
ID ABL60966 standard; DNA; 41 BP.
XX
XX
AC ABL60966;
XX
DT 23-SEP-2002 (first entry)
XX
DE Human retinoblastoma bindin (RBBP9) 13.31 cDNA specific probe 1.
XX
XX
KW Human; retinoblastoma bindin 13.31; RBBP9; retinoblastoma; cancer; probe;
KW ss.

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Query Match      1.4%; Score 32.6; DB 1; Length 41;
Best Local Similarity 89.7%; Pred. No. 5.9e+02;
Matches 35; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2103 ACCGAGTCTGCTCTGTTACCCAGGCTGGAGTGCAAGTGG 2141
    |||||
DB 41 ACTGAGTCTGCTCTGTGCACCCAGGCTTGAGTGTAAGTGG 3

RESULT 318
ABA97057
ID ABA97057 standard; DNA; 41 BP.
XX
AC ABA97057;
XX
DT 18-MAR-2002 (first entry)
XX
DE Human 2-hydroxy acid dehydrogenase 16 probe SEQ ID 9.
KW Human; 2-hydroxy acid dehydrogenase 16; cancer; haemopathy; HIV;
KW human immunodeficiency virus; infection; probe; ss.

Query Match      1.4%; Score 32.4; DB 1; Length 41;
Best Local Similarity 97.1%; Pred. No. 6e+02;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2108 GTCTTGCTCTGTTACCCAGGCTGGAGTGCAAGTGG 2141
    |||||
DB 5 GTCTTGCTCTGTCACCCAGGCTGGAGTGCAAGTGG 38

RESULT 319
ABA97056
ID ABA97056 standard; DNA; 41 BP.
XX
AC ABA97056;
XX
DT 18-MAR-2002 (first entry)
XX
DE Human 2-hydroxy acid dehydrogenase 16 probe SEQ ID 8.
KW Human; 2-hydroxy acid dehydrogenase 16; cancer; haemopathy; HIV;
KW human immunodeficiency virus; infection; probe; ss.

Query Match      1.4%; Score 32.4; DB 1; Length 41;
Best Local Similarity 97.1%; Pred. No. 6e+02;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2108 GTCTTGCTCTGTTACCCAGGCTGGAGTGCAAGTGG 2141
    |||||
DB 5 GTCTTGCTCTGTCACCCAGGCTGGAGTGCAAGTGG 38

RESULT 320
AAH91831/c
ID AAH91831 standard; DNA; 38 BP.
XX
AC AAH91831;
XX
DT 09-OCT-2001 (first entry)
XX
DE Human inflammatory bowel disease associated polymorphic site #906.
KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;

Query Match      1.4%; Score 32.2; DB 1; Length 38;
Best Local Similarity 89.5%; Pred. No. 6e+02;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2307 CTCCTGACCTCGTGATCGGCCACCTCGGCTGCCAAA 2344
    |||||
DB 38 CTCCTGACCTCGTGATCNCGCCACCTCACCTCCCAA 1
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RESULT 321
ABZ72304/c
ID ABZ72304 standard; DNA; 41 BP.
XX
AC ABZ72304;
XX
DT 03-APR-2003 (first entry)
XX
DE Gene 216 SNP reference sequence SEQ ID NO 276.
KW Human; Gene 216; chromosome 20p13-p12; antiasthmatic; anorectic;
KW antiinflammatory; gastrointestinal; gene therapy; vaccine; asthma;

Query Match      1.3%; Score 32; DB 1; Length 41;
Best Local Similarity 87.5%; Pred. No. 6.3e+02;
Matches 35; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2315 CTCGTGATCGCCACCTCGGCTCCCAAAGTGTGGAT 2354
    |||||
DB 40 CTGCTGATCTCTTACCCCGGCTTCCCAAAGTGTGGAT 1

RESULT 322
ABZ49727/c
ID ABZ49727 standard; DNA; 41 BP.
XX
AC ABZ49727;
XX
DT 26-JUN-2003 (first entry)
XX
DE Human sulphotransferase TPST2 gene polymorphic site, #6509.
KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 22;
KW polymorphic site; drug evaluation; drug screening; genotyping;

Query Match      1.3%; Score 32; DB 1; Length 41;
Best Local Similarity 87.5%; Pred. No. 6.3e+02;
Matches 35; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2263 TAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCT 2302
    |||||
DB 41 TAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCT 2

RESULT 323
ABZ43574/c
ID ABZ43574 standard; DNA; 41 BP.
XX
AC ABZ43574;
XX
DT 26-JUN-2003 (first entry)
XX
DE Human sulphotransferase TPST2 gene polymorphic site, #358.
KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 22;
KW polymorphic site; drug evaluation; drug screening; genotyping;

Query Match      1.3%; Score 32; DB 1; Length 41;
Best Local Similarity 87.5%; Pred. No. 6.3e+02;
Matches 35; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2263 TAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCT 2302
    |||||
DB 41 TAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCT 2

RESULT 324
ABX75157/c
ID ABX75157 standard; DNA; 41 BP.
XX
AC ABX75157;
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XX 25-MAR-2003 (first entry)
DT Human gene 216 DNA sequence flanking SNP #43.
DE Human; mouse; ds; gene 216; antiasthmatic; antiinflammatory; anorectic;
KW chromosome 20p13-p12; single nucleotide polymorphism; SNP; gene therapy;
KW
Query Match 1.3%; Score 32; DB 1; Length 41;
Best Local Similarity 87.5%; Pred. No. 6.3e+02;
Matches 35; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2315 CTGGTGATCGCCGACCTCGGCTCCCAAGTCTGGGAT 2354
Db 40 CTGGTGATCTCTTACCCTCCGCTTCCCAAGTCTGGGAT 1
RESULT 325
ADJ36885/C
ID ADJ36885 standard; DNA; 41 BP.
XX AC ADJ36885;
XX
XX 22-APR-2004 (first entry)
DT Gene 216 single nucleotide polymorphism seq id 276.
XX antiasthmatic; respiratory; gene therapy; asthma;
KW bronchial hyperresponsiveness; atopy; chronic obstructive lung disease;
KW
Query Match 1.3%; Score 32; DB 1; Length 41;
Best Local Similarity 87.5%; Pred. No. 6.3e+02;
Matches 35; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2315 CTGGTGATCGCCGACCTCGGCTCCCAAGTCTGGGAT 2354
Db 40 CTGGTGATCTCTTACCCTCCGCTTCCCAAGTCTGGGAT 1
RESULT 326
ADL81463/C
ID ADL81463 standard; DNA; 41 BP.
XX AC ADL81463;
XX
XX 20-MAY-2004 (first entry)
DT Gene 216 single nucleotide polymorphism #36.
XX asthma; bronchial hyperresponsiveness; obesity;
KW inflammatory bowel disease; human; gene 216; ds;
KW
Query Match 1.3%; Score 32; DB 1; Length 41;
Best Local Similarity 87.5%; Pred. No. 6.3e+02;
Matches 35; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2315 CTGGTGATCGCCGACCTCGGCTCCCAAGTCTGGGAT 2354
Db 40 CTGGTGATCTCTTACCCTCCGCTTCCCAAGTCTGGGAT 1
RESULT 327
AAH49727/C
ID AAH49727 standard; DNA; 41 BP.
XX AC AAH49727;
XX
XX 25-SEP-2001 (first entry)
DT Human DNA mismatch repair protein 11 coding sequence probe #1.
XX Human; DNA mismatch repair protein 11; cancer; haemopathy; HIV infection;
KW immunological disease; inflammation; gene therapy; probe; ss.
KW
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Query Match 1.3%; Score 31.4; DB 1; Length 41;
Best Local Similarity 85.4%; Pred. No. 6.7e+02;
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2322 TCGGCCACCTCGGCTCCCAAGTCTGGGATTACAGCA 2362
Db 41 TCTTCTGCTCGGCTCCCAAGTCTGGGATTACAGCA 1
RESULT 328
ABV74811/C
ID ABV74811 standard; DNA; 41 BP.
XX AC ABV74811;
XX
XX 31-JAN-2003 (first entry)
DT Signalase 11.22 probe #1.
XX Signalase 11.22; enzyme; tumour; haemopathy; HIV infection;
KW immunological disease; inflammation; cytostatic; anti-HIV; probe; ss.
KW
Query Match 1.3%; Score 31.4; DB 1; Length 41;
Best Local Similarity 97.0%; Pred. No. 6.7e+02;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2109 TCTTGCTCTGTACCAGGCTGGAGTGCAGTGG 2141
Db 41 TCTTGCTCTGTACCAGGCTGGAGTGCAGTGG 9
RESULT 329
ABL40963/C
ID ABL40963 standard; DNA; 41 BP.
XX AC ABL40963;
XX
XX 03-JUL-2002 (first entry)
DT Transcription regulation factor ZFM1 isomer 19.47 cDNA specific probe 1.
XX Transcription regulation factor ZFM1 isomer 19.47; human; ZFM1;
KW transcription regulation factor; cytostatic; haemostatic; virucide;
KW
Query Match 1.3%; Score 31.4; DB 1; Length 41;
Best Local Similarity 85.4%; Pred. No. 6.7e+02;
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2188 TTCTCTGCTCAGCCTCCCAATTAGCTTGGCCTACAGTCA 2228
Db 41 TTCTCTGCTCAACCTCCGAGTAGCTGGGACTACAGCA 1
RESULT 330
ABL40964/C
ID ABL40964 standard; DNA; 41 BP.
XX AC ABL40964;
XX
XX 03-JUL-2002 (first entry)
DT Transcription regulation factor ZFM1 isomer 19.47 cDNA specific probe 2.
XX Transcription regulation factor ZFM1 isomer 19.47; human; ZFM1;
KW transcription regulation factor; cytostatic; haemostatic; virucide;
KW
Query Match 1.3%; Score 31.4; DB 1; Length 41;
Best Local Similarity 85.4%; Pred. No. 6.7e+02;
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2188 TTCTCTGCTCAGCCTCCCAATTAGCTTGGCCTACAGTCA 2228
Db 41 TTCTCTGCTCAGCCTCCCAATTAGCTTGGCCTACAGTCA 1
```

Db 41 TTCTCTGCTCAACCTCCGAGTAGCTGGGACTACAGGCA 1

RESULT 331
ABZ47125/c
ID ABZ47125 standard; DNA; 41 BP.
XX
XX
XX AC ABZ47125;
XX
XX
DT 26-JUN-2003 (first entry)
XX
DE Human ATP-binding cassette ABCB4 gene polymorphic site, #3909.
XX
XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 7;
XX polymorphic site; drug evaluation; drug screening; genotyping;
KW

Query Match 1.3%; Score 31.4; DB 1; Length 41;
Best Local Similarity 85.4%; Pred. No. 6.7e+02;
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2092 TTTTGTGACCGAGCTTGTCTGTACCCAGGCTGGA 2132
DB 41 TTTTGTGAGTGAAGTCTTACTCTGTCTCACCACCAAGCTGGA 1

RESULT 332
ABZ43249/c
ID ABZ43249 standard; DNA; 41 BP.
XX
XX
XX AC ABZ43249;
XX
XX
DT 26-JUN-2003 (first entry)
XX
DE Human ATP-binding cassette ABCB4 gene polymorphic site, #33.
XX
XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 7;
XX polymorphic site; drug evaluation; drug screening; genotyping;
KW

Query Match 1.3%; Score 31.4; DB 1; Length 41;
Best Local Similarity 85.4%; Pred. No. 6.7e+02;
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2092 TTTTGTGACCGAGCTTGTCTGTACCCAGGCTGGA 2132
DB 41 TTTTGTGAGTGAAGTCTTACTCTGTCTCACCACCAAGCTGGA 1

RESULT 333
ABZ49403
ID ABZ49403 standard; DNA; 41 BP.
XX
XX
XX AC ABZ49403;
XX
XX
DT 26-JUN-2003 (first entry)
XX
DE Human UDP glycosyltransferase UGT2B15 gene polymorphic site, #6186.
XX
XX Human; drug metabolising enzyme; gene; drug metabolism; polymorphic site;
XX drug evaluation; drug screening; genotyping; genetic profiling;
KW

Query Match 1.3%; Score 31.4; DB 1; Length 41;
Best Local Similarity 85.4%; Pred. No. 6.7e+02;
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2272 CAGGTTTACCGTTAGCCAGGATGCTCGATCTCTG 2312
DB 1 CAGAGTTTACCATGTTGGCCAGGCTGCTTGAATCTCTG 41

RESULT 334
AAL51683/c
ID AAL51683 standard; DNA; 41 BP.
XX

AC AAL51683;
XX
DT 17-APR-2003 (first entry)
XX
XX
DE PC6 protease 9-9 (AIDS-associated protein) nucleotide probe #1.
XX
XX
XX KW Probe; ss; PC6 protease; 9.9; AIDS-associated protein; diabetes; AIDS.
XX

Query Match 1.3%; Score 31.2; DB 1; Length 41;
Best Local Similarity 91.7%; Pred. No. 6.8e+02;
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2106 GAGTCTTGCTCTGTACCCAGGCTGGAGTGCAGTGG 2141
DB 41 GAGTCTGCTCTGTGCGCCAGGCTGGAGTGCAGTGG 6

RESULT 335
AAF88864/c
ID AAF88864 standard; DNA; 41 BP.
XX
XX
XX AC AAF88864;
XX
XX
DT 07-JAN-2003 (first entry)
XX
DE Saccharophosphotransferase 9.46 PCR primer SEQ ID 8.
XX
XX Phosphoenolpyruvate dependent saccharophosphotransferase 9.46;
KW malignant tumour; haemopathy; HIV infection; immunological disease;

Query Match 1.3%; Score 31.2; DB 1; Length 41;
Best Local Similarity 91.7%; Pred. No. 6.8e+02;
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2106 GAGTCTTGCTCTGTACCCAGGCTGGAGTGCAGTGG 2141
DB 38 GAGTCTGCTCTGTGCGCCAGGCTGGAGTGCAGTGG 3

RESULT 336
ADC59512
ID ADC59512 standard; DNA; 41 BP.
XX
XX
XX AC ADC59512;
XX
XX
DT 18-DEC-2003 (first entry)
XX
DE Polypeptide-respiratory chain dehydrogenase-11.55 specific probe, #2.
XX
XX Polypeptide-respiratory chain dehydrogenase-11.55; cancer;
KW malignant tumour; haemopathy; human immunodeficiency virus infection;

Query Match 1.3%; Score 31.2; DB 1; Length 41;
Best Local Similarity 91.7%; Pred. No. 6.8e+02;
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2106 GAGTCTTGCTCTGTACCCAGGCTGGAGTGCAGTGG 2141
DB 3 GAGTCTTGCTCTGTGCGCTAGGCTGGAGTGCAGTGG 38

RESULT 337
ABZ57501/c
ID ABZ57501 standard; DNA; 41 BP.
XX
XX
XX AC ABZ57501;
XX
XX
DT 05-APR-2003 (first entry)
XX
DE Ser/Thr protein kinase 9.79 probe, SEQ ID NO:9.
XX
XX Ser/Thr protein kinase 9.79; recombinant production; gene therapy;
KW

XX ABL60967;
AC
XX
DT 23-SEP-2002 (first entry)
XX
DE Human retinoblastoma bindin (RBBP9) 13.31 cDNA specific probe 2.
XX
KW Human; retinoblastoma bindin 13.31; RBBP9; retinoblastoma; cancer; probe;
KW 98.

Query Match 1.3%; Score 31; DB 1; Length 41;
Best Local Similarity 87.2%; Pred. No. 6.9e+02;
Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2103 ACCGAGTCTTCTCTGTACCCAGGCTGGAGTGAGTGG 2141
DB 41 ACTGAGTCTTCTCTGTACCCAGGCTGGAGTGAGTGG 3

RESULT 345
ADE24786/c
ID ADE24786 standard; DNA; 36 BP.
XX
AC ADE24786;
XX
DT 29-JAN-2004 (first entry)
XX
DE Genetic analysis method associated target DNA seq id 11.
XX
KW genetic analysis; complementary strand extension;
KW fluorophore-tagged DNA strand; DNA analysis; genetic testing;

Query Match 1.3%; Score 30.8; DB 1; Length 36;
Best Local Similarity 88.9%; Pred. No. 6.8e+02;
Matches 32; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2305 ATCTCTGACCTCGTGATCCGCCACCTCGGCTCC 2340
DB 36 AACTCTTAACCTCGTGATCCGCCACCTCGGCTCC 1

RESULT 346
ACC84461
ID ACC84461 standard; DNA; 33 BP.
XX
AC ACC84461;
XX
DT 28-AUG-2003 (first entry)
XX
DE NTP peptide encoding sequence #8.
XX
KW Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;
KW neural thread protein; NTP; tumour; ds.

Query Match 1.3%; Score 29.8; DB 1; Length 33;
Best Local Similarity 93.9%; Pred. No. 7.4e+02;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2331 CTCGGCTCCCAAGTGTGGGATTACAGGCAT 2363
DB 1 CTCAGCTCCCAAGTGTGGGATTACAGGCAT 33

RESULT 347
AAA97662/c
ID AAA97662 standard; DNA; 29 BP.
XX
AC AAA97662;
XX
DT 15-FEB-2001 (first entry)
XX
DE Human MDM2 hybridisation probe.

KW Pseudocyclic oligonucleotide; functional segment; protective segment;
KW nucleic acid detection; mRNA cleavage; antisense therapy; PCO;

Query Match 1.2%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 649 AGGAATCATCGGACTCAGGTACATCTGTG 677
DB 29 AGGAATCATCGGACTCAGGTACATCTGTG 1

RESULT 348
ABL60508/c
ID ABL60508 standard; DNA; 29 BP.
XX
AC ABL60508;
XX
DT 12-AUG-2002 (first entry)
XX
DE Human MDM2 mRNA hybridising probe.
XX
KW Pseudo-cyclic oligonucleotide; PCO; gene expression; protein kinase A;
KW nucleic acid detection; ribozyme inhibition; gene transcription; MDM2;

Query Match 1.2%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 649 AGGAATCATCGGACTCAGGTACATCTGTG 677
DB 29 AGGAATCATCGGACTCAGGTACATCTGTG 1

RESULT 349
AAK91040
ID AAK91040 standard; DNA; 32 BP.
XX
AC AAK91040;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human digestive system antigen genomic sequence SEQ ID NO: 4616.
XX
KW Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;

Query Match 1.2%; Score 28.8; DB 1; Length 32;
Best Local Similarity 93.8%; Pred. No. 8.1e+02;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2250 TTTTGTACTTTTAGTAGAGACAGGGTTTCA 2281
DB 1 TTTTGTACTTTTAGTAGAGACAGGGTTTCA 32

RESULT 350
AAS32075
ID AAS32075 standard; DNA; 32 BP.
XX
AC AAS32075;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human liver associated genomic DNA #249.
XX
KW Liver associated protein; human; mouse; rabbit; goat; horse; cat; dog;
KW chicken; sheep; immunosuppressive; antiarthritic; vasotropic;

Query Match 1.2%; Score 28.8; DB 1; Length 32;
Best Local Similarity 93.8%; Pred. No. 8.1e+02;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 2250 TTTTTCGTACTTTTAGTAGAGACAGGGTTTCA 2281
DB 1 TTTTTCGTACTTTTAGTAGAGACAGGGTTTCA 32

RESULT 351
ABN90430
ID ABN90430 standard; DNA; 32 BP.
XX AC
XX ABN90430;
XX
DT 24-JUL-2002 (first entry)
XX
DE Human liver antigen HLDV38 genomic sequence, SEQ ID NO:551.
KW Human; liver antigen; liver disorder; hepatic disorder; infection;
KW hepatitis; viral; parasitic; bacterial; fungal; inflammatory condition;
KW

Query Match 1.2%; Score 28.8; DB 1; Length 32;
Best Local Similarity 93.8%; Pred. No. 8.1e+02;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2250 TTTTTCGTACTTTTAGTAGAGACAGGGTTTCA 2281
DB 1 TTTTTCGTACTTTTAGTAGAGACAGGGTTTCA 32

RESULT 352
ADJ15343
ID ADJ15343 standard; DNA; 32 BP.
XX AC
XX ADJ15343;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human liver-related genomic DNA - SEQ ID 551.
KW liver; virucide; fungicide; antibacterial; antiparasitic; hepatotropic;
KW antiinflammatory; cytostatic; litholytic; antirheumatic; antiarthritic;
KW

Query Match 1.2%; Score 28.8; DB 1; Length 32;
Best Local Similarity 93.8%; Pred. No. 8.1e+02;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2250 TTTTTCGTACTTTTAGTAGAGACAGGGTTTCA 2281
DB 1 TTTTTCGTACTTTTAGTAGAGACAGGGTTTCA 32

RESULT 353
AAL47196
ID AAL47196 standard; DNA; 30 BP.
XX AC
XX AAL47196;
XX
DT 22-AUG-2002 (first entry)
XX
DE Human rheumatoid arthritis associated DR3 gene related oligo #9.
KW Human; DR3; rheumatoid arthritis; antirheumatic; antiarthritic;
KW gene therapy; PCR; primer; ss.

Query Match 1.2%; Score 28.4; DB 1; Length 30;
Best Local Similarity 96.7%; Pred. No. 8.3e+02;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2295 GATGGTCTCGATCTCTGACCTCGTGATCC 2324
DB 1 GATGGTCTCTGATCTCTGACCTCGTGATCC 30

RESULT 354
AAL47197/c
ID AAL47197 standard; DNA; 30 BP.
XX AC
XX AAL47197;
XX
DT 22-AUG-2002 (first entry)
XX
DE Human rheumatoid arthritis associated DR3 gene related oligo #10.
KW Human; DR3; rheumatoid arthritis; antirheumatic; antiarthritic;
KW gene therapy; PCR; primer; ss.

Query Match 1.2%; Score 28.4; DB 1; Length 30;
Best Local Similarity 96.7%; Pred. No. 8.3e+02;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2295 GATGGTCTCGATCTCTGACCTCGTGATCC 2324
DB 30 GATGGTCTTGTGATCTCTGACCTCGTGATCC 1

RESULT 355
ADE14248/c
ID ADE14248 standard; DNA; 32 BP.
XX AC
XX ADE14248;
XX
DT 29-JAN-2004 (first entry)
XX
DE Optineurin promoter motif, repeat element or regulatory region #357.
KW Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
KW SNP; glaucoma; progressive ocular hypertensive disorder;

Query Match 1.2%; Score 28.4; DB 1; Length 32;
Best Local Similarity 96.7%; Pred. No. 8.5e+02;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2343 AAGTGTCTGGATTACAGGCATGAGCCACCG 2372
DB 32 AAGTGTCTGGATTACAGGCATGAGCCACCG 3

RESULT 356
ADE14029/c
ID ADE14029 standard; DNA; 32 BP.
XX AC
XX ADE14029;
XX
DT 29-JAN-2004 (first entry)
XX
DE Optineurin promoter motif, repeat element or regulatory region #138.
KW Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
KW SNP; glaucoma; progressive ocular hypertensive disorder;

Query Match 1.2%; Score 28.4; DB 1; Length 32;
Best Local Similarity 96.7%; Pred. No. 8.5e+02;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2343 AAGTGTCTGGATTACAGGCATGAGCCACCG 2372
DB 32 AAGTGTCTGGATTACAGGCATGAGCCACCG 3

RESULT 357
AAA97658
ID AAA97658 standard; DNA; 28 BP.
XX AC
XX AAA97658;
XX
DT 15-FEB-2001 (first entry)
XX
DE Human MDM2 gene target oligonucleotide.
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XX KW Pseudocyclic oligonucleotide; functional segment; protective segment;
KW nucleic acid detection; mRNA cleavage; antisense therapy; PCO;

Query Match 1.2%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 671 ATCTGTGAGTGAGACACAGGTGTCACTT 698
Db 1 ATCTGTGAGTGAGACACAGGTGTCACTT 28

RESULT 358
ABK65940/c
ID ABK65940 standard; DNA; 28 BP.
XX AC ABK65940;
XX DT 02-JUL-2002 (first entry)
XX DE Human gene specific PCR primer #28.
XX KW Primer; ss; DNA microarray; differential expression analysis; human.
XX

Query Match 1.2%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1204 CCTTAGCTGACTATTGGAAATGCACCTC 1231
Db 28 CCTTAGCTGACTATTGGAAATGCACCTC 1

RESULT 359
ABK65939
ID ABK65939 standard; DNA; 28 BP.
XX AC ABK65939;
XX DT 02-JUL-2002 (first entry)
XX DE Human gene specific PCR primer #27.
XX KW Primer; ss; DNA microarray; differential expression analysis; human.
XX

Query Match 1.2%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 920 GGAGATATGTTGTGAAGAAGCAGTAGC 947
Db 1 GGAGATATGTTGTGAAGAAGCAGTAGC 28

RESULT 360
ABL60504
ID ABL60504 standard; DNA; 28 BP.
XX AC ABL60504;
XX DT 12-AUG-2002 (first entry)
XX DE Human MDM2 mRNA fragment complementary oligo 16.
XX KW Pseudo-cyclic oligonucleotide; PCO; gene expression; protein kinase A;
XX nucleic acid detection; ribozyme inhibition; gene transcription; MDM2;

Query Match 1.2%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 671 ATCTGTGAGTGAGACACAGGTGTCACTT 698
Db 1 ATCTGTGAGTGAGACACAGGTGTCACTT 28

RESULT 361
ADP11597/c
ID ADP11597 standard; DNA; 28 BP.
XX AC ADP11597;
XX DT 12-AUG-2004 (first entry)
XX DE Tagman probe of the invention #280.
XX KW transplant rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss; probe.

Query Match 1.2%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1687 TGGCCTGCTTTACATGTGCAAGAGCT 1714
Db 28 TGGCCTGCTTTACATGTGCAAGAGCT 1

RESULT 362
AAI62688/c
ID AAI62688 standard; DNA; 33 BP.
XX AC AAI62688;
XX DT 19-OCT-2001 (first entry)
XX DE Human breast or ovarian antigen genomic DNA SEQ ID NO: 338.
XX KW Human; breast antigen; ovarian antigen; cancer; metastasis; gene therapy;
KW ds.

Query Match 1.2%; Score 27.8; DB 1; Length 33;
Best Local Similarity 93.5%; Pred. No. 9.1e+02;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2111 TTGCTCTGTTACCCAGGCTGGAGTGCAGTGG 2141
Db 33 TGGCTCTGTTGCCAGGCTGGAGTGCAGTGG 3

RESULT 363
AAL06807/c
ID AAL06807 standard; DNA; 33 BP.
XX AC AAL06807;
XX DT 21-NOV-2001 (first entry)
XX DE Human reproductive system related antigen DNA SEQ ID NO: 9495.
XX KW Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; ds.

Query Match 1.2%; Score 27.8; DB 1; Length 33;
Best Local Similarity 93.5%; Pred. No. 9.1e+02;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2111 TTGCTCTGTTACCCAGGCTGGAGTGCAGTGG 2141
Db 33 TGGCTCTGTTGCCAGGCTGGAGTGCAGTGG 3

RESULT 364

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AAH91537/c
ID  AAH91537 standard; DNA; 35 BP.
XX
AC  AAH91537;
XX
DT  09-OCT-2001 (first entry)
XX
DE  Human inflammatory bowel disease associated polymorphic site #612.
XX
KW  Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW  single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;

Query Match      1.2%; Score 27.6; DB 1; Length 35;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 30; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  2233 CCACCACCTGGCTAAATTTTGTACTTTTACTA 2267
    |||||
DB  35 CCACAAGCCGCGCTAAATTTTGTATTTTGGTA 1

RESULT 365
AAQ73572
ID  AAQ73572 standard; DNA; 31 BP.
XX
AC  AAQ73572;
XX
DT  25-MAR-2003 (revised)
DT  25-JUN-1995 (first entry)
XX
DE  Enhancer element ex-4 conserved basepair sequence.
XX
KW  Enhancer element; carcinoma; tumor; cancer; SLPI gene;

Query Match      1.2%; Score 27.4; DB 1; Length 31;
Best Local Similarity 90.3%; Pred. No. 9.3e+02;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2331 CTGGGCTCCCAAGTGTGGGATTACAGGC 2361
    |||||
DB  1 CTCAGCTCCCAAGTGTGGGANTACAGGC 31

RESULT 366
AAQ27389
ID  AAQ27389 standard; DNA; 32 BP.
XX
AC  AAQ27389;
XX
DT  25-MAR-2003 (revised)
DT  27-JAN-1993 (first entry)
XX
DE  Inter-Alu specific primer PDJ33A.
XX
KW  Polymerase chain reaction; PCR; repetitive element; ss.

Query Match      1.2%; Score 27.4; DB 1; Length 32;
Best Local Similarity 96.6%; Pred. No. 9.4e+02;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2332 TCGGCTCCCAAGTGTGGGATTACAGG 2360
    |||||
DB  4 TCGGCTCCCAAGTGTGGGATTACAGG 32

RESULT 367
AAQ04371
ID  AAQ04371 standard; DNA; 29 BP.
XX
AC  AAQ04371;
XX
DT  22-MAY-2000 (first entry)
XX

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DE  Polymorphic fragment of hypertension associated gene HSTSCGENE.
XX
KW  Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW  Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

Query Match      1.1%; Score 27; DB 1; Length 29;
Best Local Similarity 93.1%; Pred. No. 9.5e+02;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY  2339 CCCAAGTCTGGGATTACAGGCATGAGC 2367
    |||||
DB  1 CCCAAGTCTGGGRTTACAGGCCTGAGC 29

RESULT 368
AAQ04313
ID  AAQ04313 standard; DNA; 29 BP.
XX
AC  AAQ04313;
XX
DT  22-MAY-2000 (first entry)
XX
DE  Polymorphic fragment of hypertension associated gene GLUT4.
XX
KW  Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW  Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

Query Match      1.1%; Score 27; DB 1; Length 29;
Best Local Similarity 93.1%; Pred. No. 9.5e+02;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY  2281 ACGTGTAGCCAGGATGCTCGATCTC 2309
    |||||
DB  1 ACCATGTAGCCAGRATGCTCTCGATCTC 29

RESULT 369
AAQ03996
ID  AAQ03996 standard; DNA; 29 BP.
XX
AC  AAQ03996;
XX
DT  22-MAY-2000 (first entry)
XX
DE  Polymorphic fragment of hypertension associated gene APOC4.
XX
KW  Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW  Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

Query Match      1.1%; Score 27; DB 1; Length 29;
Best Local Similarity 93.1%; Pred. No. 9.5e+02;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY  2332 TCGGCTCCCAAGTGTGGGATTACAGG 2360
    |||||
DB  1 TTGGCTCCCAAGYGCTGGGATTACAGG 29

RESULT 370
ADE14206/c
ID  ADE14206 standard; DNA; 32 BP.
XX
AC  ADE14206;
XX
DT  29-JAN-2004 (first entry)
XX
DE  Optineurin promoter motif, repeat element or regulatory region #315.
XX
KW  Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
KW  SNP; glaucoma; progressive ocular hypertensive disorder;

Query Match      1.1%; Score 26.8; DB 1; Length 32;
Best Local Similarity 93.3%; Pred. No. 1e+03;

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Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2343 AAGTCTGGGATTACAGCATGAGCCACCG 2372
 Db |||||
 32 AAGTCTGGGATTACAGGTGTGAGCCACCG 3

RESULT 371
 AAZ37740/c
 ID AAZ37740 standard; DNA; 26 BP.
 XX
 AC AAZ37740;
 XX
 DT 07-JAN-2000 (first entry)
 XX
 DE Human mdm2 real-time reverse PCR primer #270.
 XX
 DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
 KW antisense; modulation; oligonucleotide; expression; inhibition;
 KW

Query Match 1.1%; Score 26; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 415 TGAAGTTATTAAAGTCTGTGGTGCA 440
 Db |||||
 26 TGAAGTTATTAAAGTCTGTGGTGCA 1

RESULT 372
 AAA97660
 ID AAA97660 standard; DNA; 26 BP.
 XX
 AC AAA97660;
 XX
 DT 15-FEB-2001 (first entry)
 XX
 DE Human MDM2 forward RT-PCR primer.
 XX
 DE Pseudocyclic oligonucleotide; functional segment; protective segment;
 KW nucleic acid detection; mRNA cleavage; antisense therapy; PCO;

Query Match 1.1%; Score 26; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 622 ACAGGAATTGGTAGTCAATCAG 647
 Db |||||
 1 ACAGGAATTGGTAGTCAATCAG 26

RESULT 373
 AAA50949
 ID AAA50949 standard; DNA; 26 BP.
 XX
 AC AAA50949;
 XX
 DT 27-OCT-2000 (first entry)
 XX
 DE Human mdm2 PCR primer #1.
 XX
 DE Fluorescent protein; fluorescence labelling; fusion protein; human;
 KW PCR primer; ss.

Query Match 1.1%; Score 26; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 ATGTGCAATACCAATGCTGTGTACC 337
 Db |||||
 1 ATGTGCAATACCAATGCTGTGTACC 26

RESULT 374
 AAD03619
 ID AAD03619 standard; DNA; 26 BP.
 XX
 AC AAD03619;
 XX
 DT 19-JUN-2001 (first entry)
 XX
 DE Human marathon cDNA library (Burke's lymphoma) amplifying PCR primer #1.
 DE Anthozoa; Chromoprotein; fluorescent protein; sunscreen; biosensor;
 KW analyte detection assay; selectable marker; recombinant DNA application;
 KW

Query Match 1.1%; Score 26; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 ATGTGCAATACCAATGCTGTGTACC 337
 Db |||||
 1 ATGTGCAATACCAATGCTGTGTACC 26

RESULT 375
 AAF80894/c
 ID AAF80894 standard; DNA; 26 BP.
 XX
 AC AAF80894;
 XX
 DT 02-MAY-2001 (first entry)
 XX
 DE Human mdm2 reverse primer.
 DE
 XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
 XX

Query Match 1.1%; Score 26; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 415 TGAAGTTATTAAAGTCTGTGGTGCA 440
 Db |||||
 26 TGAAGTTATTAAAGTCTGTGGTGCA 1

RESULT 376
 AAS29509/c
 ID AAS29509 standard; DNA; 26 BP.
 XX
 AC AAS29509;
 XX
 DT 21-NOV-2001 (first entry)
 XX
 DE Reverse PCR primer used to amplify human mdm2 mRNA.
 XX
 DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;
 KW

Query Match 1.1%; Score 26; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 415 TGAAGTTATTAAAGTCTGTGGTGCA 440
 Db |||||
 26 TGAAGTTATTAAAGTCTGTGGTGCA 1

RESULT 377
 ABL60506
 ID ABL60506 standard; DNA; 26 BP.
 XX
 AC ABL60506;
 XX
 DT 12-AUG-2002 (first entry)


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XX Human MDM2 mRNA amplifying RT-PCR forward primer.
DE Pseudo-cyclic oligonucleotide; PCO; gene expression; protein kinase A;
XX nucleic acid detection; ribozyme inhibition; gene transcription; MDM2;
KW
KW
Query Match 1.1%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 622 ACAGGAACCTTGGTAGTAGTCAATCAG 647
DB 1 ACAGGAACCTTGGTAGTAGTCAATCAG 26

RESULT 378
ADD21705/c
ID ADD21705 standard; DNA; 26 BP.
XX
XX
AC ADD21705;
XX
XX 15-JAN-2004 (first entry)
DE Human mdm2-specific PCR primer #2.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 1.1%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 415 TGAAGTTATTAAAGTCTGTGGTGCA 440
DB 26 TGAAGTTATTAAAGTCTGTGGTGCA 1

RESULT 379
AAA04303
ID AAA04303 standard; DNA; 29 BP.
XX
XX
AC AAA04303;
XX
XX 22-MAY-2000 (first entry)
DE Polymorphic fragment of hypertension associated gene GLUT4.
XX
XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
Query Match 1.1%; Score 26; DB 1; Length 29;
Best Local Similarity 92.9%; Pred. No. 1.e+03;
Matches 26; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2345 GTGCTGGATTACAGGATGAGCACCG 2372
DB 1 GTGCTGGATTACAGGATGAGCACCG 28

RESULT 380
AAD42705
ID AAD42705 standard; DNA; 30 BP.
XX
XX
AC AAD42705;
XX
XX 15-NOV-2002 (first entry)
DE Hdm2 cDNA amplifying PCR primer.
XX
XX Human; detection; cancer; ARF-p19 protein; cell cycle regulator; tumour;
KW cell cycle arrest; cell growth; hyperproliferative signal; therapeutic;
Query Match 1.1%; Score 25.8; DB 1; Length 30;

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Best Local Similarity 93.1%; Pred. No. 1.e+03;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 312 ATGTGCAATACCAACATGCTGTGTACCTAC 340
DB 1 ATGTGCAATACCAACATGCTGTGTGTCTAC 29

RESULT 381
AAA03956
ID AAA03956 standard; DNA; 29 BP.
XX
XX
AC AAA03956;
XX
XX 22-MAY-2000 (first entry)
DE Polymorphic fragment of hypertension associated gene APOC1.
XX
XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
Query Match 1.1%; Score 25.4; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 1.e+03;
Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2254 TTGTACTTTTAGTAGACAGAGGTTTTCAC 2282
DB 1 TTGTATTTTCAGTAKAGACAGAGGTTTTCAC 29

RESULT 382
AAA04312
ID AAA04312 standard; DNA; 29 BP.
XX
XX
AC AAA04312;
XX
XX 22-MAY-2000 (first entry)
DE Polymorphic fragment of hypertension associated gene GLUT4.
XX
XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
Query Match 1.1%; Score 25.4; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 1.e+03;
Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2275 GGTTCACCGTGTAGCCAGGATGGTCTC 2303
DB 1 GGTTCACCATGTTGCCAGAAATGGTCTC 29

RESULT 383
AAA03995
ID AAA03995 standard; DNA; 29 BP.
XX
XX
AC AAA03995;
XX
XX 22-MAY-2000 (first entry)
DE Polymorphic fragment of hypertension associated gene APOC4.
XX
XX Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
Query Match 1.1%; Score 25.4; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 1.e+03;
Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2326 CCCACTCGGCTCCCAAGTCTGGAT 2354
DB 1 CCCGCTTGGCTCTCYCAAAGTCTGGAT 29

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RESULT 384
AA04505
ID AAA04505 standard; DNA; 29 BP.
XX AC
XX AAA04505;
DT 22-MAY-2000 (first entry)
XX DE Polymorphic fragment of hypertension associated gene PGIS.
XX DE Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
KW Query Match 1.1%; Score 25.4; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 1.1e+03;
Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2319 TGATCCGCCACCTCGGCTCCCAAGTG 2347
Db 1 TGAATGCCCGCTTGGCTCCCAAGTG 29

RESULT 385
AAQ73570
ID AAQ73570 standard; DNA; 32 BP.
XX AC
XX AAQ73570;
DT 25-MAR-2003 (revised)
DT 25-JUN-1995 (first entry)
XX DE Enhancer element er-3 conserved basepair sequence.
XX KW Enhancer element; carcinoma; tumor; cancer; SLPI gene;
Query Match 1.1%; Score 25.2; DB 1; Length 32;
Best Local Similarity 87.1%; Pred. No. 1.2e+03;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2251 TTTTGTACTTTTAGTAGAGACAGGGTTTCA 2281
Db 2 TTTTGTATTTTAGTAGAGATGGGTTTCA 32

RESULT 386
AAH79009/c
ID AAH79009 standard; DNA; 33 BP.
XX AC
XX AAH79009;
DT 09-NOV-2001 (first entry)
XX DE Human signal peptidase 9 PCR primer 4.
XX DE Human; signal peptidase 9; malignant tumour; haemopathy; HIV; infection;
KW human immunodeficiency virus; immunological disease; inflammation;
Query Match 1.1%; Score 25.2; DB 1; Length 33;
Best Local Similarity 90.0%; Pred. No. 1.2e+03;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2342 AAAGTCTGGGATTACAGGCATGAGCCACC 2371
Db 33 AAAGTCTGGGATTACAGGCATGAGGATCC 4

RESULT 387
ABK50423/c
ID ABK50423 standard; DNA; 33 BP.
XX AC
XX ABK50423;
XX KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

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DT 30-JUL-2002 (first entry)
XX DE Human transfer down-regulation protein 9.79 cDNA PCR primer #2.
XX DE Human; transfer down-regulation protein 9.79; primer; ss; tumour; cancer;
KW DNA recombination; PCR.
Query Match 1.1%; Score 25.2; DB 1; Length 33;
Best Local Similarity 90.0%; Pred. No. 1.2e+03;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2342 AAAGTCTGGGATTACAGGCATGAGCCACC 2371
Db 33 AAAGTCTGGGATTACAGGCATGAGGATCC 4

RESULT 388
AAZ37741
ID AAZ37741 standard; DNA; 25 BP.
XX AC
XX AAZ37741;
DT 07-JAN-2000 (first entry)
XX DE Human mdm2 real-time reverse PCR probe #271.
XX DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 355 CCACCTCACAGATTCAGCTTCGGA 379
Db 1 CCACCTCACAGATTCAGCTTCGGA 25

RESULT 389
AAF80895
ID AAF80895 standard; DNA; 25 BP.
XX AC
XX AAF80895;
DT 02-MAY-2001 (first entry)
XX DE Human mdm2 amplification probe.
XX DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 355 CCACCTCACAGATTCAGCTTCGGA 379
Db 1 CCACCTCACAGATTCAGCTTCGGA 25

RESULT 390
AAH38447/c
ID AAH38447 standard; DNA; 25 BP.
XX AC
XX AAH38447;
DT 14-AUG-2001 (first entry)
XX DE SNP specific SNPE primer SEQ ID 1243.
XX DE Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

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Query Match      1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2185 CCATTCTCCGCTCAGCCTCCCAA 2209
DB 25 CCATTCTCCGCTCAGCCTCCCAA 1

RESULT 391
AAS29510
ID AAS29510 standard; DNA; 25 BP.
XX
AC AAS29510;
XX
DT 21-NOV-2001 (first entry)
DE Fluorescent labelled human mdm2 probe.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CCACCTCACAGATTCAGCTTCGA 379
DB 1 CCACCTCACAGATTCAGCTTCGA 25

RESULT 392
AAS15700
ID AAS15700 standard; DNA; 25 BP.
XX
AC AAS15700;
XX
DT 29-JAN-2002 (first entry)
DE Human Alu sequence PCR primer #2.
XX
KW Human; Alu sequence; ss; PCR primer; human immunodeficiency virus;
KW Latent HIV detection; LTR; long terminal repeat;

Query Match      1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAAGTCTGGGATTACAG 2359
DB 1 GCCTCCCAAAGTCTGGGATTACAG 25

RESULT 393
ADB04775
ID ADB04775 standard; DNA; 25 BP.
XX
AC ADB04775;
XX
DT 20-NOV-2003 (first entry)
DE Human MDZ7 scanning oligonucleotide SEQ ID 5761.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;

Query Match      1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2283 CGTGTAGCCAGGATGCTCGATC 2307
DB 1 CGTGTAGCCAGGATGCTCGATC 25

Query Match      1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2185 CCATTCTCCGCTCAGCCTCCCAA 2209
DB 25 CCATTCTCCGCTCAGCCTCCCAA 1

RESULT 394
ADB04766
ID ADB04766 standard; DNA; 25 BP.
XX
AC ADB04766;
XX
DT 20-NOV-2003 (first entry)
DE Human MDZ7 scanning oligonucleotide SEQ ID 5752.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;

Query Match      1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTCACCGTGTAGCCAGGATG 2298
DB 1 GGGTTTCACCGTGTAGCCAGGATG 25

RESULT 395
ADB04772
ID ADB04772 standard; DNA; 25 BP.
XX
AC ADB04772;
XX
DT 20-NOV-2003 (first entry)
DE Human MDZ7 scanning oligonucleotide SEQ ID 5758.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;

Query Match      1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGCTCG 2304
DB 1 CACCGTGTAGCCAGGATGCTCG 25

RESULT 396
ADB04781
ID ADB04781 standard; DNA; 25 BP.
XX
AC ADB04781;
XX
DT 20-NOV-2003 (first entry)
DE Human MDZ7 scanning oligonucleotide SEQ ID 5767.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;

Query Match      1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2289 AGCCAGGATGCTCGATCTCTGA 2313
DB 1 AGCCAGGATGCTCGATCTCTGA 25

RESULT 397
ADB04770
ID ADB04770 standard; DNA; 25 BP.
XX
AC ADB04770;

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XX 20-NOV-2003 (first entry)
DT Human MDZ7 scanning oligonucleotide SEQ ID 5756.
DE Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MD24; MD27; MD212; chromosome 7q22.1;
KW Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2278 TTCACCGTGTAGCCAGGATGGTCT 2302
DB 1 TTCACCGTGTAGCCAGGATGGTCT 25

RESULT 398
ADB04773
ID ADB04773 standard; DNA; 25 BP.
XX
XX ADB04773;
AC
DT 20-NOV-2003 (first entry)
DE Human MDZ7 scanning oligonucleotide SEQ ID 5759.
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MD24; MD27; MD212; chromosome 7q22.1;
KW Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2281 ACCGTGTAGCCAGGATGGTCTCGA 2305
DB 1 ACCGTGTAGCCAGGATGGTCTCGA 25

RESULT 399
ADB04771
ID ADB04771 standard; DNA; 25 BP.
XX
XX ADB04771;
AC
DT 20-NOV-2003 (first entry)
DE Human MDZ7 scanning oligonucleotide SEQ ID 5757.
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MD24; MD27; MD212; chromosome 7q22.1;
KW Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2279 TCACCGTGTAGCCAGGATGGTCTC 2303
DB 1 TCACCGTGTAGCCAGGATGGTCTC 25

RESULT 400
ADB04780
ID ADB04780 standard; DNA; 25 BP.
XX
XX ADB04780;
AC
DT 20-NOV-2003 (first entry)
DE Human MDZ7 scanning oligonucleotide SEQ ID 5766.
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MD24; MD27; MD212; chromosome 7q22.1;
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Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2288 TAGCCAGGATGGTCTCGATCTCCTG 2312
DB 1 TAGCCAGGATGGTCTCGATCTCCTG 25

RESULT 401
ADB04767
ID ADB04767 standard; DNA; 25 BP.
XX
XX ADB04767;
AC
DT 20-NOV-2003 (first entry)
DE Human MDZ7 scanning oligonucleotide SEQ ID 5753.
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MD24; MD27; MD212; chromosome 7q22.1;
KW Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2275 GGTTCACCGTGTAGCCAGGATGG 2299
DB 1 GGTTCACCGTGTAGCCAGGATGG 25

RESULT 402
ADB04769
ID ADB04769 standard; DNA; 25 BP.
XX
XX ADB04769;
AC
XX
DT 20-NOV-2003 (first entry)
DE Human MDZ7 scanning oligonucleotide SEQ ID 5755.
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MD24; MD27; MD212; chromosome 7q22.1;
KW Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2277 TTTCACCGTGTAGCCAGGATGGTC 2301
DB 1 TTTCACCGTGTAGCCAGGATGGTC 25

RESULT 403
ADB04776
ID ADB04776 standard; DNA; 25 BP.
XX
XX ADB04776;
AC
XX
DT 20-NOV-2003 (first entry)
DE Human MDZ7 scanning oligonucleotide SEQ ID 5762.
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MD24; MD27; MD212; chromosome 7q22.1;
KW Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2284 GTGTTAGCCAGGATGGTCTCGATCT 2308
DB 1 GTGTTAGCCAGGATGGTCTCGATCT 2308
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Db 1 GTGTTAGCCAGGATGGTCTCGATCT 25

RESULT 404
ADB04779
ID ADB04779 standard; DNA; 25 BP.
XX
AC ADB04779;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5765.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2287 TTAGCCAGGATGGTCTCGATCTCT 2311
DB 1 TTAGCCAGGATGGTCTCGATCTCT 25

RESULT 405
ADB04782
ID ADB04782 standard; DNA; 25 BP.
XX
AC ADB04782;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5768.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2290 GCCAGGATGGTCTCGATCTCTGAC 2314
DB 1 GCCAGGATGGTCTCGATCTCTGAC 25

RESULT 406
ADB04778
ID ADB04778 standard; DNA; 25 BP.
XX
AC ADB04778;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5764.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2286 GTTAGCCAGGATGGTCTCGATCTCC 2310
DB 1 GTTAGCCAGGATGGTCTCGATCTCC 25

RESULT 407
ADB04768
ID ADB04768 standard; DNA; 25 BP.
XX
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AC ADB04768;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5754.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2276 GTTTCACCGTGTAGCCAGGATGGT 2300
DB 1 GTTTCACCGTGTAGCCAGGATGGT 25

RESULT 408
ADB04777
ID ADB04777 standard; DNA; 25 BP.
XX
AC ADB04777;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5763.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2285 TGTAGCCAGGATGGTCTCGATCTC 2309
DB 1 TGTAGCCAGGATGGTCTCGATCTC 25

RESULT 409
ADB04774
ID ADB04774 standard; DNA; 25 BP.
XX
AC ADB04774;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5760.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2282 CCGTGTAGCCAGGATGGTCTCGAT 2306
DB 1 CCGTGTAGCCAGGATGGTCTCGAT 25

RESULT 410
ADD21706
ID ADD21706 standard; DNA; 25 BP.
XX
AC ADD21706;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 nucleotide probe.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
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KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
 Query Match 1.1%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 355 CCACCTCACAGATTCAGCTTCGGA 379
 DB 1 CCACCTCACAGATTCAGCTTCGGA 25

RESULT 411
 AAA04503
 ID AAA04503 standard; DNA; 29 BP.
 XX
 AC AAA04503;
 XX
 DT 22-MAY-2000 (first entry)
 XX
 DE Polymorphic fragment of hypertension associated gene PGIS.
 XX
 KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
 KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
 Query Match 1.1%; Score 25; DB 1; Length 29;
 Best Local Similarity 92.6%; Pred. No. 1.2e+03;
 Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2274 GGGTTTACCGTGTAGCCAGGATGGT 2300
 DB 3 GGATTTACCGTGTAGCCAGGATGGT 29

RESULT 412
 ABA94089/c
 ID ABA94089 standard; DNA; 33 BP.
 XX
 AC ABA94089;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Human tumour suppressor factor 11.77 PCR primer 3 SEQ ID NO:5.
 KW Human; tumour suppressor factor 11.77; cytostatic; haemostatic; virucide;
 KW immunomodulatory; antiinflammatory; gene therapy; malignant tumour;
 Query Match 1.1%; Score 25; DB 1; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2340 CCAAAGTCTGGGATTACAGGCATG 2364
 DB 33 CCAAAGTCTGGGATTACAGGCATG 9

RESULT 413
 ABL54842/c
 ID ABL54842 standard; DNA; 33 BP.
 XX
 AC ABL54842;
 XX
 DT 01-JUL-2002 (first entry)
 XX
 DE Human G-protein subunit 12.65 related primer#4.
 KW Human; G-protein subunit 12.65; cytostatic; analgesic; antiasthmatic;
 KW antidiarrhoeal; antiinflammatory; nootropic; hormone receptor; tumour;
 Query Match 1.1%; Score 25; DB 1; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2342 AAAGTCTGGGATTACAGGCATGAG 2366

DB 33 AAAGTCTGGGATTACAGGCATGAG 9

RESULT 414
 AAA27185
 ID AAA27185 standard; DNA; 28 BP.
 XX
 AC AAA27185;
 XX
 DT 11-SEP-2000 (first entry)
 XX
 DE Reverse primer IL10 for target sequence human interleukin 10.
 XX
 KW P2; CX5C chemokine; Chromosome 5q31; gene therapy; asthma; PCR primer;
 KW allergic rhinitis; urticaria; anaphylactic shock; hives; hay fever; human;
 Query Match 1.0%; Score 24.8; DB 1; Length 28;
 Best Local Similarity 92.9%; Pred. No. 1.2e+03;
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2111 TTGCTCTGTTCACCCAGGCTGGAGTGCAG 2138
 DB 1 TTGCTCTGTTCACCCAGGCTGGAGTGCAG 28

RESULT 415
 AAH39586/c
 ID AAH39586 standard; DNA; 31 BP.
 XX
 AC AAH39586;
 XX
 DT 14-AUG-2001 (first entry)
 XX
 DE SNP specific lower PCR primer SEQ ID 2382.
 KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
 KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
 Query Match 1.0%; Score 24.6; DB 1; Length 31;
 Best Local Similarity 87.1%; Pred. No. 1.2e+03;
 Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2256 GTACTTTTAGTAGACAGACAGCGTTTCACCGTG 2286
 DB 31 GTACTTTTAGTAGACAGACAGCGTTTCATTATG 1

RESULT 416
 AAH91712/c
 ID AAH91712 standard; DNA; 32 BP.
 XX
 AC AAH91712;
 XX
 DT 09-OCT-2001 (first entry)
 XX
 DE Human inflammatory bowel disease associated polymorphic site #787.
 KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
 Query Match 1.0%; Score 24.6; DB 1; Length 32;
 Best Local Similarity 84.4%; Pred. No. 1.2e+03;
 Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 2300 TCTCGATCTCCTGACCTCGTGATCCGCCACC 2331
 DB 32 TCTGATCTCTTGACCTCCTGATCCGCCCTGCC 1

RESULT 417
 AAH40071
 ID AAH40071 standard; DNA; 27 BP.

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XX AAH40071;
AC
XX
DT 14-AUG-2001 (first entry)
DE
DE SNP specific SNPE primer SEQ ID 2867.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
Query Match 1.0%; Score 24.4; DB 1; Length 27;
Best Local Similarity 92.6%; Pred. No. 1.2e+03;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2304 GATCTCTGACCTGCTGATCGGCCAC 2330
Db 1 GATCTCTGACCTGCTGATCGGCCAC 27

RESULT 418
AAH404504
ID AAA04504 standard; DNA; 29 BP.
AC
AC AAA04504;
XX
XX 22-MAY-2000 (first entry)
XX
XX Polymorphic fragment of hypertension associated gene PGIS.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
Query Match 1.0%; Score 24.4; DB 1; Length 29;
Best Local Similarity 89.3%; Pred. No. 1.2e+03;
Matches 25; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2274 GGGTTTCACCGTGTAGCCAGGATGGTC 2301
Db 2 GGATTTTACCGGTATYTAGCCAGGATGGTC 29

RESULT 419
AAH40498
ID AAA04498 standard; DNA; 29 BP.
AC
AC AAA04498;
XX
XX 22-MAY-2000 (first entry)
XX
XX Polymorphic fragment of hypertension associated gene PGIS.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
Query Match 1.0%; Score 24.4; DB 1; Length 29;
Best Local Similarity 89.3%; Pred. No. 1.2e+03;
Matches 25; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2140 GGGTGATCTTGGCTCACTGCAAGCTCTG 2167
Db 2 GCGTGATCTCGGCTCACTGCAAGCTCTG 29

RESULT 420
AAH403993
ID AAA03993 standard; DNA; 29 BP.
AC
AC AAA03993;
XX
XX 22-MAY-2000 (first entry)
XX
XX Polymorphic fragment of hypertension associated gene APOC4.

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KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
Query Match 1.0%; Score 24.4; DB 1; Length 29;
Best Local Similarity 89.3%; Pred. No. 1.2e+03;
Matches 25; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2343 AAGTGTGGGATTACAGGCATGAGCCAC 2370
Db 1 AAGTGTAGGATTAYAGGCGTGAGCCAC 28

RESULT 421
AAH29012/c
ID AAQ29012 standard; DNA; 25 BP.
XX
XX AAQ29012;
AC
XX
XX 25-MAR-2003 (revised)
XX 23-FEB-1993 (first entry)
XX
XX Alu family consensus sequence-derived probe #1.
XX
KW Low frequency repeat; AluI restriction digest; genetic mapping; ss.
Query Match 1.0%; Score 24.2; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.2e+03;
Matches 23; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2346 TGTCTGGGATTACAGGCATGAGCCAC 2370
Db 25 TGTCTGGGATTACAGGYRTGAGCCAC 1

RESULT 422
ACA62537
ID ACA62537 standard; DNA; 29 BP.
XX
XX ACA62537;
AC
XX
XX 18-AUG-2003 (first entry)
XX
XX Human MDM2 mutant 156-221 PCR primer #1.
XX
XX Human; ss; PCR; primer; MDM2; cancer; tumour; cytostatic; p19(ARF); p53;
XX Rb; oncoprotein; oncogenic transformation; proteosomal degradation.
Query Match 1.0%; Score 24.2; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 1.3e+03;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 964 CGCCATCGATCCGGATCTTGATGCTGGT 992
Db 1 CGCCATCTAGACCGGATCTTGATGCTGGT 29

RESULT 423
AAH91563/c
ID AAH91563 standard; DNA; 30 BP.
XX
XX AAH91563;
AC
XX
XX 09-OCT-2001 (first entry)
XX
XX Human inflammatory bowel disease associated polymorphic site #638.
XX
KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
Query Match 1.0%; Score 24.2; DB 1; Length 30;
Best Local Similarity 86.7%; Pred. No. 1.3e+03;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 2090 TATTTTGTGAGCCGAGTCTGCTGTGT 2119
DB 30 TTTTGTGAGCCGAGTCTGCTGTGT 1

RESULT 424
AAD42698
ID AAD42698 standard; DNA; 30 BP.
XX
AC AAD42698;
XX
DT 15-NOV-2002 (first entry)
XX
DE Primer #4 used to construct Hdm2 mutant plasmid.
XX
KW Human; detection; cancer; ARP-p19 protein; cell cycle regulator; tumour;
KW cell cycle arrest; cell growth; hyperproliferative signal; therapeutic;

Query Match 1.0%; Score 24.2; DB 1; Length 30;
Best Local Similarity 89.7%; Pred. No. 1.3e+03;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 934 AAAGAAGCAGTAGCAGTGAATCTACAGG 962
DB 2 ATATGAGCAGTAGCAGTGAATCTACAGG 30

RESULT 425
AAQ73573
ID AAQ73573 standard; DNA; 31 BP.
XX
AC AAQ73573;
XX
DT 25-MAR-2003 (revised)
DT 25-JUN-1995 (first entry)
XX
DE Enhancer element er-3 conserved basepair sequence.
XX
KW Enhancer element; carcinoma; tumor; cancer; SLP1 gene;

Query Match 1.0%; Score 24.2; DB 1; Length 31;
Best Local Similarity 83.9%; Pred. No. 1.3e+03;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2197 CTCAGCCTCCCAANTAGTTCGCTACAGTC 2227
DB 1 CTCAGCCTCCCAANTAGTTCGCTACAGGC 31

RESULT 426
AAZ89375
ID AAZ89375 standard; DNA; 24 BP.
XX
AC AAZ89375;
XX
DT 15-JUN-2000 (first entry)
XX
DE Human mdm-2 PCR primer mdm2Pr11.
XX
KW Human; mdm-2; PCR primer; reaction container; quantitation; diagnosis;
KW food analysis; ss.

Query Match 1.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1591 GAGAGTGTGGAATCTAGTTTCC 1604
DB 1 GAGAGTGTGGAATCTAGTTTCC 24

RESULT 427
AAH45830/c

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ID AAH45830 standard; DNA; 24 BP.
XX
AC AAH45830;
XX
DT 11-SEP-2001 (first entry)
XX
DE Telomere size determination method related oligonucleotide #3.
XX
KW Telomere size determination; chromosomal DNA; probe; primer;
KW repetitive sequence; tissue aging; cancer progression; ds.

Query Match 1.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAGTCTGGGATTACA 2358
DB 24 GCCTCCCAAGTCTGGGATTACA 1

RESULT 428
AAH45828
ID AAH45828 standard; DNA; 24 BP.
XX
AC AAH45828;
XX
DT 11-SEP-2001 (first entry)
XX
DE Telomere size determination method related oligonucleotide #1.
XX
KW Telomere size determination; chromosomal DNA; probe; primer;
KW repetitive sequence; tissue aging; cancer progression; ds.

Query Match 1.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAGTCTGGGATTACA 2358
DB 1 GCCTCCCAAGTCTGGGATTACA 24

RESULT 429
AAI69885/c
ID AAI69885 standard; DNA; 24 BP.
XX
AC AAI69885;
XX
DT 14-DEC-2001 (first entry)
XX
DE Human transglutaminase 12 PCR primer #1.
XX
KW Human; transglutaminase 12; cytostatic; virucidal; immunomodulatory;
KW antiinflammatory; haemostatic; gene therapy; malignant tumour;

Query Match 1.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2341 CAAAGTGTGGGATTACAGGCATG 2364
DB 24 CAAAGTGTGGGATTACAGGCATG 1

RESULT 430
ADK66042
ID ADK66042 standard; DNA; 24 BP.
XX
AC ADK66042;
XX
DT 06-MAY-2004 (first entry)
XX
DE Standardized polynucleotide system polynucleotide #9 PCR primer #1.

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XX ss; standardized polynucleotide system; medical diagnosis;
KW functional genomics; sample analysis; pharmacogenomics; sample analysis;

Query Match      1.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1581 GAGAGTGTGGAATCTAGTTTGCCC 1604
DB 1 GAGAGTGTGGAATCTAGTTTGCCC 24

RESULT 431
AAQ25353/c
ID AAQ25353 standard; DNA; 25 BP.
XX
AC AAQ25353;
XX
DT 21-NOV-1992 (first entry)
XX
DE Sequence of probe Alu 1.
XX
KW Hybridisation rate; chondroitin sulphate; probe; probe cocktail; Alu 1;
KW ss.

Query Match      1.0%; Score 24; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAGTGTGGGATTACA 2358
DB 24 GCCTCCCAAGTGTGGGATTACA 1

RESULT 432
ADB04765
ID ADB04765 standard; DNA; 25 BP.
XX
AC ADB04765;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5751.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match      1.0%; Score 24; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGCTTTCACCGTGTAGCCAGGAT 2297
DB 2 GGCTTTCACCGTGTAGCCAGGAT 25

RESULT 433
ADB04783
ID ADB04783 standard; DNA; 25 BP.
XX
AC ADB04783;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5769.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match      1.0%; Score 24; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2291 CCAGGATGCTCTCGATCTCTCTGAC 2314
DB 1 CCAGGATGCTCTCGATCTCTCTGAC 24

RESULT 434
AAA04506
ID AAA04506 standard; DNA; 29 BP.
XX
AC AAA04506;
XX
DT 22-MAY-2000 (first entry)
XX
DE Polymorphic fragment of hypertension associated gene PGIS.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

Query Match      1.0%; Score 24; DB 1; Length 29;
Best Local Similarity 92.3%; Pred. No. 1.3e+03;
Matches 24; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2347 GCTGGATTACAGGCATGAGCCACCG 2372
DB 1 GCTGGATTACAGGVTGAGCCACCG 26

RESULT 435
AAA03879/c
ID AAA03879 standard; DNA; 29 BP.
XX
AC AAA03879;
XX
DT 22-MAY-2000 (first entry)
XX
DE Polymorphic fragment of hypertension associated gene AEL.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

Query Match      1.0%; Score 23.8; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 1.3e+03;
Matches 25; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2098 TTGAGACCGAGTCTTGCTCTGTATCCAG 2126
DB 29 TTGAGACAGGGTCTGCTCTGTGCCAG 1

RESULT 436
AAA03958
ID AAA03958 standard; DNA; 29 BP.
XX
AC AAA03958;
XX
DT 22-MAY-2000 (first entry)
XX
DE Polymorphic fragment of hypertension associated gene APOC1.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

Query Match      1.0%; Score 23.8; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 1.3e+03;
Matches 25; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2303 CGATCTCTCGACTCTGATCGCCACCG 2331
DB 1 CGATCTCTGACTTGTGATCGCCCTGCC 29

RESULT 437

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AAA04485/c
ID AAA04485 standard; DNA; 29 BP.
XX
AC AAA04485;
XX
DT 22-MAY-2000 (first entry)
XX
DE Polymorphic fragment of hypertension associated gene PGIS.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
Query Match 1.0%; Score 23.8; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 1.3e+03;
Matches 25; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2267 AGAGACGGGTTTCACCGTGTAGCCAGG 2295
Db 29 AGAGACGGGTTTCRCCATGTTGCCAGG 1
RESULT 438
AAA03985/c
ID AAA03985 standard; DNA; 29 BP.
XX
AC AAA03985;
XX
DT 22-MAY-2000 (first entry)
XX
DE Polymorphic fragment of hypertension associated gene APOC3.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
Query Match 1.0%; Score 23.8; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 1.3e+03;
Matches 25; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2110 CTTCCTCTGTACCCAGGCTGGAGTGCGAG 2138
Db 29 CTTCCTCTGTACCCAGGCTGGAGTGCGAG 1
RESULT 439
AAA04389/c
ID AAA04389 standard; DNA; 29 BP.
XX
AC AAA04389;
XX
DT 22-MAY-2000 (first entry)
XX
DE Polymorphic fragment of hypertension associated gene IAPP.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
Query Match 1.0%; Score 23.8; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 1.3e+03;
Matches 25; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2105 CGAGTCTGTCTGTATACCCAGGCTGGAG 2133
Db 29 CGAGTCTGTCTGTATACCCAGGCTGGAG 1
RESULT 440
AAA04314
ID AAA04314 standard; DNA; 29 BP.
XX
AC AAA04314;
XX
DT 22-MAY-2000 (first entry)
XX

DE Polymorphic fragment of hypertension associated gene GLUT4.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
Query Match 1.0%; Score 23.8; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 1.3e+03;
Matches 25; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2303 CGATCTCCTGACCTCGTGATCCGCCACC 2331
Db 1 CGATCTCCTGACCTGATCTGCTGCC 29
RESULT 441
AAV19047
ID AAV19047 standard; DNA; 30 BP.
XX
AC AAV19047;
XX
DT 28-JUL-1998 (first entry)
XX
DE Alu PCR primer 4.
XX
KW PCR; primer; amplification; Alu repeat sequence; vector;
KW circular yeast artificial chromosome; YAC; ss.
Query Match 1.0%; Score 23.6; DB 1; Length 30;
Best Local Similarity 86.7%; Pred. No. 1.4e+03;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2097 TTTGAGACCGAGTCTGCTCTGTATACCCAG 2126
Db 1 TTTGAGACCGAGTCTGCTCTGTGCCCCAG 30
RESULT 442
ABL59103
ID ABL59103 standard; DNA; 30 BP.
XX
AC ABL59103;
XX
DT 27-SEP-2002 (first entry)
XX
DE PCR primer used to amplify an 82 bp Alu probe.
XX
KW Yeast artificial chromosome; YAC; pPD39;
KW transformation-associated recombination; PCR; primer; ss.
Query Match 1.0%; Score 23.6; DB 1; Length 30;
Best Local Similarity 86.7%; Pred. No. 1.4e+03;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2097 TTTGAGACCGAGTCTGCTCTGTATACCCAG 2126
Db 1 TTTGAGACCGAGTCTGCTCTGTGCCCCAG 30
RESULT 443
ACC85703
ID ACC85703 standard; DNA; 30 BP.
XX
AC ACC85703;
XX
DT 22-APR-2004 (first entry)
XX
DE Human protease MDT59 related DNA sequence SEQ ID NO: 18.
XX
KW Promoter; human; protease; MDT59; chronic kidney failure; nephrotropic;
KW gene; ds.
Query Match 1.0%; Score 23.6; DB 1; Length 30;
Best Local Similarity 86.7%; Pred. No. 1.4e+03;

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Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2097 TTTGAGACCGAGTCTGCTGTGTACCCAG 2126
|||||
Db 1 TTTGAGACCGAGTCTGCTGTGTGCCAG 30

RESULT 444
AAH40799
ID AAH40799 standard; DNA; 25 BP.
XX AC
XX AAH40799;
XX DT
XX 14-AUG-2001 (first entry)
XX DE
XX SNP specific SNPE primer SEQ ID 3595.
XX KW
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
Query Match 1.0%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.3e+03;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2343 AAGTGTGGGATTACAGCGATGAGC 2367
|||||
Db 1 AAGTGTGGGATTACAGCGGTGAGC 25

RESULT 445
AAS14584
ID AAS14584 standard; DNA; 25 BP.
XX AC
XX AAS14584;
XX DT
XX 18-DEC-2001 (first entry)
XX DE
XX Human SNAP23 SNP region #2 PCR primer #1.
XX KW
XX Human; single-nucleotide polymorphism; SNP; SNAP23; ss; PCR primer;
XX synaptosome associated protein of 23 kilodaltons; diabetes; obesity;
Query Match 1.0%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.3e+03;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2336 CCTCCCAAGTCTGGGATTACAGG 2360
|||||
Db 1 CCTCCCAAGTACTGGGATTACAGG 25

RESULT 446
AAS14581
ID AAS14581 standard; DNA; 25 BP.
XX AC
XX AAS14581;
XX DT
XX 18-DEC-2001 (first entry)
XX DE
XX Human SNAP23 SNP region #1 PCR primer #1.
XX KW
XX Human; single-nucleotide polymorphism; SNP; SNAP23; ss; PCR primer;
XX synaptosome associated protein of 23 kilodaltons; diabetes; obesity;
Query Match 1.0%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.3e+03;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2336 CCTCCCAAGTCTGGGATTACAGG 2360
|||||
Db 1 CCTCCCAAGTACTGGGATTACAGG 25

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RESULT 447
ABT03658
ID ABT03658 standard; DNA; 25 BP.
XX AC
XX ABT03658;
XX DT
XX 13-SEP-2002 (first entry)
XX DE
XX Human Med-6 gene PCR primer SEQ ID NO: 179.
XX KW
XX Human; cancer; neoplastic disease; tumour specific marker; cytostatic;
XX transcription factor; PCR; primer; ss.
Query Match 1.0%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.3e+03;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2341 CAAAGTCTGGGATTACAGCGATGA 2365
|||||
Db 1 CAAAGTCTGGGATTACAGCGGTGA 25

RESULT 448
ADI17385
ID ADI17385 standard; DNA; 25 BP.
XX AC
XX ADI17385;
XX DT
XX 15-APR-2004 (first entry)
XX DE
XX PCR primer used for exon linking to confirm human NOVX DNA SeqID921.
XX KW
XX human; PCR; primer; ss; exon linking; NOVX; cardiomyopathy;
XX atherosclerosis; cancer; diabetes; inflammation; autoimmune disorder;
Query Match 1.0%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.3e+03;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2295 GATGGTCTCGATCTCCTGACCTCGT 2319
|||||
Db 1 GATGGTCTCGATCTCCTGACCTCTT 25

RESULT 449
ADN42474
ID ADN42474 standard; DNA; 25 BP.
XX AC
XX ADN42474;
XX DT
XX 17-JUN-2004 (first entry)
XX DE
XX Human NOV22c exon linking PCR primer #2.
XX KW
XX Human; ss; NOVX; cancer; diabetes; cardiomyopathy; atherosclerosis; PCR;
XX primer; exon linking.
Query Match 1.0%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.3e+03;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2295 GATGGTCTCGATCTCCTGACCTCGT 2319
|||||
Db 1 GATGGTCTCGATCTCCTGACCTCTT 25

RESULT 450
AAH40327
ID AAH40327 standard; DNA; 27 BP.
XX AC
XX AAH40327;
XX DT
XX 14-AUG-2001 (first entry)

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XX SNP specific SNPE primer SEQ ID 3123.
DE
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
Query Match 1.0%; Score 23.4; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 1.4e+03;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2302 TCGATCTCTGACCTCGTGATCCGCC 2328
DB 1 TCGNTCTCTGACCTCGTGTCGTCC 27
RESULT 451
ABX15004/c
ID ABX15004 standard; DNA; 29 BP.
XX
AC ABX15004;
XX
DT 14-MAR-2003 (first entry)
XX Human delta opioid receptor OPRD1-7 SNP genotyping PCR probe #2.
DE
XX Human; delta opioid receptor; OPRD1-7; ss; PCR; probe; SNP;
KW single nucleotide polymorphism; eating disorder; anorexia nervosa;
Query Match 1.0%; Score 23.2; DB 1; Length 29;
Best Local Similarity 89.3%; Pred. No. 1.4e+03;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2249 ATTTTGTACTTTTAGTAGACAGGG 2276
DB 28 AATTTTGTACTTTTAGTAAGATAGG 1
RESULT 452
ABT34292/c
ID ABT34292 standard; DNA; 29 BP.
XX
AC ABT34292;
XX
DT 12-JUN-2003 (first entry)
XX Opioid receptor D1 probe SEQ ID No 78.
DE
XX Eating disorder; polymorphism; dataset; allele; HGBASE identification;
KW serotonin receptor 1D; delta-opioid receptor; dopamine receptor D2;
Query Match 1.0%; Score 23.2; DB 1; Length 29;
Best Local Similarity 89.3%; Pred. No. 1.4e+03;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2249 ATTTTGTACTTTTAGTAGACAGGG 2276
DB 28 AATTTTGTACTTTTAGTAAGATAGG 1
RESULT 453
AAH40734
ID AAH40734 standard; DNA; 30 BP.
XX
AC AAH40734;
XX
DT 14-AUG-2001 (first entry)
XX SNP specific lower PCR primer SEQ ID 3530.
DE
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
Query Match 1.0%; Score 23.2; DB 1; Length 30;

Best Local Similarity 89.3%; Pred. No. 1.4e+03;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2249 ATTTTGTACTTTTAGTAGACAGGG 2276
DB 3 AATTTTGTACTTTTAGTAGACAGGG 30
RESULT 454
AAF77571/c
ID AAF77571 standard; DNA; 23 BP.
XX
AC AAF77571;
XX
DT 29-MAY-2001 (first entry)
XX Human mdm2 RNA PCR primer #2.
DE
XX Human; p53; proliferative disease; diterpenoid triepoxides;
KW multi-drug resistance; cancer; restenosis; atherosclerosis; psoriasis;
Query Match 1.0%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1374 GAGGGCTTTGATGTTCTGATTG 1396
DB 23 GAGGGCTTTGATGTTCTGATTG 1
RESULT 455
ADE12183/c
ID ADE12183 standard; DNA; 23 BP.
XX
AC ADE12183;
XX
DT 29-JAN-2004 (first entry)
XX PCR primer #2 for mdm2 cDNA from human MCF-7 (breast cancer) cell line.
DE
XX Tumour; synergistic combination therapy; tumour cell; p21waf1/cip1;
KW diterpenoid triepoxide; vinca alkaloid; triptolide; anti-proliferative;
Query Match 1.0%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1374 GAGGGCTTTGATGTTCTGATTG 1396
DB 23 GAGGGCTTTGATGTTCTGATTG 1
RESULT 456
ADG72450/c
ID ADG72450 standard; DNA; 23 BP.
XX
AC ADG72450;
XX
DT 11-MAR-2004 (first entry)
XX PCR primer #2 for human mdm2 cDNA.
DE
XX Hyperproliferative disorder; antiproliferative; diterpenoid triepoxide;
KW tumour; p21; waf1/cip1; carcinoma; cancer; multi-drug resistance; p53;
Query Match 1.0%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1374 GAGGGCTTTGATGTTCTGATTG 1396
DB 23 GAGGGCTTTGATGTTCTGATTG 1

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RESULT 457
ADP11845
ID ADP11845 standard; DNA; 23 BP.
XX
XX
AC ADP11845;
XX
DT 12-AUG-2004 (first entry)
DE
DE Set 2 left PCR primer for marker probe #197.
XX
XX
XX
KW transplant rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss; primer.

Query Match 1.0%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1528 GCAGCCCAAGAAGATGTGAAAGAG 1550
Db 1 GCAGCCCAAGAAGATGTGAAAGAG 23

RESULT 458
ABI99962
ID ABI99962 standard; DNA; 24 BP.
XX
XX
AC ABI99962;
XX
DT 31-MAY-2002 (first entry)
DE
DE Human phosphatidic acid phosphatase 2-12 RT-PCR primer, SEQ ID NO:4.
XX
XX
KW Human; phosphatidic acid phosphatase 2-12; recombinant production;
KW cancer; HIV infection; human immunodeficiency virus; gene therapy;

Query Match 1.0%; Score 23; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGACACAGGGTTTCAC 2282
Db 2 TTTTAGTAGACACAGGGTTTCAC 24

RESULT 459
ACA90127
ID ACA90127 standard; DNA; 24 BP.
XX
XX
AC ACA90127;
XX
DT 10-JUL-2003 (first entry)
DE
DE Human kinesin gene(s) antisense oligonucleotide #10.
XX
XX
KW Human; ss; antisense; kinesin; CENP-E; Eg5; MCAK; colon cancer; stroke;
KW T cell cancer; B cell lymphoma; pancreatic cancer; breast cancer;

Query Match 1.0%; Score 23; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2350 GGGATTACAGCATGAGCCACCG 2372
Db 1 GGGATTACAGCATGAGCCACCG 23

RESULT 460
ADB04764
ID ADB04764 standard; DNA; 25 BP.
XX
XX
AC ADB04764;
XX

DT 20-NOV-2003 (first entry)
DE
DE Human MDZ7 scanning oligonucleotide SEQ ID 5750.
XX
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;

Query Match 1.0%; Score 23; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTCACCGTGTAGCCAGGA 2296
Db 3 GGGTTTCACCGTGTAGCCAGGA 25

RESULT 461
ADO56443/C
ID ADO56443 standard; DNA; 30 BP.
XX
XX
AC ADO56443;
XX
DT 12-AUG-2004 (first entry)
DE
DE Human cyclin-dependent kinase 10, CDK10 proximal SNP PCR primer #166.
XX
XX
KW gene therapy; human; ss; melanoma;
KW melanoma associated polymorphic variation; SNP;

Query Match 1.0%; Score 23; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2341 CAAAGTCTGGGATTACAGGCAT 2363
Db 30 CAAAGTCTGGGATTACAGGCAT 8

RESULT 462
ADO56349/C
ID ADO56349 standard; DNA; 30 BP.
XX
XX
AC ADO56349;
XX
DT 12-AUG-2004 (first entry)
DE
DE Human cyclin-dependent kinase 10, CDK10 proximal SNP PCR primer #72.
XX
XX
KW gene therapy; human; ss; melanoma;
KW melanoma associated polymorphic variation; SNP;

Query Match 1.0%; Score 23; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2341 CAAAGTCTGGGATTACAGGCAT 2363
Db 30 CAAAGTCTGGGATTACAGGCAT 8

RESULT 463
AAV59189
ID AAV59189 standard; DNA; 26 BP.
XX
XX
AC AAV59189;
XX
DT 21-DEC-1998 (first entry)
DE
DE Human bak gene promoter NF-kappa B site 2.
XX
XX
KW Bak gene; promoter; human; apoptosis; ischaemia; tumour; cancer;
KW infection; HIV; neurodegenerative disorder; hair loss;

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```
Query Match 1.0%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 1.4e+03;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2264 AGTAGAGACAGGGTTTCACCGTGTGA 2289
DB 1 AGTAGAGACGGGGTTTCACCATGTGA 26

RESULT 464
ABK65978
ID ABK65978 standard; DNA; 26 BP.
XX
AC ABK65978;
XX
DT 02-JUL-2002 (first entry)
DE Human gene specific PCR primer #66.
XX
KW Primer; ss; DNA microarray; differential expression analysis; human.
XX

Query Match 1.0%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 1.4e+03;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2342 AAAGTGCTGGGATTACAGGCATGAGC 2367
DB 1 AAAGTGCTAGGATTACAGGCGTGAGC 26

RESULT 465
AAH40487
ID AAH40487 standard; DNA; 27 BP.
XX
AC AAH40487;
XX
DT 14-AUG-2001 (first entry)
DE SNP specific SNPE primer SEQ ID 3283.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 1.0%; Score 22.8; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 1.4e+03;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2332 TCGGCTCCCAAGTGTGGGATTACA 2358
DB 1 TTGGCTCNCACAGTGTGGGATTACA 27

RESULT 466
AAH39279
ID AAH39279 standard; DNA; 27 BP.
XX
AC AAH39279;
XX
DT 14-AUG-2001 (first entry)
DE SNP specific SNPE primer SEQ ID 2075.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 1.0%; Score 22.8; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 1.4e+03;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2344 AGTGCTGGGATTACAGGCATGAGCCAC 2370
DB 1 AGTCTGGGATTACAGGCATGAGGCAC 27
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RESULT 467
AAA04311
ID AAA04311 standard; DNA; 29 BP.
XX
AC AAA04311;
XX
DT 22-MAY-2000 (first entry)
DE Polymorphic fragment of hypertension associated gene GLUT4.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

Query Match 1.0%; Score 22.8; DB 1; Length 29;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 24; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2271 ACAGGGTTTCACCGTGTAGCCAGGATG 2298
DB 2 ACCGGTTTCACCGTGTAGCCAGGATG 29

RESULT 468
AAA04497
ID AAA04497 standard; DNA; 29 BP.
XX
AC AAA04497;
XX
DT 22-MAY-2000 (first entry)
DE Polymorphic fragment of hypertension associated gene PGIS.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

Query Match 1.0%; Score 22.8; DB 1; Length 29;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 24; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2106 GAGTCTGCTCTCTTACCAGGCTGGAG 2133
DB 2 GAGTCTGCTCTCTTACCAGGCTGGAG 29

RESULT 469
AAH38989
ID AAH38989 standard; DNA; 30 BP.
XX
AC AAH38989;
XX
DT 14-AUG-2001 (first entry)
DE SNP specific upper PCR primer SEQ ID 1785.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 1.0%; Score 22.8; DB 1; Length 30;
Best Local Similarity 92.3%; Pred. No. 1.5e+03;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2250 TTTTGTACTTTTAGTAGAGACAGG 2275
DB 5 TTTTGTATTATTTTAGTAGAGACGGG 30

RESULT 470
ADO56348/c
ID ADO56348 standard; DNA; 30 BP.
XX
AC ADO56348;
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XX 12-AUG-2004 (first entry)
DT Human cyclin-dependent kinase 10, CDK10 proximal SNP PCR primer #71.
DE gene therapy; human; ss; melanoma;
KW melanoma associated polymorphic variation; SNP;

Query Match 1.0%; Score 22.8; DB 1; Length 30;
Best Local Similarity 92.3%; Pred. No. 1.5e+03;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2337 CTCCCAAAGTCTGGGATTACAGCA 2362
DB 30 CTCCCAAAGTCTGGGATTACATCCA 5

RESULT 471
ADP08583/c
ID ADP08583 standard; DNA; 30 BP.
XX AC ADP08583;
XX AC ADP08583;
XX AC ADP08583;
DT 26-AUG-2004 (first entry)
DE PCR primer 167 used to genotype human glycoprotein VI (GP6) polymorphism.
DE breast cancer; cytostatic; gene therapy; human; platelet glycoprotein VI;
KW GP6; GPIV; GPII; chromosome 19q13.4; ss; PCR; primer; SNP;

Query Match 1.0%; Score 22.8; DB 1; Length 30;
Best Local Similarity 92.3%; Pred. No. 1.5e+03;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2337 CTCCCAAAGTCTGGGATTACAGCA 2362
DB 30 CTCCCAAAGTCTGGGATTACATCCA 5

RESULT 472
ADO79710/c
ID ADO79710 standard; DNA; 30 BP.
XX AC ADO79710;
XX AC ADO79710;
XX AC ADO79710;
DT 26-AUG-2004 (first entry)
DE DP3 PCR primer #44.
DE Cytostatic; Gene therapy; breast cancer; human; DLG1; KIAA0783; DP3;
KW CENPC1; SNP; single nucleotide polymorphism;

Query Match 1.0%; Score 22.8; DB 1; Length 30;
Best Local Similarity 92.3%; Pred. No. 1.5e+03;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2337 CTCCCAAAGTCTGGGATTACAGCA 2362
DB 30 CTCCCAAAGTCTGGGATTACATCCA 5

RESULT 473
AAQ77890/c
ID AAQ77890 standard; cDNA; 30 BP.
XX AC AAQ77890;
XX AC AAQ77890;
XX AC AAQ77890;
DT 25-MAR-2003 (revised)
DT 06-JUL-1995 (first entry)
DE Neural thread protein AD10-7 cDNA 5' antisense oligonucleotide.
DE Neural thread protein AD10-7; Alzheimer's; neuroectodermal tumours;
KW

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```

Query Match 1.0%; Score 22.6; DB 1; Length 30;
Best Local Similarity 86.2%; Pred. No. 1.5e+03;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2179 TTGCGACCAATTCCTGCTCAGCCTCC 2207
DB 30 TTCAAGCGATTCTCTGCTCAGCCTCC 2

RESULT 474
AAT27744/c
ID AAT27744 standard; DNA; 30 BP.
XX AC AAT27744;
XX AC AAT27744;
XX AC AAT27744;
DT 14-NOV-1996 (first entry)
DE Neural thread protein antisense sequence.
DE Neural thread protein; NTP; diagnosis; detection; Alzheimer's disease;
KW neuroectodermal tumour; malignant astrocytoma; monoclonal antibody;

Query Match 1.0%; Score 22.6; DB 1; Length 30;
Best Local Similarity 86.2%; Pred. No. 1.5e+03;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2179 TTGCGACCAATTCCTGCTCAGCCTCC 2207
DB 30 TTCAAGCGATTCTCTGCTCAGCCTCC 2

RESULT 475
AAF92888
ID AAF92888 standard; DNA; 24 BP.
XX AC AAF92888;
XX AC AAF92888;
XX AC AAF92888;
DT 17-MAY-2001 (first entry)
DE Human ABC1 transcription factor binding site #49.
DE High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.
KW

Query Match 0.9%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 1.4e+03;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2301 CTCGATCTCTGACCTCGTGATCC 2324
DB 1 CTCGATCTCTGACCTCGTGATCC 24

RESULT 476
ABA03268/c
ID ABA03268 standard; DNA; 24 BP.
XX AC ABA03268;
XX AC ABA03268;
XX AC ABA03268;
DT 14-FEB-2002 (first entry)
DE Human chorine ion channel 9 PCR primer #1.
DE Human; chorine ion channel 9; cytostatic; virucide; immunomodulator;
KW antiinflammatory; haemostatic; gene therapy; tumour; haemopathy;

Query Match 0.9%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 1.4e+03;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2265 GTAGACAGGGTTTCCCGTGT 2288
DB 1 GTAGACAGGGTTTCCCGTGT 2288

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Db      24 GTAGAGACGGGGTTTCACCGTGT 1

RESULT 477
ABA05118/c
ID ABA05118 standard; DNA; 24 BP.
XX
XX
AC ABA05118;
XX
DT 04-MAR-2002 (first entry)
XX
DE Human Pax protein 22 coding sequence PCR primer #2.
XX
KW Human; Pax protein 22; cancer; haemopathy; HIV infection; cytostatic;
KW haemostatic; virucide; immunomodulatory; antiinflammatory; inflammation;

Query Match      0.9%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 1.4e+03;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2307 CTCCTGACCTCGTGATCGCCAC 2330
Db      24 CTCCTGACCTCGTGATCGCCGC 1

RESULT 478
ADL07545/c
ID ADL07545 standard; DNA; 24 BP.
XX
XX
AC ADL07545;
XX
DT 06-MAY-2004 (first entry)
XX
DE Sec24 protein-31.35 RT-PCR primer #1.
XX
DE ss; primer; Sec24 protein-31.35; cancer; HIV infection; PCR; RT-PCR;
KW reverse transcriptase PCR.

Query Match      0.9%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 1.4e+03;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2347 GCTGGATTACAGGATGAGCCAC 2370
Db      24 GCTGGATTACAGGCGTGAGCCAC 1

RESULT 479
AAQ63846/c
ID AAQ63846 standard; DNA; 25 BP.
XX
XX
AC AAQ63846;
XX
DT 25-MAR-2003 (revised)
DT 29-JAN-1995 (first entry)
XX
DE PCR primer ALU for tumour specific DNA.
XX
KW Arbitrary primers; AP-PCR; amplification; tumour cells; cancer;

Query Match      0.9%; Score 22.4; DB 1; Length 25;
Best Local Similarity 95.8%; Pred. No. 1.5e+03;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2260 TTTTAGTAGACAGGGTTTCACC 2283
Db      24 TTTTAGTAGACAGGATTTCACC 1

RESULT 480
AAAX24391
ID AAAX24391 standard; DNA; 25 BP.
XX

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AC AAX24391;
XX
XX 07-JUN-1999 (first entry)
XX
DE Chemokine receptor CCR8 PCR primer CY6.
XX
KW Chemokine receptor; CCR8; human; G protein coupled receptor; HIV;
KW infection; therapy; immunomodulator; chemotaxis; apoptosis; PCR; primer;

Query Match      0.9%; Score 22.4; DB 1; Length 25;
Best Local Similarity 95.8%; Pred. No. 1.5e+03;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2347 GCTGGATTACAGGATGAGCCAC 2370
Db      1 GCTAGGATTACAGGCGATGAGCCAC 24

RESULT 481
ADB97611/c
ID ADB97611 standard; DNA; 25 BP.
XX
XX
AC ADB97611;
XX
DT 04-DEC-2003 (first entry)
XX
DE Tumour tissue arbitrary PCR primer #10.
XX
DE ss; PCR; primer; tumour; tumour tissue; colorectal tumour cell;
KW stomach tumour cell; pancreatic tumour cell; cancer risk; cancer.

Query Match      0.9%; Score 22.4; DB 1; Length 25;
Best Local Similarity 95.8%; Pred. No. 1.5e+03;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2260 TTTTAGTAGACAGGGTTTCACC 2283
Db      24 TTTTAGTAGACAGGATTTCACC 1

RESULT 482
ADO04045/c
ID ADO04045 standard; DNA; 25 BP.
XX
XX
AC ADO04045;
XX
DT 29-JUL-2004 (first entry)
XX
DE AP-PCR primer J, used to identify deletions in human gene.
XX
KW Neoplasm identification; tumour; colorectal; stomach; pancreatic;
KW arbitrarily primed; AP; PCR; primer; human; ss.

Query Match      0.9%; Score 22.4; DB 1; Length 25;
Best Local Similarity 95.8%; Pred. No. 1.5e+03;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2260 TTTTAGTAGACAGGGTTTCACC 2283
Db      24 TTTTAGTAGACAGGATTTCACC 1

RESULT 483
AAH91455/c
ID AAH91455 standard; DNA; 29 BP.
XX
XX
AC AAH91455;
XX
DT 09-OCT-2001 (first entry)
XX
DE Human inflammatory bowel disease associated polymorphic site #530.
KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;

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KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;

Query Match 0.9%; Score 22.4; DB 1; Length 29;
 Best Local Similarity 92.0%; Pred. No. 1.5e+03;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2230 CTGCCACACACCTGGCTAATTTT 2254
 DB 25 CTGCCACCNCACCTGGCTAATTTT 1

RESULT 484
 AAA04010/c
 ID AAA04010 standard; DNA; 29 BP.
 XX
 AC AAA04010;
 XX
 DT 22-MAY-2000 (first entry)
 XX Polymorphic fragment of hypertension associated gene APOC4.
 DE Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
 KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
 KW

Query Match 0.9%; Score 22.2; DB 1; Length 29;
 Best Local Similarity 92.8%; Pred. No. 1.5e+03;
 Matches 24; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAGTGTGGATTACAGGCAT 2363
 DB 29 GCCTCCGAGTAGCGGGATTACAGGCAT 1

RESULT 485
 AAA04663
 ID AAA04663 standard; DNA; 29 BP.
 XX
 AC AAA04663;
 XX
 DT 22-MAY-2000 (first entry)
 XX Polymorphic fragment of hypertension associated gene TBXA2R.
 DE Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
 KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
 KW

Query Match 0.9%; Score 22.2; DB 1; Length 29;
 Best Local Similarity 92.8%; Pred. No. 1.5e+03;
 Matches 24; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2179 TTGCACCAATTCCTCGCTCAGCTCCC 2207
 DB 1 TTCAGCGATTCGTGCTCCTCAGCTCCC 29

RESULT 486
 AAA04486/c
 ID AAA04486 standard; DNA; 29 BP.
 XX
 AC AAA04486;
 XX
 DT 22-MAY-2000 (first entry)
 XX Polymorphic fragment of hypertension associated gene PGIS.
 DE Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
 KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
 KW

Query Match 0.9%; Score 22.2; DB 1; Length 29;
 Best Local Similarity 92.8%; Pred. No. 1.5e+03;
 Matches 24; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2262 TTAGTAGACAGGGTTTCACCGTGTAG 2290

DB 29 TTAGTAGACAGGGTTTCACCGTGTAG 1

RESULT 487
 AAA04496
 ID AAA04496 standard; DNA; 29 BP.
 XX
 AC AAA04496;
 XX
 DT 22-MAY-2000 (first entry)
 XX Polymorphic fragment of hypertension associated gene PGIS.
 DE Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
 KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
 KW

Query Match 0.9%; Score 22.2; DB 1; Length 29;
 Best Local Similarity 92.8%; Pred. No. 1.5e+03;
 Matches 24; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2098 TTGAGACCGAGTCTTGCTCTGTATCCAG 2126
 DB 1 TTGAGATGGAGTCTGTGCTCTGTGCCCCAG 29

RESULT 488
 AAA04500
 ID AAA04500 standard; DNA; 29 BP.
 XX
 AC AAA04500;
 XX
 DT 22-MAY-2000 (first entry)
 XX Polymorphic fragment of hypertension associated gene PGIS.
 DE Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
 KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
 KW

Query Match 0.9%; Score 22.2; DB 1; Length 29;
 Best Local Similarity 92.8%; Pred. No. 1.5e+03;
 Matches 24; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2193 CTGCTCAGCTCCCAATTAGCTTGGCCT 2221
 DB 1 CTGCTCAGCTCCCGTAGTAGTGGGACT 29

RESULT 489
 AAA04009/c
 ID AAA04009 standard; DNA; 29 BP.
 XX
 AC AAA04009;
 XX
 DT 22-MAY-2000 (first entry)
 XX Polymorphic fragment of hypertension associated gene APOC4.
 DE Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
 KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
 KW

Query Match 0.9%; Score 22.2; DB 1; Length 29;
 Best Local Similarity 92.8%; Pred. No. 1.5e+03;
 Matches 24; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2222 ACAGTCATCTGCCACACACCTGGCTAAT 2250
 DB 29 ACAGGTCATCTGCCAYCATGCCGCTAAT 1

RESULT 490
 AAA03983/c
 ID AAA03983 standard; DNA; 29 BP.

XX AAA03983;
 AC
 DT 22-MAY-2000 (first entry)
 XX
 DE Polymorphic fragment of hypertension associated gene APOC3.
 XX
 KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
 KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
 KW
 Query Match 0.9%; Score 22.2; DB 1; Length 29;
 Best Local Similarity 82.8%; Pred. No. 1.5e+03;
 Matches 24; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 2270 GACAGGGTTTACCGTGTAGCCAGGATG 2298
 Db 29 GATGGGGTTTCCACCTGTGGCCAGGTTG 1
 RESULT 491
 AAV29285
 ID AAV29285 standard; cDNA; 22 BP.
 XX
 AC AAV29285;
 XX
 DT 21-AUG-1998 (first entry)
 XX
 DE Nucleotide sequence of PCR primer P2.
 XX
 KW Human; tumorigenesis gene; T-gene; PLAG2; PLAG1; CTNNB1; antibody;
 KW benign tumour; malignant tumour; leukaemia; lymphoma; cancer; inhibition;
 KW
 Query Match 0.9%; Score 22; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2338 TCCCAAGTGTGGGATTACAG 2359
 Db 1 TCCCAAGTGTGGGATTACAG 22
 RESULT 492
 AAC69376/c
 ID AAC69376 standard; DNA; 22 BP.
 XX
 AC AAC69376;
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE Human ABC1 BAC contig polymorphic site, SEQ ID NO:275.
 XX
 KW Human ABC1 cholesterol transporter; chromosome 9q31;
 KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
 KW
 Query Match 0.9%; Score 22; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2188 TTCTCTGCTCAGCTCCCAA 2209
 Db 22 TTCTCTGCTCAGCTCCCAA 1
 RESULT 493
 AAZ89376/c
 ID AAZ89376 standard; DNA; 22 BP.
 XX
 AC AAZ89376;
 XX
 DT 15-JUN-2000 (first entry)
 XX
 KW Human mdm-2 PCR primer mdm2Pr21.
 XX

KW Human; mdm-2; PCR primer; reaction container; quantitation; diagnosis;
 KW food analysis; ss.
 Query Match 0.9%; Score 22; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1638 GGTGCGACCTAAAAAATGGTTGCA 1659
 Db 22 GGTGCGACCTAAAAAATGGTTGCA 1
 RESULT 494
 AA97661/c
 ID AA97661 standard; DNA; 22 BP.
 XX
 AC AA97661;
 XX
 DT 15-FEB-2001 (first entry)
 XX
 DE Human MDM2 reverse RT-PCR primer 1.
 XX
 KW Pseudocyclic oligonucleotide; functional segment; protective segment;
 KW nucleic acid detection; mRNA cleavage; antisense therapy; PCO;
 KW
 Query Match 0.9%; Score 22; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 679 GTGAGAACAGGTGTCACTTGA 700
 Db 22 GTGAGAACAGGTGTCACTTGA 1
 RESULT 495
 AAF77570
 ID AAF77570 standard; DNA; 22 BP.
 XX
 AC AAF77570;
 XX
 DT 29-MAY-2001 (first entry)
 XX
 DE Human mdm2 RNA PCR primer #1.
 XX
 KW Human; p53; proliferative disease; diterpenoid triepoxides;
 KW multi-drug resistance; cancer; restenosis; atherosclerosis; psoriasis;
 KW
 Query Match 0.9%; Score 22; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 639 GTCAATCAGCAGGAATCATCGG 660
 Db 1 GTCAATCAGCAGGAATCATCGG 22
 RESULT 496
 AAC87596
 ID AAC87596 standard; DNA; 22 BP.
 XX
 AC AAC87596;
 XX
 DT 16-MAR-2001 (first entry)
 XX
 DE Human Alu sequence PCR primer, CL1.
 XX
 KW Human; keratinocyte growth factor; KGF; chromosome 9p11; abnormality;
 KW cancer; miscarriage; spontaneous abortion; genetic susceptibility;
 KW
 Query Match 0.9%; Score 22; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2338 TCCCAAAAGTGTGGGATTACAG 2359
Db 1 TCCCAAAAGTGTGGGATTACAG 22

RESULT 497
AAF88160
ID AAF88160 standard; DNA; 22 BP.
XX
AC
XX AAF88160;
XX
DT 17-JUL-2001 (first entry)
XX
DE Human thyroid malfunction-associated protein RITA PCR primer #1.
KW KRAB domain; hyperplasia; thyroid; tumor; zinc finger motif; primer;
KW cytosstatic; antithyroid; gene therapy; chromosome 19; 19q13; ss.

Query Match 0.9%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2338 TCCCAAAAGTGTGGGATTACAG 2359
Db 1 TCCCAAAAGTGTGGGATTACAG 22

RESULT 498
ABL60507/c
ID ABL60507 standard; DNA; 22 BP.
XX
AC ABL60507;
XX
DT 12-AUG-2002 (first entry)
XX
DE Human MDM2 mRNA amplifying RT-PCR reverse primer.
KW Pseudo-cyclic oligonucleotide; PCO; gene expression; protein kinase A;
KW nucleic acid detection; ribozyme inhibition; gene transcription; MDM2;

Query Match 0.9%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 679 GTGAGAACAGGTGCACCTTGA 700
Db 22 GTGAGAACAGGTGCACCTTGA 1

RESULT 499
ADE12182
ID ADE12182 standard; DNA; 22 BP.
XX
AC ADE12182;
XX
DT 29-JAN-2004 (first entry)
XX
DE PCR primer #1 for mdm2 cDNA from human MCF-7 (breast cancer) cell line.
KW Tumour; synergistic combination therapy; tumour cell; p21waft1/cipl;
KW diterpenoid triepoxide; vinca alkaloid; triptolide; anti-proliferative;

Query Match 0.9%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 639 GTCAATCAGCAGGAATCATCGG 660
Db 1 GTCAATCAGCAGGAATCATCGG 22

RESULT 500
ADK66043/c

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ID ADK66043 standard; DNA; 22 BP.
XX
AC ADK66043;
XX
DT 06-MAY-2004 (first entry)
XX
DE Standardized polynucleotide system polynucleotide #9 PCR primer #2.
KW ss; standardized polynucleotide system; medical diagnosis;
KW functional genomics; sample analysis; pharmacogenomics; sample analysis;

Query Match 0.9%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1638 GGTCGACCTAAAAAATGTTGCA 1659
Db 22 GGTCGACCTAAAAAATGTTGCA 1

RESULT 501
ADK66047/c
ID ADK66047 standard; DNA; 22 BP.
XX
AC ADK66047;
XX
DT 06-MAY-2004 (first entry)
XX
DE Standardized polynucleotide system polynucleotide #10 PCR primer #2.
KW ss; standardized polynucleotide system; medical diagnosis;
KW functional genomics; sample analysis; pharmacogenomics; sample analysis;

Query Match 0.9%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1253 CCTTCCATCACATTGCAACAGA 1274
Db 22 CCTTCCATCACATTGCAACAGA 1

RESULT 502
ADG72449
ID ADG72449 standard; DNA; 22 BP.
XX
AC ADG72449;
XX
DT 11-MAR-2004 (first entry)
XX
DE PCR primer #1 for human mdm2 cDNA.
KW Hyperproliferative disorder; antiproliferative; diterpenoid triepoxide;
KW tumour; p21; waf1/cipl; carcinoma; cancer; multi-drug resistance; p53;

Query Match 0.9%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 639 GTCAATCAGCAGGAATCATCGG 660
Db 1 GTCAATCAGCAGGAATCATCGG 22

RESULT 503
AAF69748
ID AAF69748 standard; DNA; 23 BP.
XX
AC AAF69748;
XX
DT 18-APR-2001 (first entry)
XX
DE Human IL4Ralpha gene PCR primer #84.

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XX Polymorphism; human; interleukin 4 receptor-alpha; IL4R-alpha;
KW allergic disease; PCR primer; ss.

Query Match      0.9%; Score 22; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2233 CCACCACACCTGGCTAAATTTT 2254
Db 1 CCACCACACCTGGCTAAATTTT 22

RESULT 504
AAL56647/c
ID AAL56647 standard; DNA; 24 BP.
XX
AC AAL56647;
XX
DT 09-OCT-2003 (first entry)
DE
DE HS2+ primer nested for HS3+, which amplifies the human tp53 gene.
XX
KW Genomics; DNA sequencing; random fragmentation; primer linked fragment;
KW HS3+; positional amplification; PCR; primer; ss; human; tp53; HS2+.

Query Match      0.9%; Score 22; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2286 GTTACCCAGGATGGTCTCGATC 2307
Db 22 GTTACCCAGGATGGTCTCGATC 1

RESULT 505
ADB04763
ID ADB04763 standard; DNA; 25 BP.
XX
AC ADB04763;
XX
DT 20-NOV-2003 (first entry)
DE
DE Human MDZ7 scanning oligonucleotide SEQ ID 5749.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MD24; MD27; MD212; chromosome 7q22.1;

Query Match      0.9%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTCACCGTGTAGCCAGG 2295
Db 4 GGGTTTCACCGTGTAGCCAGG 25

RESULT 506
AAA04309
ID AAA04309 standard; DNA; 29 BP.
XX
AC AAA04309;
XX
DT 22-MAY-2000 (first entry)
DE
DE Polymorphic fragment of hypertension associated gene GLUT4.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

Query Match      0.9%; Score 22; DB 1; Length 29;
Best Local Similarity 91.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 2231 TGCACCACACCTGGCTAAATTTT 2254
Db 6 TGCACCACACCTGGCTAAATTTAT 29

RESULT 507
AAA03981/c
ID AAA03981 standard; DNA; 29 BP.
XX
AC AAA03981;
XX
DT 22-MAY-2000 (first entry)
DE
DE Polymorphic fragment of hypertension associated gene APOC3.
XX
KW Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;

Query Match      0.9%; Score 22; DB 1; Length 29;
Best Local Similarity 91.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2349 TGGGATTACAGGCATGAGCCACCG 2372
Db 29 TGGGATTACAGGCATGAGCCACTG 6

RESULT 508
AAF84351/c
ID AAF84351 standard; DNA; 25 BP.
XX
AC AAF84351;
XX
DT 20-JUN-2001 (first entry)
DE
DE Human CYP2C18i PCR primer #7.
XX
KW Gene polymorphism; drug-metabolising enzyme; PCR primer; CYP2C18i; ss.

Query Match      0.9%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.6e+03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2269 AGACAGGTTTCACCGTGTAGCCA 2293
Db 25 AGACAGGTTTCACCATGTTGGCCA 1

RESULT 509
ADB04739
ID ADB04739 standard; DNA; 25 BP.
XX
AC ADB04739;
XX
DT 20-NOV-2003 (first entry)
DE
DE Human MDZ7 scanning oligonucleotide SEQ ID 5725.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MD24; MD27; MD212; chromosome 7q22.1;

Query Match      0.9%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.6e+03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2248 AATTTTGTACTTTTAGTAGACAC 2272
Db 1 AATATTTTGTATTTTAGTAGACAC 25

RESULT 510

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ADB04737
ID ADB04737 standard; DNA; 25 BP.
XX
AC ADB04737;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5723.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
Query Match 0.9%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.6e+03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2246 CTAATTTTGTACTTTTAGTAGAG 2270
DB 1 CTAATATTTGTATTTTAGTAGAG 25
RESULT 511
ADB04667
ID ADB04667 standard; DNA; 25 BP.
XX
AC ADB04667;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5653.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
Query Match 0.9%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.6e+03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2176 GGGTTCGACCACTTCCTGCCTCA 2200
DB 1 GGGTTCACACACTTCCTGCTCA 25
RESULT 512
ADB04738
ID ADB04738 standard; DNA; 25 BP.
XX
AC ADB04738;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5724.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
Query Match 0.9%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.6e+03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2247 TAATTTTGTACTTTTAGTAGAGA 2271
DB 1 TAATATTTGTATTTTAGTAGAGA 25
RESULT 513
ADB04743
ID ADB04743 standard; DNA; 25 BP.
XX
AC ADB04743;
XX
DT 20-NOV-2003 (first entry)
XX

DE Human MD27 scanning oligonucleotide SEQ ID 5729.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
Query Match 0.9%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.6e+03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2252 TTTTGTACTTTTAGTAGACAGGG 2276
DB 1 TTTTGTATTTTAGTAGACAGGG 25
RESULT 514
ADB04674
ID ADB04674 standard; DNA; 25 BP.
XX
AC ADB04674;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5660.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
Query Match 0.9%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.6e+03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2183 CACCATTCCTGCCTCAGCTCCC 2207
DB 1 CACCATTCCTGCTTCAGTCTCCC 25
RESULT 515
ADB04668
ID ADB04668 standard; DNA; 25 BP.
XX
AC ADB04668;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5654.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
Query Match 0.9%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.6e+03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2177 GGTTCGACCACTTCCTGCCTCAG 2201
DB 1 GGTTCACACCACTTCCTGCTTCAG 25
RESULT 516
AAH91552
ID AAH91552 standard; DNA; 27 BP.
XX
AC AAH91552;
XX
DT 09-OCT-2001 (first entry)
XX
DE Human inflammatory bowel disease associated polymorphic site #627.
XX
KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
Query Match 0.9%; Score 21.8; DB 1; Length 27;
Best Local Similarity 88.5%; Pred. No. 1.6e+03;

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Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2335 GCCTCCCAAGTCTGGGATTACAGG 2360
Db 1 GCCTTCCCAAGTGCNAGGATTACAGG 26

RESULT 517
ADO12902
ID ADO12902 standard; DNA; 29 BP.
XX
AC ADO12902;
XX
DT 15-JUL-2004 (first entry)
DE Single multiplex PCR primer #2274.
XX
KW ss; primer; simultaneous amplification;
KW single multiplex polymerase chain reaction; multifactorial disease;
Query Match 0.9%; Score 21.8; DB 1; Length 29;
Best Local Similarity 92.0%; Pred. No. 1.6e+03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2332 TCGGCTCCCAAGTCTGGGATTA 2356
Db 5 TCGGCTCCCAAAATTCGGGATTA 29

RESULT 518
ADO12945/c
ID ADO12945 standard; DNA; 29 BP.
XX
AC ADO12945;
XX
DT 15-JUL-2004 (first entry)
DE Single multiplex PCR primer #2317.
XX
KW ss; primer; simultaneous amplification;
KW single multiplex polymerase chain reaction; multifactorial disease;
Query Match 0.9%; Score 21.8; DB 1; Length 29;
Best Local Similarity 92.0%; Pred. No. 1.6e+03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2332 TCGGCTCCCAAGTCTGGGATTA 2356
Db 25 TCGGCTCCCAAAATTCGGGATTA 1

RESULT 519
AAT12509
ID AAT12509 standard; DNA; 28 BP.
XX
AC AAT12509;
XX
DT 09-SEP-1996 (first entry)
DE
DE Primer Alu B corresp. to bases 294-267.
KW Primer; PCR; polymerase chain reaction; amplification; Alu repeat; ss;
KW quantitation; internal standard; plasmid; contamination; therapeutic.
Query Match 0.9%; Score 21.6; DB 1; Length 28;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2100 GAGACGAGTCTGCTCTGTACCCAGG 2127
Db 1 GAGACAGAGTCTCGCTCTGTGCGCCAGG 28

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RESULT 520
AAx83037/c
ID AAx83037 standard; DNA; 23 BP.
XX
AC AAx83037;
XX
DT 31-AUG-1999 (first entry)
DE
DE Primer E2C to isolate human WRN gene 3' exons.
XX
KW Human; WRN; Werner's syndrome; detection; diagnosis; autosomal;
KW recessive disorder; phenotype; primer; RT-PCR; amplification; ss.
Query Match 0.9%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2336 CCTCCCAAGTCTGGGATTACA 2358
Db 23 CCTCCCAAGTCTGGGATTACA 1

RESULT 521
ADH47847
ID ADH47847 standard; DNA; 23 BP.
XX
AC ADH47847;
XX
DT 25-MAR-2004 (first entry)
DE
DE NOV14 PCR primer, SEQ ID 260.
XX
KW Antidiabetic; anorectic; cardiant; hypotensive; antiarteriosclerotic;
KW anorectic; virucide; antibacterial; fungicide; protozoacide; nootropic;
Query Match 0.9%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2097 TTTGACACCGAGTCTTGCTCTGT 2119
Db 1 TTTGACACCGAGTCTTGCTCTGT 23

RESULT 522
ADA74797/c
ID ADA74797 standard; DNA; 23 BP.
XX
AC ADA74797;
XX
DT 20-NOV-2003 (first entry)
DE
DE PCR primer F1209 used to sequence human LDLR DNA.
XX
KW discriminant function coefficient; DC; ethnic affiliation; haplotype;
KW descent predictor; forensic analysis; Alu repeat; hot spot; diversity;
Query Match 0.9%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2344 AGTGCTGGGATTACAGCGATGAG 2366
Db 23 AGTGCTGGGATTACAGCGGTGAG 1

RESULT 523
ADP68378
ID ADP68378 standard; DNA; 23 BP.
XX
AC ADP68378;
XX
DT 12-AUG-2004 (first entry)

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XX PCR primer used to amplify human NOV14 DNA (Ag210) SeqID 262.
DE human; PCR; ss; NOVX; Alzheimer's disease; Huntington's; inflammatory;
KW Crohn's disease; rheumatoid arthritis; immunological; endocrine;
KW

Query Match      0.9%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2097 TTTGAGACCGAGTCTGCTGT 2119
DB 1 TTTGAGACCGAGTCTGCTGT 23

RESULT 524
ADL25729
ID ADL25729 standard; DNA; 23 BP.
XX
AC ADL25729;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human NOVX gene, reverse PCR primer #29.
XX
KW ss; PCR; primer; Cytostatic; Neuroprotective; Immunosuppressive;
KW Gene therapy; Vaccine; human; neurodegenerative disorder;
KW

Query Match      0.9%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2097 TTTGAGACCGAGTCTGCTGT 2119
DB 1 TTTGAGACCGAGTCTGCTGT 23

RESULT 525
ABV75668/c
ID ABV75668 standard; DNA; 24 BP.
XX
AC ABV75668;
XX
DT 28-JAN-2003 (first entry)
XX
DE Human FD16.06 PCR primer 2.
XX
KW Human; FD16.06; cancer; HIV; PCR; primer; ss.
XX

Query Match      0.9%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2108 GTCTTGCTCTGTACCCAGGCTG 2130
DB 24 GTCTTGCTCTGTGTCAGGCTG 2

RESULT 526
ABQ83396
ID ABQ83396 standard; DNA; 24 BP.
XX
AC ABQ83396;
XX
DT 21-JAN-2003 (first entry)
XX
DE Human proteasome p40.5 subunit 20.24 PCR primer 2 SEQ ID NO:4.
XX
KW Human; proteasome p40.5 subunit 20.24; malignant tumour; haemopathy;
KW Human immunodeficiency virus infection; HIV infection; inflammation;
KW

Query Match      0.9%; Score 21.4; DB 1; Length 24;

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Best Local Similarity 95.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2266 TAGAGACAGGGTTTCACCGTGT 2288
DB 1 TAGAGACAGGGTTTCACCGTGT 23

RESULT 527
ADE43814/c
ID ADE43814 standard; DNA; 24 BP.
XX
AC ADE43814;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human LIPA PCR primer, SEQ ID 419.
XX
KW Neurodegenerative disease; uPA; SNGG; IDE; KNSL1; LIPA; TNFRSF6;
KW Alzheimer's disease; neuroprotective; neurotropic; gene therapy;
KW

Query Match      0.9%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2261 TTTAGTAGACAGGGTTTCACC 2283
DB 23 TTTAGTAGATACAGGGTTTCACC 1

RESULT 528
ADL06343/c
ID ADL06343 standard; DNA; 24 BP.
XX
AC ADL06343;
XX
DT 06-MAY-2004 (first entry)
XX
DE RT-PCR primer #1 for cDNA encoding human protein-13.2.
XX
KW Human; protein-13.2; site-specific recombinase;
KW growth development disorder; tumour; reverse transcriptase-PCR; RT-PCR;
KW

Query Match      0.9%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2185 CCATTCTCTGCTCAGCCTCCC 2207
DB 24 CGATTCTCTGCTCAGCCTCCC 2

RESULT 529
ADH54292/c
ID ADH54292 standard; DNA; 24 BP.
XX
AC ADH54292;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human neurodegenerative disease-related PCR primer SeqID419.
XX
KW human; neurodegenerative disease; urokinase plasminogen activator; uPA;
KW gamma-synuclein; SNGG; insulin degrading enzyme; IDE;
KW

Query Match      0.9%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2261 TTTAGTAGACAGGGTTTCACC 2283
DB 23 TTTAGTAGATACAGGGTTTCACC 1

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RESULT 530
AAH16609
ID AAX16609 standard; DNA; 25 BP.
XX AC
XX AAX16609;
DT 29-APR-1999 (first entry)
XX AC
DE Interleukin 1 (44112332) haplotype PCR primer #3.
KW Interleukin 1; IL-1; haplotype; inflammatory disorder; alopecia areata;
KW coronary artery disease; osteoporosis; nephropathy; diabetes mellitus;

Query Match 0.9%; Score 21.4; DB 1; Length 25;
Best Local Similarity 95.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2350 GGGATTACAGGCGTGAGCCACCG 2372
DB 1 GGGATTACAGGCGTGAGCCACCG 23

RESULT 531
AAD27391
ID AAD27391 standard; DNA; 25 BP.
XX AC
XX AAD27391;
DT 18-APR-2002 (first entry)
XX AC
DE PCR primer #1, used for genotyping human IL-1A (gz5/gz6) marker.
KW Human; interleukin-1; inflammatory disorder; coronary artery disease;
KW periodontal disease; Alzheimer's disease; atherosclerosis; osteoporosis;

Query Match 0.9%; Score 21.4; DB 1; Length 25;
Best Local Similarity 95.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2350 GGGATTACAGGCGTGAGCCACCG 2372
DB 1 GGGATTACAGGCGTGAGCCACCG 23

RESULT 532
ADN48862
ID ADN48862 standard; DNA; 25 BP.
XX AC
XX ADN48862;
DT 15-JUL-2004 (first entry)
XX AC
DE Human interleukin-1A (gz5/gz6) amplifying PCR primer #1.
KW Early-onset menopause; EOM; diagnosis; therapy; human; interleukin-1A;
KW IL-1A; PCR; primer; ss.

Query Match 0.9%; Score 21.4; DB 1; Length 25;
Best Local Similarity 95.7%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2350 GGGATTACAGGCGTGAGCCACCG 2372
DB 1 GGGATTACAGGCGTGAGCCACCG 23

RESULT 533
AAH39523
ID AAH39523 standard; DNA; 27 BP.
XX AC
XX AAH39523;

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DT 14-AUG-2001 (first entry)
XX AC
DE SNP specific SNPE primer SEQ ID 2319.
XX AC
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 0.9%; Score 21.2; DB 1; Length 27;
Best Local Similarity 85.2%; Pred. No. 1.7e+03;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2257 TACTTTTAGTAGACAGGCTTTCACC 2283
DB 1 TATTTTAGTAGAGATGGGNTTTCACC 27

RESULT 534
AAH38059/c
ID AAH38059 standard; DNA; 27 BP.
XX AC
XX AAH38059;
DT 14-AUG-2001 (first entry)
XX AC
DE SNP specific SNPE primer SEQ ID 855.
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 0.9%; Score 21.2; DB 1; Length 27;
Best Local Similarity 85.2%; Pred. No. 1.7e+03;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2142 GTGATCTTGCTCACTGCAAGCTCTGC 2168
DB 27 GTGATCTTAGTCACTGCAACCTCCGC 1

RESULT 535
AAH40803
ID AAH40803 standard; DNA; 27 BP.
XX AC
XX AAH40803;
DT 14-AUG-2001 (first entry)
XX AC
DE SNP specific SNPE primer SEQ ID 3599.
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 0.9%; Score 21.2; DB 1; Length 27;
Best Local Similarity 85.2%; Pred. No. 1.7e+03;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2344 AGTGCTGGGATTACAGGCATGCCAC 2370
DB 1 AGTGCTGAAATTACAGNCGTGAGCCAC 27

RESULT 536
AAV27991/c
ID AAV27991 standard; DNA; 21 BP.
XX AC
XX AAV27991;
DT 25-SEP-1998 (first entry)
XX AC
DE Ataxia telangiectasia exon 17 primer 2.
KW ss; PCR; primer; amplification; ataxia telangiectasia; diagnosis; human;
KW radiation; breast cancer.

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Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2122 CCCAGGCTGGAGTGCAGTGGG 2142
    |||||
Db 21 CCCAGGCTGGAGTGCAGTGGG 1

RESULT 537
AAZ37739
ID AAZ37739 standard; DNA; 21 BP.
XX
AC AAZ37739;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 real-time forward PCR primer #269.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 307 GGCATAATGTGCAATACCAACA 327
    |||||
Db 1 GGCATAATGTGCAATACCAACA 21

RESULT 538
AAX35114
ID AAX35114 standard; DNA; 21 BP.
XX
AC AAX35114;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide S7-3 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
    inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1007 AGGTGATTGGTTGGATCAGGA 1027
    |||||
Db 1 AGGTGATTGGTTGGATCAGGA 21

RESULT 539
AAX35136/c
ID AAX35136 standard; DNA; 21 BP.
XX
AC AAX35136;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide AS7-3 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
    inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1007 AGGTGATTGGTTGGATCAGGA 1027
    |||||
Db 21 AGGTGATTGGTTGGATCAGGA 1

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RESULT 540
AAA62471/c
ID AAA62471 standard; DNA; 21 BP.
XX
AC AAA62471;
XX
DT 21-NOV-2000 (first entry)
XX
DE Human SECX 2826468 forward primer.
XX
KW Human; secreted protein; SECX; cancer; cytostatic; vaccine; primer;
    expression analysis; ss.

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2300 TCTCGATCTCCTGACCTCGTG 2320
    |||||
Db 21 TCTCGATCTCCTGACCTCGTG 1

RESULT 541
AAA97663/c
ID AAA97663 standard; DNA; 21 BP.
XX
AC AAA97663;
XX
DT 15-FEB-2001 (first entry)
XX
DE Human MDM2 reverse RT-PCR primer 2.
XX
KW Pseudocyclic oligonucleotide; functional segment; protective segment;
    nucleic acid detection; mRNA cleavage; antisense therapy; PCO;

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 726 GTACAAGAGCTTCAGGAAGAG 746
    |||||
Db 21 GTACAAGAGCTTCAGGAAGAG 1

RESULT 542
AAA50950/c
ID AAA50950 standard; DNA; 21 BP.
XX
AC AAA50950;
XX
DT 27-OCT-2000 (first entry)
XX
DE Human mdm2 PCR primer #2.
XX
KW Fluorescent protein; fluorescence labelling; fusion protein; human;
    PCR primer; ss.

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1767 GTGCTAACTATTTCCTCCCTAG 1787
    |||||
Db 21 GTGCTAACTATTTCCTCCCTAG 1

RESULT 543
AAD03620/c
ID AAD03620 standard; DNA; 21 BP.
XX
AC AAD03620;

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XX 19-JUN-2001 (first entry)
DT Human marathon cDNA library (Burke's lymphoma) amplifying PCR primer #2.
DE Anthozoa; Chromoprotein; fluorescent protein; sunscreen; biosensor;
KW analyte detection assay; selectable marker; recombinant DNA application;

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1767 GTGCTAACTTATTTCCCTAG 1787
DB 21 GTGCTAACTTATTTCCCTAG 1

RESULT 544
AAF95738
ID AAF95738 standard; DNA; 21 BP.
XX
AC AAF95738;
XX
DT 06-JUN-2001 (first entry)
DE Human gene single nucleotide polymorphism #499.
XX
KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW polymorphism; vascular disease; coronary artery disease; forensics;

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2336 CCTCCAAAGTCTGGGATTA 2356
DB 1 CCTCCAAAGTCTGGGATTA 21

RESULT 545
AAF80893
ID AAF80893 standard; DNA; 21 BP.
XX
AC AAF80893;
XX
DT 02-MAY-2001 (first entry)
DE Human mdm2 forward primer.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 307 GGCAATGTGCAATACCAACA 327
DB 1 GGCAATGTGCAATACCAACA 21

RESULT 546
AAH40326
ID AAH40326 standard; DNA; 21 BP.
XX
AC AAH40326;
XX
DT 14-AUG-2001 (first entry)
DE SNP specific lower PCR primer SEQ ID 3122.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

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Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2286 GTTAGCCAGGATGCTCTCGAT 2306
DB 1 GTTAGCCAGGATGCTCTCGAT 21

RESULT 547
AAH22714/c
ID AAH22714 standard; DNA; 21 BP.
XX
AC AAH22714;
XX
DT 07-SEP-2001 (first entry)
DE Human secreted protein (SECX) specific oligo.
XX
KW Secreted protein; SECX; cancer; human; cytostatic; gene therapy;
KW PCR primer; probe; ss.

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2300 TCTCGATCTCTGACCTCGTG 2320
DB 21 TCTCGATCTCTGACCTCGTG 1

RESULT 548
AAS29508
ID AAS29508 standard; DNA; 21 BP.
XX
AC AAS29508;
XX
DT 21-NOV-2001 (first entry)
DE Forward PCR primer used to amplify human mdm2 mRNA.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 307 GGCAATGTGCAATACCAACA 327
DB 1 GGCAATGTGCAATACCAACA 21

RESULT 549
ABS98157
ID ABS98157 standard; DNA; 21 BP.
XX
AC ABS98157;
XX
DT 23-DEC-2002 (first entry)
DE Human multidrug resistance gene polymorphic sequence #59.
XX
KW Human; ds; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1;
KW cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTF;

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2278 TTCACCGTGTAGCCAGGATG 2298
DB 1 TTCACCGTGTAGCCAGGATG 2298

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Db      1 TTCACCGTGTAGCCAGGATG 21

RESULT 550
ABL60509/c
ID      ABL60509 standard; DNA; 21 BP.
AC      ABL60509;
XX
XX      12-AUG-2002 (first entry)
XX
XX      Human MDM2 mRNA amplifying RT-PCR reverse primer 2.
XX
XX      Pseudo-cyclic oligonucleotide; PCO; gene expression; protein kinase A;
KW      nucleic acid detection; ribozyme inhibition; gene transcription; MDM2;

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      726 GTACAAGAGCTTCAGGAAGAG 746
Db      21 GTACAAGAGCTTCAGGAAGAG 1

RESULT 551
ADD21704
ID      ADD21704 standard; DNA; 21 BP.
XX
AC      ADD21704;
XX
XX      15-JAN-2004 (first entry)
XX
XX      Human mdm2-specific PCR primer #1.
XX
KW      antisense oligonucleotide; human; mdm2; hyperproliferation;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      307 GGCAAAATGTGCAATACCAACA 327
Db      1 GGCAAAATGTGCAATACCAACA 21

RESULT 552
AAD64997
ID      AAD64997 standard; DNA; 21 BP.
XX
AC      AAD64997;
XX
XX      11-MAR-2004 (first entry)
XX
XX      Human mouse double minute (MDM2) sense oligonucleotide S7-3.
XX
XX      MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW      therapeutic; antisense therapy; human; ss.

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1007 AGGTGATTGGTTGGATCAGGA 1027
Db      1 AGGTGATTGGTTGGATCAGGA 21

RESULT 553
AAD65018/c
ID      AAD65018 standard; DNA; 21 BP.
XX

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AC      AAD65018;
XX
XX      11-MAR-2004 (first entry)
XX
XX      Human mouse double minute (MDM2) antisense oligonucleotide AS7-3.
XX
XX      MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW      therapeutic; antisense therapy; human; antisense; ss.

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1007 AGGTGATTGGTTGGATCAGGA 1027
Db      21 AGGTGATTGGTTGGATCAGGA 1

RESULT 554
ADK66046
ID      ADK66046 standard; DNA; 21 BP.
XX
AC      ADK66046;
XX
XX      06-MAY-2004 (first entry)
XX
XX      Standardized polynucleotide system polynucleotide #10 PCR primer #1.
XX
XX      ss; standardized polynucleotide system; medical diagnosis;
KW      functional genomics; sample analysis; pharmacogenomics; sample analysis;

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      359 CTCACAGATTCACAGCTTCGGA 379
Db      1 CTCACAGATTCACAGCTTCGGA 21

RESULT 555
ADI23732
ID      ADI23732 standard; DNA; 21 BP.
XX
AC      ADI23732;
XX
XX      06-MAY-2004 (first entry)
XX
XX      Human LPDLR PCR primer #12.
XX
XX      lipase; LPDLR; lipase deficiency; atherosclerosis;
KW      fatty liver disease; dyslipidaemia; hypercholesterolaemia;

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2346 TGCTGGGATTACGGCATGAG 2366
Db      1 TGCTGGGATTACAGGCATGAG 21

RESULT 556
AAF93028/c
ID      AAF93028 standard; DNA; 22 BP.
XX
AC      AAF93028;
XX
XX      17-MAY-2001 (first entry)
XX
XX      Polymorphic sequence for ABC1 polymorphic site #38.
XX
XX      High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.

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XX
Query Match      0.9%; Score 21; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2188 TTCTCTGCTCAGCTCCCAA 2209
DB 22 TTCTCTGCTNAGCTCCCAA 1

RESULT 557
ADB04762
ID ADB04762 standard; DNA; 25 BP.
XX
AC ADB04762;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5748.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
  zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match      0.9%; Score 21; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTACCGGTGTAGCCAG 2294
DB 5 GGGTTTACCGGTGTAGCCAG 25

RESULT 558
AAF92891
ID AAF92891 standard; DNA; 24 BP.
XX
AC AAF92891;
XX
DT 17-MAY-2001 (first entry)
XX
DE Human ABC1 transcription factor binding site #52.
XX
KW High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.

Query Match      0.9%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2301 CTCGATCTCTGACCTCGATCC 2324
DB 1 CTCGATCTCTGACCTCGATCC 24

RESULT 559
AAF92843
ID AAF92843 standard; DNA; 24 BP.
XX
AC AAF92843;
XX
DT 17-MAY-2001 (first entry)
XX
DE Human ABC1 transcription factor binding site #6.
XX
KW High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.

Query Match      0.9%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2293 AGGATGGTCTCGATCTCTGACCT 2316
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Db 1 AGGCTGGTCTCGAAGCTCTGACCT 24

RESULT 560
AAI65098
ID AAI65098 standard; DNA; 24 BP.
XX
AC AAI65098;
XX
DT 28-NOV-2001 (first entry)
XX
DE Human zinc finger protein 15 PCR primer #1.
XX
KW Human; zinc finger protein 15; cytostatic; virucidal; immunomodulatory;
  antiinflammatory; haemostatic; gene therapy; malignant neoplasm;

Query Match      0.9%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2349 TGGGATTACAGGCATGAGCCACCG 2372
DB 1 TGGGATTACAGGTGTGAGCCACCG 24

RESULT 561
ABK51390
ID ABK51390 standard; DNA; 24 BP.
XX
AC ABK51390;
XX
DT 30-JUL-2002 (first entry)
XX
DE Human Mch2 protein 9.57, RT-PCR primer 2.
XX
KW Human; Mch2 protein 9.57; cancer; human immunodeficiency virus infection;
  HIV; reverse transcriptase PCR; RT-PCR; primer; ss.

Query Match      0.9%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2102 GACCGAGTCTTGCTCTGTACCCA 2125
DB 1 GACAGAGTCTTGCTCTGTGCCCA 24

RESULT 562
ABL56667
ID ABL56667 standard; DNA; 24 BP.
XX
AC ABL56667;
XX
DT 30-JUL-2002 (first entry)
XX
DE PCR primer #2 for human prollyl oligomeric peptidase 13.2 cDNA.
XX
KW Human; prollyl oligomeric peptidase 13.2; enzyme; angiocardiodiopathy;
  nervous system retrograde disease; gene therapy; PCR; primer; ss.

Query Match      0.9%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2100 GAGACCGAGTCTTGCTCTGTACC 2123
DB 1 GAGACAGAGTCTTGCTCTGTGCC 24

RESULT 563
AAL46337/c
ID AAL46337 standard; DNA; 24 BP.
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XX AAL46337;
AC
XX
DT 19-JUL-2002 (first entry)
DE Human M30 protein coding sequence PCR primer hm30_nn_s5.
XX
KW Neurodegenerative disease; M30; M31; M32; M33; stroke;
KW fragile X syndrome; Huntington's disease; Parkinson's disease;
Query Match 0.9%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2106 GAGTCTTGCTCTGTACCCAGGCT 2129
      ||||| ||||| ||||| ||||| |||||
Db 24 GAGTCTTGCTCTGTGCTAGGCT 1

RESULT 564
AAS20575
ID AAS20575 standard; DNA; 24 BP.
XX
AC AAS20575;
XX
DT 23-APR-2002 (first entry)
DE Human uterine globulin 12 cDNA RT-PCR primer #2.
XX
KW Human; uterine globulin 12; malignant tumour; cancer; haemopathy;
KW human immunodeficiency virus; HIV; immunological disease; inflammation;
Query Match 0.9%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2264 AGTAGACACAGGGTTTCCCGTGT 2287
      ||||| ||||| ||||| ||||| |||||
Db 1 AGTAGAACACAGGGTTTCCACCATGT 24

RESULT 565
ABQ77823
ID ABQ77823 standard; DNA; 24 BP.
XX
AC ABQ77823;
XX
DT 20-DEC-2002 (first entry)
DE Human protein phosphatase 13.64 RT-PCR primer, SEQ ID NO:3.
XX
KW Human; protein phosphatase 13.64; recombinant production; gene therapy;
KW female genital development disorder; abnormal female sex characteristic;
Query Match 0.9%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2265 GTAGACACAGGGTTTCCCGTGT 2288
      ||||| ||||| ||||| ||||| |||||
Db 1 GTAGAGATGGGGTTTCCACCGTGT 24

RESULT 566
ABT08420
ID ABT08420 standard; DNA; 24 BP.
XX
AC ABT08420;
XX
DT 27-NOV-2002 (first entry)
DE Human PSF promoter PCR primer SEQ ID NO: 55.
XX
XX

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KW Human; cyclin-dependent kinase; CDK; cyclin-dependent kinase inhibitor;
KW inhibitor; cancer; age-related disease; promoter; atherosclerosis;
Query Match 0.9%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2342 AAAGTCTGGGATTACAGGCATGA 2365
      ||||| ||||| ||||| ||||| |||||
Db 1 AAAGTCTGGGATTAGAGGGGTGA 24

RESULT 567
ABZ57256/c
ID ABZ57256 standard; DNA; 24 BP.
XX
AC ABZ57256;
XX
DT 01-APR-2003 (first entry)
DE Human RAGE4 renal cancer antigen 11.44 RT-PCR primer, SEQ ID NO:3.
XX
KW Human; RAGE4 renal cancer antigen 11.44; recombinant production;
KW gene therapy; renal tumour; renal cancer; cytostatic;
Query Match 0.9%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2260 TTTTGTAGACACAGGGTTTCCACC 2283
      ||||| ||||| ||||| ||||| |||||
Db 24 TTTTGTAGACACGGGATTTCACC 1

RESULT 568
ACA90120
ID ACA90120 standard; DNA; 24 BP.
XX
AC ACA90120;
XX
DT 10-JUL-2003 (first entry)
DE Human kinesin gene(s) antisense oligonucleotide #3.
XX
KW Human; ss; antisense; kinesin; CENP-E; Eg5; MCAK; colon cancer; stroke;
KW T cell cancer; B cell lymphoma; pancreatic cancer; breast cancer;
Query Match 0.9%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2100 GAGACCGAGTCTTGCTCTGTACC 2123
      ||||| ||||| ||||| ||||| |||||
Db 1 GAGACCGACTCTTGCTCTGTGCC 24

RESULT 569
ACF35685/c
ID ACF35685 standard; DNA; 24 BP.
XX
AC ACF35685;
XX
DT 13-OCT-2003 (first entry)
DE Human TGNP promoter amplifying forward primer.
XX
KW Trans-Golgi network integral membrane protein; TGNP; chromosome 2p11.2;
KW cytostatic; antiinflammatory; immunomodulator; neuroprotective; human;
Query Match 0.9%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 2114 CTCTGTTACCCAGGCTGGAGTGCA 2137
DB 24 CTCTGTCACCCAGGCTTGAGTGCA 1

RESULT 570
ADG28972
ID ADG28972 standard; DNA; 24 BP.
XX
AC
XX
AC ADG28972;
XX
DT 26-FEB-2004 (first entry)
XX
DE PCR primer SEQ ID 55 used to amplify human PSF promoter DNA.
XX
KW recombinant expression construct; cyclin-dependent kinase inhibitor; CDK;
KW virucide; cytostatic; neuroprotective; nootropic; antiarteriosclerotic;

Query Match 0.9%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2342 AAGTGTGGGATTACAGGCATGA 2365
DB 1 AAGTGTGGGATTAGAGCGTGA 24

RESULT 571
ADQ30417/c
ID ADQ30417 standard; DNA; 24 BP.
XX
AC ADQ30417;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human VRI exon 1d transcription factor binding fragment #136.
DE ds; VRI receptor; vanilloid receptor type 1; modulator;
KW pain transmission; primary sensory neuron; transcription factor;

Query Match 0.9%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2340 CCAAGTGTGGGATTACAGGCAT 2363
DB 24 CCAAGTGTGGGATTCCAGGCGT 1

RESULT 572
AAH38671
ID AAH38671 standard; DNA; 25 BP.
XX
AC AAH38671;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific SNPE primer SEQ ID 1467.
DE
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2249 ATTTTTCGTTTATTAGTAGAGAC 2272
DB 1 AATTTTGTATTATTAGTAGAGAC 24

RESULT 573
AAH38231
ID AAH38231 standard; DNA; 25 BP.
XX
AC AAH38231;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific SNPE primer SEQ ID 1027.
DE
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2249 ATTTTTCGTTTATTAGTAGAGAC 2272
DB 1 AATTTTGTATTATTAGTAGAGAC 24

RESULT 574
ADB04675
ID ADB04675 standard; DNA; 25 BP.
XX
AC ADB04675;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5661.
DE
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;

Query Match 0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2184 ACCATTCTCTGCTCAGCTCCC 2207
DB 1 ACCATTCTCTGCTCAGTCTCCC 24

RESULT 575
ADB04744
ID ADB04744 standard; DNA; 25 BP.
XX
AC ADB04744;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5730.
DE
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;

Query Match 0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2253 TTGTACTTTTATTAGTAGAGACGGG 2276
DB 1 TTGTATTATTATTAGTAGAGCGGG 24

RESULT 576
ADB04673
ID ADB04673 standard; DNA; 25 BP.
XX
AC ADB04673;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5659.

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XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match      0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2183 CACCAATTCCTCTGCTCAGCCTCC 2206
DB 2 CACCAATTCCTCTGCTCAGCCTCC 25

RESULT 577
ADB04664
ID ADB04664 standard; DNA; 25 BP.
XX
AC ADB04664;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5650.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match      0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2173 CCGGGTTCGACCAATTCCTCTGC 2196
DB 1 CCGGGTTCGACCAATTCCTCTGC 24

RESULT 578
ADB04736
ID ADB04736 standard; DNA; 25 BP.
XX
AC ADB04736;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5722.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match      0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2246 CTAATTTTGTACTTTTAGTAGA 2269
DB 2 CTAATTTTGTACTTTTAGTAGA 25

RESULT 579
ADB04740
ID ADB04740 standard; DNA; 25 BP.
XX
AC ADB04740;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5726.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match      0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 2249 ATTTTGTACTTTTAGTAGAGAC 2272
DB 1 ATATTTTGTATTTTAGTAGAGAC 24

RESULT 580
ADB04666
ID ADB04666 standard; DNA; 25 BP.
XX
AC ADB04666;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5652.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match      0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2176 GGGTTCGACCAATTCCTCTGCCTC 2199
DB 2 GGGTTCGACCAATTCCTCTGCCTC 25

RESULT 581
ADB04669
ID ADB04669 standard; DNA; 25 BP.
XX
AC ADB04669;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5655.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match      0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2178 GTTCGACCAATTCCTCTGCCTCAG 2201
DB 1 GTTCGACCAATTCCTCTGCCTCAG 24

RESULT 582
ADB04663
ID ADB04663 standard; DNA; 25 BP.
XX
AC ADB04663;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5649.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match      0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2173 CCGGGTTCGACCAATTCCTCTGC 2196
DB 2 CCGGGTTCGACCAATTCCTCTGC 25

RESULT 583

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ADB04742
ID ADB04742 standard; DNA; 25 BP.
XX
AC ADB04742;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5728.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match 0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2252 TTTTGTACTTTTAGTAGAGACAGG 2275
DB 2 TTTTGTATTTTAGTAGAGACGG 25

RESULT 584
ADJ94629
ID ADJ94629 standard; DNA; 25 BP.
XX
AC ADJ94629;
XX
DT 06-MAY-2004 (first entry)
XX
DE Promoter related PCR primer, SEQ ID 7.
XX
KW Promoter; human; fat cell; PCR; primer; ss.

Query Match 0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGAGACAGGGTTTCACC 2283
DB 1 TTTTAGTAGAGACAGGGTTTCACC 24

RESULT 585
AAZ37279/c
ID AAZ37279 standard; DNA; 27 BP.
XX
AC AAZ37279;
XX
DT 01-FEB-2000 (first entry)
XX
DE PCR primer for SGRF coding sequence.
XX
KW SGRF; human; Interleukin-6 G-CSF related factor; cell proliferation;
immune system; haematopoietic system; therapy; PCR primer; ss.

Query Match 0.9%; Score 20.8; DB 1; Length 27;
Best Local Similarity 91.7%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2192 CCTGCTCAGCTCCCAATTAGCT 2215
DB 27 CCTGCTCAGCTCCCAAGCAGCT 4

RESULT 586
AAH39267
ID AAH39267 standard; DNA; 27 BP.
XX
AC AAH39267;
XX
DT 14-AUG-2001 (first entry)
XX

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DE SNP specific SNPE primer SEQ ID 2063.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 0.9%; Score 20.8; DB 1; Length 27;
Best Local Similarity 84.6%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2346 TGCTGGATTACAGGCATGAGCCACC 2371
DB 1 TGCTGNGATTATAGNCACGAGCCACC 26

RESULT 587
AAH91322/c
ID AAH91322 standard; DNA; 27 BP.
XX
AC AAH91322;
XX
DT 09-OCT-2001 (first entry)
XX
DE Human inflammatory bowel disease associated polymorphic site #397.
XX
KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;

Query Match 0.9%; Score 20.8; DB 1; Length 27;
Best Local Similarity 88.0%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2185 CGATTCTCTGCTCAGCCTCCCAA 2209
DB 25 CGATTCTCTGCTCAGCCTCCCAA 1

RESULT 588
ACC84460
ID ACC84460 standard; DNA; 27 BP.
XX
AC ACC84460;
XX
DT 28-AUG-2003 (first entry)
XX
DE NTP peptide encoding sequence #7.
XX
KW Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;
neural thread protein; NTP; tumour; ds.

Query Match 0.9%; Score 20.6; DB 1; Length 27;
Best Local Similarity 85.2%; Pred. No. 1.8e+03;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2331 CTGGGCTCCCAAGTCTGGGATTAC 2357
DB 1 CTCAGCCTCCCAAGCAGCTGGGATTAC 27

RESULT 589
AAC69375/c
ID AAC69375 standard; DNA; 22 BP.
XX
AC AAC69375;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human ABC1 BAC contig polymorphic site, SEQ ID NO:274.
XX
KW Human ABC1 cholesterol transporter; chromosome 9q31;
ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;

Query Match 0.9%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.7e+03;

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Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2188 TTCTCTGCTCAGCCTCCCA 2209
DB 22 TTCTCTGCTTAGCCTCCCA 1

RESULT 590
AAF84349/c
ID AAF84349 standard; DNA; 22 BP.
XX
AC AAF84349;
XX
DT 20-JUN-2001 (first entry)
XX
DE Human CYP2C18i PCR primer #5.
XX
KW Gene polymorphism; drug-metabolising enzyme; PCR primer; CYP2C18i; ss.
XX

Query Match 0.9%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.7e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2344 AGTGCTGGGATTACAGGCATGA 2365
DB 22 AATGCTGGGATTACAGGCATGA 1

RESULT 591
AAD31453/c
ID AAD31453 standard; DNA; 22 BP.
XX
AC AAD31453;
XX
DT 31-MAY-2002 (first entry)
XX
DE Human chromosome 17 92Kb gene fragment amplifying PCR primer, wt1R.
KW Human; Van Buchem's disease; genomic deletion; craniofacial; hypertension;
autosomal recessive disorder; chromosome 17; chromosome 17q21;

Query Match 0.9%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.7e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2187 ATTCTCTGCTCAGCCTCCCA 2208
DB 22 ATTCTCTGCTCAGCCTCCCA 1

RESULT 592
AAD31457/c
ID AAD31457 standard; DNA; 22 BP.
XX
AC AAD31457;
XX
DT 31-MAY-2002 (first entry)
XX
DE Human chromosome 17 92Kb gene fragment amplifying PCR primer, wt3R.
KW Human; Van Buchem's disease; genomic deletion; craniofacial; hypertension;
autosomal recessive disorder; chromosome 17; chromosome 17q21;

Query Match 0.9%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.7e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2187 ATTCTCTGCTCAGCCTCCCA 2208
DB 22 ATTCTCTGCTCAGCCTCCCA 1
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RESULT 593
ADB88578
ID ADB88578 standard; DNA; 22 BP.
XX
AC ADB88578;
XX
DT 04-DEC-2003 (first entry)
XX
DE Frizzled-4 (FZD4) modulating agent related oligo, SEQ ID No 25.
KW Frizzled-4; FZD4; immunomodulatory compound; ophthalmological; vasotropic;
antiinflammatory; vulnery; osteopathic; antimicrobial; antipsoriatic;

Query Match 0.9%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.7e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2109 TCTTGCTCTGTACCCAGGCTG 2130
DB 1 TCTTGCTCTGTACCCAGGCTG 22

RESULT 594
ADB88579
ID ADB88579 standard; DNA; 22 BP.
XX
AC ADB88579;
XX
DT 04-DEC-2003 (first entry)
XX
DE Frizzled-4 (FZD4) modulating agent related oligo, SEQ ID No 26.
KW Frizzled-4; FZD4; immunomodulatory compound; ophthalmological; vasotropic;
antiinflammatory; vulnery; osteopathic; antimicrobial; antipsoriatic;

Query Match 0.9%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.7e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2109 TCTTGCTCTGTACCCAGGCTG 2130
DB 1 TCTTGCTCTGTACCCAGGCTG 22

RESULT 595
ADM65599
ID ADM65599 standard; DNA; 22 BP.
XX
AC ADM65599;
XX
DT 03-JUN-2004 (first entry)
XX
DE NRY polymorphism detection primer #505.
KW ethnic origin determination; polymorphic site determination;
Y chromosome; paternity testing; forensic; diagnosis;

Query Match 0.9%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.7e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2092 TTTTCTTGTGAGACCGAGTCTTG 2113
DB 1 TTTTCTTGTGAGACCGAGTCTTG 22

RESULT 596
ADM65602
ID ADM65602 standard; DNA; 22 BP.
XX
AC ADM65602;
XX
DT 03-JUN-2004 (first entry)
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XX NRY polymorphism detection primer #507.
DE ethnic origin determination; polymorphic site determination;
KW Y chromosome; paternity testing; forensic; diagnosis;
Query Match      0.9%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.7e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2092 TTTTGTGAGACCGAGTCTTG 2113
DB 1 TTTTGTGAGACCGAGTCTTG 22

RESULT 597
ADM65605
ID ADM65605 standard; DNA; 22 BP.
XX AC
XX ADM65605;
XX
DT 03-JUN-2004 (first entry)
DE
DE NRY polymorphism detection primer #509.
KW ethnic origin determination; polymorphic site determination;
KW Y chromosome; paternity testing; forensic; diagnosis;
Query Match      0.9%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.7e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2092 TTTTGTGAGACCGAGTCTTG 2113
DB 1 TTTTGTGAGACCGAGTCTTG 22

RESULT 598
ABS58183/C
ID ABS58183 standard; DNA; 24 BP.
XX AC
XX ABS58183;
XX
DT 26-FEB-2003 (first entry)
DE
DE RT-PCR primer #1 for cDNA encoding human zinc finger protein 10.01.
KW Human; zinc finger protein 10.01; malignant tumour; haemopathy;
KW human immunodeficiency virus infection; HIV infection; inflammation;
Query Match      0.9%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.8e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2351 GGATTACAGGCATGAGCCACCG 2372
DB 24 GGATTACAGGCATGAGCCACCG 3

RESULT 599
ABA96912/C
ID ABA96912 standard; DNA; 24 BP.
XX AC
XX ABA96912;
XX
DT 15-MAY-2002 (first entry)
DE
DE Human arginase 9 RT-PCR primer, SEQ ID NO:3 version #1.
XX Human; arginase 9; recombinant production; argininaemia;
KW arginine metabolism disorder; urea metabolism disorder;
Query Match      0.9%; Score 20.4; DB 1; Length 24;

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Best Local Similarity 95.5%; Pred. No. 1.8e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2351 GGATTACAGGCATGAGCCACCG 2372
DB 24 GGATTACAGGCATGAGCCACCG 3

RESULT 600
ABX15537
ID ABX15537 standard; DNA; 25 BP.
XX AC
XX ABX15537;
XX
DT 11-APR-2003 (first entry)
DE
DE Human IL-1 genotyping marker gz51gz6 primer #1.
KW Human; ss; PCR; primer; interleukin-1; IL-1; marker gz51gz6; nephropathy;
KW inflammatory disease; Systemic Inflammatory Response; SIRS; genotyping;
Query Match      0.9%; Score 20.4; DB 1; Length 25;
Best Local Similarity 91.3%; Pred. No. 1.8e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2350 GGGATTACAGGCATGAGCCACCG 2372
DB 1 GGGATTACAGGCATGAGCCACCG 23

RESULT 601
AAH38991/C
ID AAH38991 standard; DNA; 25 BP.
XX AC
XX AAH38991;
XX
DT 14-AUG-2001 (first entry)
DE
DE SNP specific SNPE primer SEQ ID 1787.
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
Query Match      0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2326 CCACCTCGCCCTCCCAAGTGCTG 2350
DB 25 CCACCTCGCCCTCCCAAGTGCTG 1

RESULT 602
AAH37598
ID AAH37598 standard; DNA; 25 BP.
XX AC
XX AAH37598;
XX
DT 14-AUG-2001 (first entry)
DE
DE SNP specific lower PCR primer SEQ ID 394.
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
Query Match      0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2090 TATTTTGTGAGACCGAGTCTTG 2114
DB 1 TATTTTGTGAGATGGAGTCTTG 25

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RESULT 603
AAH38423
ID AAH38423 standard; DNA; 25 BP.
XX
AC AAH38423;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific SNPE primer SEQ ID 1219.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2185 CCATTCCTGCTCAGCTCCCA 2209
Db 1 CAATTCCTGCTCAGCTCCCA 25

RESULT 604
AAH40563/c
ID AAH40563 standard; DNA; 25 BP.
XX
AC AAH40563;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific SNPE primer SEQ ID 3359.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2188 TTCTCCTGCTCAGCTCCCAATTA 2212
Db 25 TTGTCCTGCTCAGCTCCCAATTA 1

RESULT 605
AAH37859
ID AAH37859 standard; DNA; 25 BP.
XX
AC AAH37859;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific SNPE primer SEQ ID 655.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2188 TTCTCCTGCTCAGCTCCCAATTA 2212
Db 25 TTGTCCTGCTCAGCTCCCAATTA 1

RESULT 606
AAH40067/c
ID AAH40067 standard; DNA; 25 BP.
XX
AC AAH40067;
XX

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DT 14-AUG-2001 (first entry)
XX
DE SNP specific SNPE primer SEQ ID 2863.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match 0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2188 TTCTCCTGCTCAGCTCCCAATTA 2212
Db 25 TTCTCCTGCTCAGCTCCCAATTA 1

RESULT 607
ABL51377/c
ID ABL51377 standard; DNA; 25 BP.
XX
AC ABL51377;
XX
DT 28-JUN-2002 (first entry)
XX
DE Mutant DSPP gene detection related 5' PCR primer D4S2932.
XX
KW Mutant DSPP gene detection; chromosome 4q21; dentin sialophosphoprotein;
KW hereditary opalescent dentin; periodontal; gene therapy; mineralisation;

Query Match 0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2092 TTTTCTTTCGACCGAGCTTTGCTC 2116
Db 25 TTAATTTTCGACGAGCTTTGCTC 1

RESULT 608
ADB04671
ID ADB04671 standard; DNA; 25 BP.
XX
AC ADB04671;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5657.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match 0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2180 TCCACCATTCCTCCTCAGCT 2204
Db 1 TCACACCATTCCTCCTCAGCT 25

RESULT 609
ADB04676
ID ADB04676 standard; DNA; 25 BP.
XX
AC ADB04676;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5662.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

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Query Match      0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2185 CCATTCTCTGCTCAGCCTCCCAA 2209
DB 1 CCATTCTCTGCTCAGTCTCCCGA 25

RESULT 610
ADB04670
ID ADB04670 standard; DNA; 25 BP.
XX
AC ADB04670;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5656.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match      0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2179 TTCGCACCATTCCTCTGCTCAGCC 2203
DB 1 TTCACACCATTCCTCTGCTTCAGTC 25

RESULT 611
ADB04745
ID ADB04745 standard; DNA; 25 BP.
XX
AC ADB04745;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5731.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match      0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2254 TTGTACTTTTGTAGTACAGAGCGGTT 2278
DB 1 TTGTATTTTGTAGACAGCGGGGT 25

RESULT 612
ADB04579
ID ADB04579 standard; DNA; 25 BP.
XX
AC ADB04579;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5565.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match      0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2087 TATTATTTTGTAGACCGAGTCT 2111
DB 1 TTTTATTTTGTAGACAGAGTCT 25
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RESULT 613
ADB04665
ID ADB04665 standard; DNA; 25 BP.
XX
AC ADB04665;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5651.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match      0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2174 CCGGGTTTCGACCATTCCTCTGCTT 2198
DB 1 CTGGGTTTCACACCATTCCTCTGCTT 25

RESULT 614
ADB04578
ID ADB04578 standard; DNA; 25 BP.
XX
AC ADB04578;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5564.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match      0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2086 TTATTATTTTGTAGACCGAGTC 2110
DB 1 TTTTATTTTGTAGACAGAGTC 25

RESULT 615
ADB04746
ID ADB04746 standard; DNA; 25 BP.
XX
AC ADB04746;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5732.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match      0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2255 TGTACTTTTGTAGACAGCGGTTT 2279
DB 1 TGTATTTTGTAGACAGCGGGTT 25

RESULT 616
ADB04672
ID ADB04672 standard; DNA; 25 BP.
XX
AC ADB04672;
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Db      1  GGTCTGGGATTAGGTTGTAACAC 26

RESULT 623
AAH91096/c
ID  AAH91096 standard; DNA; 26 BP.
XX
XX
AC  AAH91096;
XX
DT  09-OCT-2001 (first entry)
XX
DE  Human inflammatory bowel disease associated polymorphic site #171.
XX
KW  Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW  single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;

Query Match      0.9%; Score 20.2; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2345 GTGCTGGGATTACAGGCATGAGCCAC 2370
Db      26 GTGCTGGGATTGCANGTGTGAGCCAC 1

RESULT 624
AD112547/c
ID  AD112547 standard; DNA; 26 BP.
XX
XX
AC  AD112547;
XX
DT  22-APR-2004 (first entry)
XX
DE  Mutant human BRCA1 genomic DNA resulting from deletion 4 SegID 30.
XX
KW  ds; cancer; human; tumour suppressor;
KW  breast cancer susceptibility gene 1; BRCA1; repetitive Alu;

Query Match      0.9%; Score 20.2; DB 1; Length 26;
Best Local Similarity 88.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2144 GATCTTGCTCACTGCAAGCTCTGC 2168
Db      25 GATCTTGCTCACTGAACCTCTGC 1

RESULT 625
AAT73703/c
ID  AAT73703 standard; DNA; 20 BP.
XX
XX
AC  AAT73703;
XX
DT  27-FEB-1998 (first entry)
XX
DE  PCR primer SRI used to prepare probes for diagnosing Alzheimer's.
XX
KW  PCR primer SRI; Alzheimer's disease; probe; diagnosis; fluorochrome;
KW  yeast artificial chromosome library; YAC; chromosome 14; presenile; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2122 CCCAGGCTGGAGTGCAGTGG 2141
Db      20 CCCAGGCTGGAGTGCAGTGG 1

RESULT 626
AAV85762/c
ID  AAV85762 standard; DNA; 20 BP.
XX

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AC  AAV85762;
XX
DT  10-FEB-1999 (first entry)
XX
XX
DE  LRP5 exon primer 57-4 1r.
XX
KW  LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis;
KW  insulin dependent diabetes mellitus; autoimmune disease;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2344 AGTGCTGGGATTACAGGCAT 2363
Db      20 AGTGCTGGGATTACAGGCAT 1

RESULT 627
AAV85840/c
ID  AAV85840 standard; DNA; 20 BP.
XX
XX
AC  AAV85840;
XX
DT  10-FEB-1999 (first entry)
XX
DE  LRP5 SNP primer 57-4 1r.
XX
KW  LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis;
KW  insulin dependent diabetes mellitus; autoimmune disease;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2344 AGTGCTGGGATTACAGGCAT 2363
Db      20 AGTGCTGGGATTACAGGCAT 1

RESULT 628
AAZ37506/c
ID  AAZ37506 standard; DNA; 20 BP.
XX
XX
AC  AAZ37506;
XX
DT  07-JAN-2000 (first entry)
XX
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #36.
XX
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW  antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      29 GCCTGTGTGCCCCTGTGTGT 48
Db      20 GCCTGTGTGCCCCTGTGTGT 1

RESULT 629
AAZ37519/c
ID  AAZ37519 standard; DNA; 20 BP.
XX
XX
AC  AAZ37519;
XX
DT  07-JAN-2000 (first entry)
XX
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #49.
XX
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;

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KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 174 TGGCCCGAGAGTGGAAATGA 193
DB 20 TGGCCCGAGAGTGGAAATGA 1

RESULT 630
AAZ37547/c
ID AAZ37547 standard; DNA; 20 BP.
XX
AC AAZ37547;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #77.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 351 GTAACCACTTCACAGATTCC 370
DB 20 GTAACCACTTCACAGATTCC 1

RESULT 631
AAZ37566/c
ID AAZ37566 standard; DNA; 20 BP.
XX
AC AAZ37566;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #96.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 575 GCCAAGCTTCTCTGTGAAAG 594
DB 20 GCCAAGCTTCTCTGTGAAAG 1

RESULT 632
AAZ37584/c
ID AAZ37584 standard; DNA; 20 BP.
XX
AC AAZ37584;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #114.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 774 AGACCATCTACCTCATCTAG 793
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DB 20 AGACCATCTACCTCATCTAG 1

RESULT 633
AAZ37597/c
ID AAZ37597 standard; DNA; 20 BP.
XX
AC AAZ37597;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #127.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 927 TGTGTGAAAGAGCAGTAG 946
DB 20 TGTGTGAAAGAGCAGTAG 1

RESULT 634
AAZ37608/c
ID AAZ37608 standard; DNA; 20 BP.
XX
AC AAZ37608;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #138.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1046 TAGTGTAGAAATTTGAAGTTG 1065
DB 20 TAGTGTAGAAATTTGAAGTTG 1

RESULT 635
AAZ37632/c
ID AAZ37632 standard; DNA; 20 BP.
XX
AC AAZ37632;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #162.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1292 GAATTGGCTTCTCTGAAGATA 1311
DB 20 GAATTGGCTTCTCTGAAGATA 1

RESULT 636
AAZ37639/c
ID AAZ37639 standard; DNA; 20 BP.
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XX AAZ37639;
AC
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #169.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1368 GCTGAGAGGGCTTTGATGT 1387
Db 20 GCTGAGAGGGCTTTGATGT 1

RESULT 637
AAZ37643/c
ID AAZ37643 standard; DNA; 20 BP.
XX
XX AAZ37643;
AC
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #173.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1434 GTTGAGGAAATGATGATAA 1453
Db 20 GTTGAGGAAATGATGATAA 1

RESULT 638
AAZ37651/c
ID AAZ37651 standard; DNA; 20 BP.
XX
XX AAZ37651;
AC
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #181.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1506 ACTTCTAGTAGCATTATTTA 1525
Db 20 ACTTCTAGTAGCATTATTTA 1

RESULT 639
AAZ37654/c
ID AAZ37654 standard; DNA; 20 BP.
XX
XX AAZ37654;
AC
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #184.
XX

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KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1533 CAAGAAGATGTGAAGAGTT 1552
Db 20 CAAGAAGATGTGAAGAGTT 1

RESULT 640
AAZ37664/c
ID AAZ37664 standard; DNA; 20 BP.
XX
XX AAZ37664;
AC
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #194.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1657 GCATTGTCCATGGCAAAACA 1676
Db 20 GCATTGTCCATGGCAAAACA 1

RESULT 641
AAZ37677/c
ID AAZ37677 standard; DNA; 20 BP.
XX
XX AAZ37677;
AC
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #207.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1798 TATAAGAGAATTATATATTT 1817
Db 20 TATAAGAGAATTATATATTT 1

RESULT 642
AAZ37693/c
ID AAZ37693 standard; DNA; 20 BP.
XX
XX AAZ37693;
AC
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #223.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1913 AGTATAATTGACCTACTTTG 1932
DB 20 AGTATAATTGACCTACTTTG 1

RESULT 643
AAZ37701/c
ID AAZ37701 standard; DNA; 20 BP.
XX
AC
AAZ37701;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #231.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1982 ATCCTTTACACCACTCCTTA 2001
DB 20 ATCCTTTACACCACTCCTTA 1

RESULT 644
AAZ37715/c
ID AAZ37715 standard; DNA; 20 BP.
XX
AC
AAZ37715;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #245.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2140 GGGTGATCTTGGCTCACTGC 2159
DB 20 GGGTGATCTTGGCTCACTGC 1

RESULT 645
AAZ37717/c
ID AAZ37717 standard; DNA; 20 BP.
XX
AC
AAZ37717;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #247.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 TCACTGCAAGCTCTGCCCTC 2172
DB 20 TCACTGCAAGCTCTGCCCTC 1

RESULT 646
AAZ37487/c
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ID AAZ37487 standard; DNA; 20 BP.
XX
AC
AAZ37487;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #17.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1785 TAGTTGACCTGCTATAGA 1804
DB 20 TAGTTGACCTGCTATAGA 1

RESULT 647
AAZ37495/c
ID AAZ37495 standard; DNA; 20 BP.
XX
AC
AAZ37495;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #25.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 GGCCCTGTGTGCGGAAGA 56
DB 20 GGCCCTGTGTGCGGAAGA 1

RESULT 648
AAZ37507/c
ID AAZ37507 standard; DNA; 20 BP.
XX
AC
AAZ37507;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #37.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 TGTGGCCCTGTGTGCGGAA 53
DB 20 TGTGGCCCTGTGTGCGGAA 1

RESULT 649
AAZ37526/c
ID AAZ37526 standard; DNA; 20 BP.
XX
AC
AAZ37526;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #56.
```

```
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 294 ATGGTGAGGACGAGCAAT 313
DB 20 ATGGTGAGGACGAGCAAT 1

RESULT 650
AAZ37536/c
ID AAZ37536 standard; DNA; 20 BP.
XX
AC AAZ37536;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #66.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 AGGCAATGTGCAATACCA 325
DB 20 AGGCAATGTGCAATACCA 1

RESULT 651
AAZ37539/c
ID AAZ37539 standard; DNA; 20 BP.
XX
AC AAZ37539;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #69.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 309 CAAATGTGCAATACCAAT 328
DB 20 CAAATGTGCAATACCAAT 1

RESULT 652
AAZ37540/c
ID AAZ37540 standard; DNA; 20 BP.
XX
AC AAZ37540;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #70.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1.1
QY 310 AAATGTGCAATACCAATG 329
DB 20 AAATGTGCAATACCAATG 1

RESULT 653
AAZ37558/c
ID AAZ37558 standard; DNA; 20 BP.
XX
AC AAZ37558;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #88.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 503 ACGATTATATGATGAGAAGC 522
DB 20 ACGATTATATGATGAGAAGC 1

RESULT 654
AAZ37559/c
ID AAZ37559 standard; DNA; 20 BP.
XX
AC AAZ37559;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #89.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 515 TGAGAAGCAACAATATTG 534
DB 20 TGAGAAGCAACAATATTG 1

RESULT 655
AAZ37569/c
ID AAZ37569 standard; DNA; 20 BP.
XX
AC AAZ37569;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #99.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 600 AGGAAATATATACCATGAT 619
DB 20 AGGAAATATATACCATGAT 1

RESULT 656
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AAZ37614/c
ID AAZ37614 standard; DNA; 20 BP.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
AC AAZ37614;
XX
XX antisease; modulation; oligonucleotide; expression; inhibition;
DT 07-JAN-2000 (first entry)
XX
XX Human mdm2 phosphorothioate oligodeoxynucleotide #144.
DE
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1092 CTTAGTGAAGAGCAAGA 1111
DB 20 CTTAGTGAAGAGCAAGA 1
RESULT 657
AAZ37616/c
ID AAZ37616 standard; DNA; 20 BP.
XX
XX AAZ37616;
AC
XX
XX 07-JAN-2000 (first entry)
DT
XX
XX Human mdm2 phosphorothioate oligodeoxynucleotide #146.
DE
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1105 GACAAGAACTCTCAGATGAA 1124
DB 20 GACAAGAACTCTCAGATGAA 1
RESULT 658
AAZ37617/c
ID AAZ37617 standard; DNA; 20 BP.
XX
XX AAZ37617;
AC
XX
XX 07-JAN-2000 (first entry)
DT
XX
XX Human mdm2 phosphorothioate oligodeoxynucleotide #147.
DE
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1115 CTCAGATGAAGATGATGAGG 1134
DB 20 CTCAGATGAAGATGATGAGG 1
RESULT 659
AAZ37670/c
ID AAZ37670 standard; DNA; 20 BP.
XX
XX AAZ37670;
AC
XX
XX 07-JAN-2000 (first entry)
DT
XX
XX Human mdm2 phosphorothioate oligodeoxynucleotide #200.
DE
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1710 AAGCTAAAGAAAGGAATAA 1729
DB 20 AAGCTAAAGAAAGGAATAA 1
RESULT 660
AAZ37675/c
ID AAZ37675 standard; DNA; 20 BP.
XX
XX AAZ37675;
AC
XX
XX 07-JAN-2000 (first entry)
DT
XX
XX Human mdm2 phosphorothioate oligodeoxynucleotide #205.
DE
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1757 TCAAATGATTGTGCTAACTT 1776
DB 20 TCAAATGATTGTGCTAACTT 1
RESULT 661
AAZ37685/c
ID AAZ37685 standard; DNA; 20 BP.
XX
XX AAZ37685;
AC
XX
XX 07-JAN-2000 (first entry)
DT
XX
XX Human mdm2 phosphorothioate oligodeoxynucleotide #215.
DE
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1855 TTTATTTCATATATCAAAAG 1874
DB 20 TTTATTTCATATATCAAAAG 1
RESULT 662
AAZ37721/c
ID AAZ37721 standard; DNA; 20 BP.
XX
XX AAZ37721;
AC
XX
XX 07-JAN-2000 (first entry)
DT
XX
XX Human mdm2 phosphorothioate oligodeoxynucleotide #251.
DE
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2198 TCAGCCTCCCAATTAGCTTG 2217
Db 20 TCAGCCTCCCAATTAGCTTG 1
RESULT 663
AAZ37729/c
ID AAZ37729 standard; DNA; 20 BP.
XX
AC AAZ37729;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #259.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2274 GGGTTTCACCGTTAGCCA 2293
Db 20 GGGTTTCACCGTTAGCCA 1
RESULT 664
AAZ37483/c
ID AAZ37483 standard; DNA; 20 BP.
XX
AC AAZ37483;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #13.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1047 AGTGAGAAATTGAAGTTGA 1066
Db 20 AGTGAGAAATTGAAGTTGA 1
RESULT 665
AAZ37492/c
ID AAZ37492 standard; DNA; 20 BP.
XX
AC AAZ37492;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #22.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2256 GTACTTTTGTAGAGACAGG 2275
Db 20 GTACTTTTGTAGAGACAGG 1
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RESULT 666
AAZ37509/c
ID AAZ37509 standard; DNA; 20 BP.
XX
AC AAZ37509;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #39.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 50 GGAAGATGGAGCAAGAAGC 69
Db 20 GGAAGATGGAGCAAGAAGC 1
RESULT 667
AAZ37515/c
ID AAZ37515 standard; DNA; 20 BP.
XX
AC AAZ37515;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #45.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 120 GCAGCCAGGAGCACCGTCCC 139
Db 20 GCAGCCAGGAGCACCGTCCC 1
RESULT 668
AAZ37615/c
ID AAZ37615 standard; DNA; 20 BP.
XX
AC AAZ37615;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #145.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1100 AGAAGGACCAAGAACTCTCAG 1119
Db 20 AGAAGGACCAAGAACTCTCAG 1
RESULT 669
AAZ37669/c
ID AAZ37669 standard; DNA; 20 BP.
XX
AC AAZ37669;
XX
DT 07-JAN-2000 (first entry)
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XX Human mdm2 phosphorothioate oligodeoxynucleotide #199.
DE
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1702 GTGCAAGAGCTAAAGAAA 1721
DB 20 GTGCAAGAGCTAAAGAAA 1

RESULT 670
AAZ37672/c
ID AAZ37672 standard; DNA; 20 BP.
XX
AC AAZ37672;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #202.
XX
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1726 ATAAGCCCTGCCAGTATGT 1745
DB 20 ATAAGCCCTGCCAGTATGT 1

RESULT 671
AAZ37702/c
ID AAZ37702 standard; DNA; 20 BP.
XX
AC AAZ37702;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #232.
XX
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1990 CACCAACTCTTAATTTAAA 2009
DB 20 CACCAACTCTTAATTTAAA 1

RESULT 672
AAZ37707/c
ID AAZ37707 standard; DNA; 20 BP.
XX
AC AAZ37707;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #237.
XX
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;

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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2051 TTTTCTTAATATGTATATG 2070
DB 20 TTTTCTTAATATGTATATG 1

RESULT 673
AAZ37510/c
ID AAZ37510 standard; DNA; 20 BP.
XX
AC AAZ37510;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #40.
XX
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 62 CAAGAAGCCGAGCCCGAGGG 81
DB 20 CAAGAAGCCGAGCCCGAGGG 1

RESULT 674
AAZ37511/c
ID AAZ37511 standard; DNA; 20 BP.
XX
AC AAZ37511;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #41.
XX
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 70 CGAGCCCGAGGGCGGCCGC 89
DB 20 CGAGCCCGAGGGCGGCCGC 1

RESULT 675
AAZ37529/c
ID AAZ37529 standard; DNA; 20 BP.
XX
AC AAZ37529;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #59.
XX
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 298 TGAGGAGCAGGCAATGTGC 317
DB 20 TGAGGAGCAGGCAATGTGC 1

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RESULT 676
AAZ37581/c
ID AAZ37581 standard; DNA; 20 BP.
XX
AC AAZ37581;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #111.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
  antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 740 GGAGAGAAACCTTCATCTT 759
DB 20 GGAGAGAAACCTTCATCTT 1

RESULT 677
AAZ37583/c
ID AAZ37583 standard; DNA; 20 BP.
XX
AC AAZ37583;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #113.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
  antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 761 ACATTGGTTCTAGACCAT 780
DB 20 ACATTGGTTCTAGACCAT 1

RESULT 678
AAZ37598/c
ID AAZ37598 standard; DNA; 20 BP.
XX
AC AAZ37598;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #128.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
  antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 936 AGAGCAGTAGCAGTGAATC 955
DB 20 AGAGCAGTAGCAGTGAATC 1

RESULT 679
AAZ37603/c
ID AAZ37603 standard; DNA; 20 BP.
XX
AC AAZ37603;
XX

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DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #133.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
  antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 996 AGTGAACATTCAGTGATTG 1015
DB 20 AGTGAACATTCAGTGATTG 1

RESULT 680
AAZ37604/c
ID AAZ37604 standard; DNA; 20 BP.
XX
AC AAZ37604;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #134.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
  antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1006 CAGGTGATGGTTGGATCAG 1025
DB 20 CAGGTGATGGTTGGATCAG 1

RESULT 681
AAZ37622/c
ID AAZ37622 standard; DNA; 20 BP.
XX
AC AAZ37622;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #152.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
  antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1170 GATACAGATTCATTTGAAGA 1189
DB 20 GATACAGATTCATTTGAAGA 1

RESULT 682
AAZ37623/c
ID AAZ37623 standard; DNA; 20 BP.
XX
AC AAZ37623;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #153.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
  antisense; modulation; oligonucleotide; expression; inhibition;

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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1184 TGAAGAGATCCTGAAATTT 1203
DB 20 TGAAGAAGATCCTGAAATTT 1

RESULT 683
AAZ37647/c
ID AAZ37647 standard; DNA; 20 BP.
XX
AC AAZ37647;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #177.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1466 TTCACATCAACAAGAAAGTG 1485
DB 20 TTCACATCAACAAGAAAGTG 1

RESULT 684
AAZ37650/c
ID AAZ37650 standard; DNA; 20 BP.
XX
AC AAZ37650;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #180.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1499 GCCATCAACTTCTAGTAGCA 1518
DB 20 GCCATCAACTTCTAGTAGCA 1

RESULT 685
AAZ37653/c
ID AAZ37653 standard; DNA; 20 BP.
XX
AC AAZ37653;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #183.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 TTTATAGCAGCCAGAGAT 1541
DB 20 TTTATAGCAGCCAGAGAT 1
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RESULT 686
AAZ37662/c
ID AAZ37662 standard; DNA; 20 BP.
XX
AC AAZ37662;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #192.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1624 GTGTGATTTGTCAAGGTGCA 1643
DB 20 GTGTGATTTGTCAAGGTGCA 1

RESULT 687
AAZ37668/c
ID AAZ37668 standard; DNA; 20 BP.
XX
AC AAZ37668;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #198.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1690 CCTGCTTTACATGTGCAAG 1709
DB 20 CCTGCTTTACATGTGCAAG 1

RESULT 688
AAZ37671/c
ID AAZ37671 standard; DNA; 20 BP.
XX
AC AAZ37671;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #201.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1720 AAAGGAATAAGCCCTGCCCA 1739
DB 20 AAAGGAATAAGCCCTGCCCA 1

RESULT 689
AAZ37694/c
ID AAZ37694 standard; DNA; 20 BP.
XX
AC AAZ37694;
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XX 07-JAN-2000 (first entry)
DT
DE Human mdm2 phosphorothioate oligodeoxynucleotide #224.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
  antisense; modulation; oligonucleotide; expression; inhibition;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1920 TTGACCTACTTTGGTAGTGG 1939
DB 20 TTGACCTACTTTGGTAGTGG 1
RESULT 690
AAZ37695/c
ID AAZ37695 standard; DNA; 20 BP.
XX
AC AAZ37695;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #225.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
  antisense; modulation; oligonucleotide; expression; inhibition;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1933 GTAGTGGAAATGTAATACT 1952
DB 20 GTAGTGGAAATGTAATACT 1
RESULT 691
AAZ37719/c
ID AAZ37719 standard; DNA; 20 BP.
XX
AC AAZ37719;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #249.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
  antisense; modulation; oligonucleotide; expression; inhibition;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2185 CCATTCTCTGCTCAGCCT 2204
DB 20 CCATTCTCTGCTCAGCCT 1
RESULT 692
AAZ37723/c
ID AAZ37723 standard; DNA; 20 BP.
XX
AC AAZ37723;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #253.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
  antisense; modulation; oligonucleotide; expression; inhibition;
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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2210 TTAGCTTGGCCTACAGTCAT 2229
DB 20 TTAGCTTGGCCTACAGTCAT 1
RESULT 693
AAZ37477/c
ID AAZ37477 standard; DNA; 20 BP.
XX
AC AAZ37477;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #7.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
  antisense; modulation; oligonucleotide; expression; inhibition;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 181 GAGAGTGGAAATGATCCCGA 200
DB 20 GAGAGTGGAAATGATCCCGA 1
RESULT 694
AAZ37512/c
ID AAZ37512 standard; DNA; 20 BP.
XX
AC AAZ37512;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #42.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
  antisense; modulation; oligonucleotide; expression; inhibition;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 98 TGACCGAGATCCTGCTGCTT 117
DB 20 TGACCGAGATCCTGCTGCTT 1
RESULT 695
AAZ37516/c
ID AAZ37516 standard; DNA; 20 BP.
XX
AC AAZ37516;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #46.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
  antisense; modulation; oligonucleotide; expression; inhibition;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 150 AGTGCCTACGAGCGCCAGT 169
DB 150 AGTGCCTACGAGCGCCAGT 169
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KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1560 GAAGAAACCCCAAGACAAGA 1579
DB 20 GAAGAAACCCCAAGACAAGA 1

RESULT 703
AAZ37682/c
ID AAZ37682 standard; DNA; 20 BP.
XX
AC AAZ37682;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #212.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1832 CTAGGAATTTAGACAACCTG 1851
DB 20 CTAGGAATTTAGACAACCTG 1

RESULT 704
AAZ37713/c
ID AAZ37713 standard; DNA; 20 BP.
XX
AC AAZ37713;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #243.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2123 CCAGGCTGGAGTCAGTGGG 2142
DB 20 CCAGGCTGGAGTCAGTGGG 1

RESULT 705
AAZ37731/c
ID AAZ37731 standard; DNA; 20 BP.
XX
AC AAZ37731;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #261.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2290 GCCAGGATGGTCTCGATCTC 2309
DB 20 GCCAGGATGGTCTCGATCTC 1

KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 CTCCAAGCGCGAAACCCCG 292
DB 20 CTCCAAGCGCGAAACCCCG 1

RESULT 707
AAZ37517/c
ID AAZ37517 standard; DNA; 20 BP.
XX
AC AAZ37517;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #47.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 CGAGCGCCCGAGTCCCTGGC 177
DB 20 CGAGCGCCCGAGTCCCTGGC 1

RESULT 708
AAZ37530/c
ID AAZ37530 standard; DNA; 20 BP.
XX
AC AAZ37530;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #60.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 299 GAGGAGCAGGCAAAATGTGCA 318
DB 20 GAGGAGCAGGCAAAATGTGCA 1

RESULT 709
AAZ37534/c
ID AAZ37534 standard; DNA; 20 BP.
```

XX AAZ37534;
 XX
 DT 07-JAN-2000 (first entry)
 DE Human mdm2 phosphorothioate oligodeoxynucleotide #64.
 XX
 KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
 KW antisense; modulation; oligonucleotide; expression; inhibition;
 Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 304 GCAGGCAAAATGTGCATACC 323
 Db 20 GCAGGCAAAATGTGCATACC 1
 RESULT 710
 AAZ37546/c
 ID AAZ37546 standard; DNA; 20 BP.
 XX
 AC AAZ37546;
 XX
 DT 07-JAN-2000 (first entry)
 DE Human mdm2 phosphorothioate oligodeoxynucleotide #76.
 XX
 KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
 KW antisense; modulation; oligonucleotide; expression; inhibition;
 Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 334 TACCTACTGATGTGCTGTA 353
 Db 20 TACCTACTGATGTGCTGTA 1
 RESULT 711
 AAZ37552/c
 ID AAZ37552 standard; DNA; 20 BP.
 XX
 AC AAZ37552;
 XX
 DT 07-JAN-2000 (first entry)
 DE Human mdm2 phosphorothioate oligodeoxynucleotide #82.
 XX
 KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
 KW antisense; modulation; oligonucleotide; expression; inhibition;
 Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 403 AGCCATTGCTTTTGAAGTTA 422
 Db 20 AGCCATTGCTTTTGAAGTTA 1
 RESULT 712
 AAZ37556/c
 ID AAZ37556 standard; DNA; 20 BP.
 XX
 AC AAZ37556;
 XX
 DT 07-JAN-2000 (first entry)
 DE Human mdm2 phosphorothioate oligodeoxynucleotide #86.
 XX

KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
 KW antisense; modulation; oligonucleotide; expression; inhibition;
 Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 490 ATATTATGACTAAACGATTGA 509
 Db 20 ATATTATGACTAAACGATTGA 1
 RESULT 713
 AAZ37573/c
 ID AAZ37573 standard; DNA; 20 BP.
 XX
 AC AAZ37573;
 XX
 DT 07-JAN-2000 (first entry)
 DE Human mdm2 phosphorothioate oligodeoxynucleotide #103.
 XX
 KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
 KW antisense; modulation; oligonucleotide; expression; inhibition;
 Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 646 AGCAGGAATCATCGGACTCA 665
 Db 20 AGCAGGAATCATCGGACTCA 1
 RESULT 714
 AAZ37620/c
 ID AAZ37620 standard; DNA; 20 BP.
 XX
 AC AAZ37620;
 XX
 DT 07-JAN-2000 (first entry)
 DE Human mdm2 phosphorothioate oligodeoxynucleotide #150.
 XX
 KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
 KW antisense; modulation; oligonucleotide; expression; inhibition;
 Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1149 GTGTATCAGCGGGGAGAG 1168
 Db 20 GTGTATCAGCGGGGAGAG 1
 RESULT 715
 AAZ37649/c
 ID AAZ37649 standard; DNA; 20 BP.
 XX
 AC AAZ37649;
 XX
 DT 07-JAN-2000 (first entry)
 DE Human mdm2 phosphorothioate oligodeoxynucleotide #179.
 XX
 KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
 KW antisense; modulation; oligonucleotide; expression; inhibition;
 Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1489 ACTATTCTCAGCCATCAACT 1508
Db 20 ACTATTCTCAGCCATCAACT 1

RESULT 716
AAZ37663/c
ID AAZ37663 standard; DNA; 20 BP.
XX
AC AAZ37663;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #193.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1648 AAAATGGTTGCATTGTCCAT 1667
Db 20 AAAATGGTTGCATTGTCCAT 1

RESULT 717
AAZ37703/c
ID AAZ37703 standard; DNA; 20 BP.
XX
AC AAZ37703;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #233.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1997 TCCTAAATTTAAATAATTTC 2016
Db 20 TCCTAAATTTAAATAATTTC 1

RESULT 718
AAZ37722/c
ID AAZ37722 standard; DNA; 20 BP.
XX
AC AAZ37722;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #252.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2202 CCTCCCAATTAGCTTGGCCT 2221
Db 20 CCTCCCAATTAGCTTGGCCT 1

RESULT 719
AAZ37738/c

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ID AAZ37738 standard; DNA; 20 BP.
XX
AC AAZ37738;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #268.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2351 GGATTACAGGCATGAGCCAC 2370
Db 20 GGATTACAGGCATGAGCCAC 1

RESULT 720
AAZ37481/c
ID AAZ37481 standard; DNA; 20 BP.
XX
AC AAZ37481;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #11.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 331 CTGTACTACTGATGGTGCT 350
Db 20 CTGTACTACTGATGGTGCT 1

RESULT 721
AAZ37484/c
ID AAZ37484 standard; DNA; 20 BP.
XX
AC AAZ37484;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #14.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1381 TTGATGTTCTCTGATTGTAAA 1400
Db 20 TTGATGTTCTCTGATTGTAAA 1

RESULT 722
AAZ37488/c
ID AAZ37488 standard; DNA; 20 BP.
XX
AC AAZ37488;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #18.

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XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1818 CTAACCTATATACCCCTAGGA 1837
DB 20 CTAACCTATATACCCCTAGGA 1
RESULT 723
AAZ37538/c
ID AAZ37538 standard; DNA; 20 BP.
XX AAZ37538;
AC AAZ37538;
XX 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #68.
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 308 GCAAAATGTGCAATACCAACA 327
DB 20 GCAAAATGTGCAATACCAACA 1
RESULT 724
AAZ37550/c
ID AAZ37550 standard; DNA; 20 BP.
XX AAZ37550;
AC AAZ37550;
XX 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #80.
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 386 GACCCCTGGTTAGACCAAGC 405
DB 20 GACCCCTGGTTAGACCAAGC 1
RESULT 725
AAZ37553/c
ID AAZ37553 standard; DNA; 20 BP.
XX AAZ37553;
AC AAZ37553;
XX 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #83.
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 422 ATTAAAGTCTGTTGGTGCAC 441
DB 20 ATTAAAGTCTGTTGGTGCAC 1
RESULT 726
AAZ37579/c
ID AAZ37579 standard; DNA; 20 BP.
XX AAZ37579;
AC AAZ37579;
XX 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #109.
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 718 AGGACCTTGTTACAAAGAGCTT 737
DB 20 AGGACCTTGTTACAAAGAGCTT 1
RESULT 727
AAZ37582/c
ID AAZ37582 standard; DNA; 20 BP.
XX AAZ37582;
AC AAZ37582;
XX 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #112.
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 752 TTCATCTTCACATTTGGTTT 771
DB 20 TTCATCTTCACATTTGGTTT 1
RESULT 728
AAZ37606/c
ID AAZ37606 standard; DNA; 20 BP.
XX AAZ37606;
AC AAZ37606;
XX 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #136.
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1023 CAGGATTTCAGTTTCAGATCA 1042
DB 20 CAGGATTTCAGTTTCAGATCA 1
RESULT 729

AAZ37609/c
ID AAZ37609 standard; DNA; 20 BP.
XX
AC AAZ37609;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #139.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1051 TAGAATTTGAAGTTGAATCT 1070
DB 20 TAGAATTTGAAGTTGAATCT 1
RESULT 730
AAZ37612/c
ID AAZ37612 standard; DNA; 20 BP.
XX
AC AAZ37612;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #142.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1077 TCAGAAGATTATAGCCTTAG 1096
DB 20 TCAGAAGATTATAGCCTTAG 1
RESULT 731
AAZ37635/c
ID AAZ37635 standard; DNA; 20 BP.
XX
AC AAZ37635;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #165.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1325 AGGGGAATCTCTGAGAAAG 1344
DB 20 AGGGGAATCTCTGAGAAAG 1
RESULT 732
AAZ37640/c
ID AAZ37640 standard; DNA; 20 BP.
XX
AC AAZ37640;
XX
DT 07-JAN-2000 (first entry)
XX

DE Human mdm2 phosphorothioate oligodeoxynucleotide #170.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1401 AAAACTATAGTGAATGATTC 1420
DB 20 AAACTATAGTGAATGATTC 1
RESULT 733
AAZ37642/c
ID AAZ37642 standard; DNA; 20 BP.
XX
AC AAZ37642;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #172.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1421 CAGAGAGTCATGTGTTGAGG 1440
DB 20 CAGAGAGTCATGTGTTGAGG 1
RESULT 734
AAZ37645/c
ID AAZ37645 standard; DNA; 20 BP.
XX
AC AAZ37645;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #175.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1449 GATAAAATTACACAGCTTC 1468
DB 20 GATAAAATTACACAGCTTC 1
RESULT 735
AAZ37674/c
ID AAZ37674 standard; DNA; 20 BP.
XX
AC AAZ37674;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #204.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1745 TAGACCAACCAATTCAAATGA 1764
ID AAZ37716 standard; DNA; 20 BP.
XX ||||||||||||||||||
AC AAZ37716;
DT 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #211.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1823 TATATAACCCCTAGGAATTGA 1842
ID AAZ37727 standard; DNA; 20 BP.
XX ||||||||||||||||||
AC AAZ37727;
DT 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #229.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1969 GAATATGTAGCTCATCTTT 1988
ID AAZ37709 standard; DNA; 20 BP.
XX ||||||||||||||||||
AC AAZ37709;
DT 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #239.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2072 CATTTAAATGTAACCTTATTA 2091
ID AAZ37485 standard; DNA; 20 BP.
XX ||||||||||||||||||
AC AAZ37485;
DT 07-JAN-2000 (first entry)
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RESULT 739
AAZ37716/c
ID AAZ37716 standard; DNA; 20 BP.
XX ||||||||||||||||||
AC AAZ37716;
DT 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #246.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2146 TCTTGGCTCACTGCAAGCTC 2165
ID AAZ37727 standard; DNA; 20 BP.
XX ||||||||||||||||||
AC AAZ37727;
DT 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #257.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2253 TTTGTACTTTTAGTAGAGAC 2272
ID AAZ37476 standard; DNA; 20 BP.
XX ||||||||||||||||||
AC AAZ37476;
DT 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #6.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 147 ATTAGTGCCTACGAGCGCCC 166
ID AAZ37485/c
XX ||||||||||||||||||
AC AAZ37485;
DT 07-JAN-2000 (first entry)
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```
XX Human mdm2 phosphorothioate oligodeoxynucleotide #15.
DE
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1695 TTTACATGTGCAAGAAGCT 1714
Db 20 TTTACATGTGCAAGAAGCT 1

RESULT 743
AAZ37489/c
ID AAZ37489 standard; DNA; 20 BP.
XX
AC AAZ37489;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #19.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1934 TAGTGGATAGTGAATACCT 1953
Db 20 TAGTGGATAGTGAATACCT 1

RESULT 744
AAZ37491/c
ID AAZ37491 standard; DNA; 20 BP.
XX
AC AAZ37491;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #21.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2224 AGTCATCTGCCACACACCT 2243
Db 20 AGTCATCTGCCACACACCT 1

RESULT 745
AAZ37508/c
ID AAZ37508 standard; DNA; 20 BP.
XX
AC AAZ37508;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #38.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
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```
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 GTGTGTCGGAAGATGGAGC 62
Db 20 GTGTGTCGGAAGATGGAGC 1

RESULT 746
AAZ37522/c
ID AAZ37522 standard; DNA; 20 BP.
XX
AC AAZ37522;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #52.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 CTTCCGCACTAGTCAGTCCC 236
Db 20 CTTCCGCACTAGTCAGTCCC 1

RESULT 747
AAZ37533/c
ID AAZ37533 standard; DNA; 20 BP.
XX
AC AAZ37533;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #63.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 GAGCAGGCAAAATGTGCAATA 321
Db 20 GAGCAGGCAAAATGTGCAATA 1

RESULT 748
AAZ37571/c
ID AAZ37571 standard; DNA; 20 BP.
XX
AC AAZ37571;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #101.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 TCTACAGGAACCTGGTAGTA 638
Db 20 TCTACAGGAACCTGGTAGTA 1
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RESULT 749
AAZ37572/c
ID AAZ37572 standard; DNA; 20 BP.
XX
XX
AC AAZ37572;
XX
DT 07-JAN-2000. (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #102.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 634 TAGTAGTCAATCAGCAGGAA 653
Db 20 TAGTAGTCAATCAGCAGGAA 1

RESULT 750
AAZ37574/c
ID AAZ37574 standard; DNA; 20 BP.
XX
XX
AC AAZ37574;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #104.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 656 ATCGGACTCAGTACATCTG 675
Db 20 ATCGGACTCAGTACATCTG 1

RESULT 751
AAZ37607/c
ID AAZ37607 standard; DNA; 20 BP.
XX
XX
AC AAZ37607;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #137.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1034 TTCAGATCAGTTAGTGTAG 1053
Db 20 TTCAGATCAGTTAGTGTAG 1

RESULT 752
AAZ37611/c
ID AAZ37611 standard; DNA; 20 BP.
XX
XX
AC AAZ37611;
XX
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DT 07-JAN-2000 (first entry)
XX
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #141.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1068 TCTCTCGACTCAGACAGATTA 1087
Db 20 TCTCTCGACTCAGACAGATTA 1

RESULT 753
AAZ37619/c
ID AAZ37619 standard; DNA; 20 BP.
XX
XX
AC AAZ37619;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #149.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1135 TATATCAAGTTACTGTGTAT 1154
Db 20 TATATCAAGTTACTGTGTAT 1

RESULT 754
AAZ37630/c
ID AAZ37630 standard; DNA; 20 BP.
XX
XX
AC AAZ37630;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #160.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1275 TGTGGGCCCTTCGTGAGAA 1294
Db 20 TGTGGGCCCTTCGTGAGAA 1

RESULT 755
AAZ37633/c
ID AAZ37633 standard; DNA; 20 BP.
XX
XX
AC AAZ37633;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #163.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1301 TCCTGAAGATAAAGGGAAG 1320
DB 20 TCCTGAAGATAAAGGGAAG 1

RESULT 756
AAZ37656/c
ID AAZ37656 standard; DNA; 20 BP.
XX
AC AAZ37656;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #186.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1550 GTTTGAAGGGAAGAACCC 1569
DB 20 GTTTGAAGGGAAGAACCC 1

RESULT 757
AAZ37658/c
ID AAZ37658 standard; DNA; 20 BP.
XX
AC AAZ37658;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #188.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1566 ACCCAAGACAAGAGAGAG 1585
DB 20 ACCCAAGACAAGAGAGAG 1

RESULT 758
AAZ37660/c
ID AAZ37660 standard; DNA; 20 BP.
XX
AC AAZ37660;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #190.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1605 CTTAATGCCATTGAACCTTG 1624
DB 20 CTTAATGCCATTGAACCTTG 1
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RESULT 759
AAZ37678/c
ID AAZ37678 standard; DNA; 20 BP.
XX
AC AAZ37678;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #208.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1804 AGAATTATATATTTCTAACT 1823
DB 20 AGAATTATATATTTCTAACT 1

RESULT 760
AAZ37720/c
ID AAZ37720 standard; DNA; 20 BP.
XX
AC AAZ37720;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #250.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2191 TCCTGCTCAGCCTCCCAAT 2210
DB 20 TCCTGCTCAGCCTCCCAAT 1

RESULT 761
AAZ37479/c
ID AAZ37479 standard; DNA; 20 BP.
XX
AC AAZ37479;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #9.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 295 TGGTGAGGAGCAGGCAATG 314
DB 20 TGGTGAGGAGCAGGCAATG 1

RESULT 762
AAZ37482/c
ID AAZ37482 standard; DNA; 20 BP.
XX
AC AAZ37482;
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XX 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #12.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX antisense; modulation; oligonucleotide; expression; inhibition;
KW
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 617 GATCTACAGGAAGCTGTAG 636
DB 20 GATCTACAGGAAGCTGTAG 1

RESULT 763
AAZ37505/c
ID AAZ37505 standard; DNA; 20 BP.
XX
AC AAZ37505;
XX
DT 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #35.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX antisense; modulation; oligonucleotide; expression; inhibition;
KW
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 GCTTCTGGGGCCTGTGGC 39
DB 20 GCTTCTGGGGCCTGTGGC 1

RESULT 764
AAZ37527/c
ID AAZ37527 standard; DNA; 20 BP.
XX
AC AAZ37527;
XX
DT 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #57.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX antisense; modulation; oligonucleotide; expression; inhibition;
KW
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 296 GGTGAGGAGCAGGCAATGT 315
DB 20 GGTGAGGAGCAGGCAATGT 1

RESULT 765
AAZ37528/c
ID AAZ37528 standard; DNA; 20 BP.
XX
AC AAZ37528;
XX
DT 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #58.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX antisense; modulation; oligonucleotide; expression; inhibition;
KW
KW

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Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 297 GTGAGGAGCAGGCAATGTG 316
DB 20 GTGAGGAGCAGGCAATGTG 1

RESULT 766
AAZ37537/c
ID AAZ37537 standard; DNA; 20 BP.
XX
AC AAZ37537;
XX
DT 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #67.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX antisense; modulation; oligonucleotide; expression; inhibition;
KW
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 307 GGCARATGTGCATACCAAC 326
DB 20 GGCARATGTGCATACCAAC 1

RESULT 767
AAZ37551/c
ID AAZ37551 standard; DNA; 20 BP.
XX
AC AAZ37551;
XX
DT 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #81.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX antisense; modulation; oligonucleotide; expression; inhibition;
KW
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 392 GGTAGACCAAGCCATTGC 411
DB 20 GGTAGACCAAGCCATTGC 1

RESULT 768
AAZ37596/c
ID AAZ37596 standard; DNA; 20 BP.
XX
AC AAZ37596;
XX
DT 07-JAN-2000 (first entry)
XX Human mdm2 phosphorothioate oligodeoxynucleotide #126.
DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX antisense; modulation; oligonucleotide; expression; inhibition;
KW
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 915 ATAAGGAGATATGTTGTA 934
DB 20 ATAAGGAGATATGTTGTA 1

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Db      20 ATAGGAGATATGTTGTGA 1

RESULT 769
AAZ37599/c
ID  AAZ37599 standard; DNA; 20 BP.
XX
XX
AC  AAZ37599;
XX
DT  07-JAN-2000 (first entry)
XX
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #129.
XX
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      949 GTGAATCTACAGGACGCCA 968
Db      20 GTGAATCTACAGGACGCCA 1

RESULT 770
AAZ37624/c
ID  AAZ37624 standard; DNA; 20 BP.
XX
XX
AC  AAZ37624;
XX
DT  07-JAN-2000 (first entry)
XX
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #154.
XX
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1196 TGAAATTTTCCTTAGCTGACT 1215
Db      20 TGAAATTTTCCTTAGCTGACT 1

RESULT 771
AAZ37636/c
ID  AAZ37636 standard; DNA; 20 BP.
XX
XX
AC  AAZ37636;
XX
DT  07-JAN-2000 (first entry)
XX
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #166.
XX
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1333 TCTCTGAGAAAGCCAAACTG 1352
Db      20 TCTCTGAGAAAGCCAAACTG 1

RESULT 772
AAZ37661/c
ID  AAZ37661 standard; DNA; 20 BP.
XX
XX
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AC  AAZ37661;
XX
DT  07-JAN-2000 (first entry)
XX
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #191.
XX
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1617 GAACCTTGCTGATTTGTCA 1636
Db      20 GAACCTTGCTGATTTGTCA 1

RESULT 773
AAZ37680/c
ID  AAZ37680 standard; DNA; 20 BP.
XX
XX
AC  AAZ37680;
XX
DT  07-JAN-2000 (first entry)
XX
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #210.
XX
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1816 TTCTAACTATATAACCCCTAG 1835
Db      20 TTCTAACTATATAACCCCTAG 1

RESULT 774
AAZ37696/c
ID  AAZ37696 standard; DNA; 20 BP.
XX
XX
AC  AAZ37696;
XX
DT  07-JAN-2000 (first entry)
XX
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #226.
XX
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1940 AATAGTGAATACTTACTATA 1959
Db      20 AATAGTGAATACTTACTATA 1

RESULT 775
AAZ37710/c
ID  AAZ37710 standard; DNA; 20 BP.
XX
XX
AC  AAZ37710;
XX
DT  07-JAN-2000 (first entry)
XX
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #240.
XX
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
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KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2103 ACCGAGTCTTGCTGTTAC 2122
| | | | | | | | | | | | | | | | | |
DB 20 ACCGAGTCTTGCTGTTAC 1

RESULT 776
AAZ37714/c
ID AAZ37714 standard; DNA; 20 BP.
XX
AC AAZ37714;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #244.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2133 GTGCAGTGGTGATCTTGGC 2152
| | | | | | | | | | | | | | | | | |
DB 20 GTGCAGTGGTGATCTTGGC 1

RESULT 777
AAZ37726/c
ID AAZ37726 standard; DNA; 20 BP.
XX
AC AAZ37726;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #256.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2232 GCCACACACCTGGCTAATT 2251
| | | | | | | | | | | | | | | | | |
DB 20 GCCACACACCTGGCTAATT 1

RESULT 778
AAZ37475/c
ID AAZ37475 standard; DNA; 20 BP.
XX
AC AAZ37475;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #5.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 CTCTGACCGAGATCCTGCTG 114
| | | | | | | | | | | | | | | | | |
DB 20 CTCTGACCGAGATCCTGCTG 1

RESULT 779
AAZ37480/c
ID AAZ37480 standard; DNA; 20 BP.
XX
AC AAZ37480;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #10.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 AGCAGCGCAATGTGCAATAC 322
| | | | | | | | | | | | | | | | | |
DB 20 AGCAGCGCAATGTGCAATAC 1

RESULT 780
AAZ37524/c
ID AAZ37524 standard; DNA; 20 BP.
XX
AC AAZ37524;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #54.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 289 CCGGATGTGTGAGGAGCAGG 308
| | | | | | | | | | | | | | | | | |
DB 20 CCGGATGTGTGAGGAGCAGG 1

RESULT 781
AAZ37542/c
ID AAZ37542 standard; DNA; 20 BP.
XX
AC AAZ37542;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #72.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 ATGTGCAATACCAACATGTC 331
| | | | | | | | | | | | | | | | | |
DB 20 ATGTGCAATACCAACATGTC 1

RESULT 782
AAZ37545/c
ID AAZ37545 standard; DNA; 20 BP.
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XX AAZ37545;
AC
XX
DT 07-JAN-2000 (first entry)
DE
XX Human mdm2 phosphorothioate oligodeoxynucleotide #75.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 CAACATGCTGTACTACTG 342
Db 20 CAACATGCTGTACTACTG 1

RESULT 783
AAZ37565/c
ID AAZ37565 standard; DNA; 20 BP.
XX
XX AAZ37565;
AC
XX
DT 07-JAN-2000 (first entry)
DE
XX Human mdm2 phosphorothioate oligodeoxynucleotide #95.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 566 GTTGGCGTGCCAGCTTCT 585
Db 20 GTTGGCGTGCCAGCTTCT 1

RESULT 784
AAZ37577/c
ID AAZ37577 standard; DNA; 20 BP.
XX
XX AAZ37577;
AC
XX
DT 07-JAN-2000 (first entry)
DE
XX Human mdm2 phosphorothioate oligodeoxynucleotide #107.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 691 GTCACCTTGAAGTGGGAGT 710
Db 20 GTCACCTTGAAGTGGGAGT 1

RESULT 785
AAZ37587/c
ID AAZ37587 standard; DNA; 20 BP.
XX
XX AAZ37587;
AC
XX
DT 07-JAN-2000 (first entry)
DE
XX Human mdm2 phosphorothioate oligodeoxynucleotide #117.
XX
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```
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 810 GAGACAGAGAAAATTCAGA 829
Db 20 GAGACAGAGAAAATTCAGA 1

RESULT 786
AAZ37621/c
ID AAZ37621 standard; DNA; 20 BP.
XX
XX AAZ37621;
AC
XX
DT 07-JAN-2000 (first entry)
DE
XX Human mdm2 phosphorothioate oligodeoxynucleotide #151.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1161 GGGGAGAGTGATACAGATTC 1180
Db 20 GGGGAGAGTGATACAGATTC 1

RESULT 787
AAZ37627/c
ID AAZ37627 standard; DNA; 20 BP.
XX
XX AAZ37627;
AC
XX
DT 07-JAN-2000 (first entry)
DE
XX Human mdm2 phosphorothioate oligodeoxynucleotide #157.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1226 CACTTCATGCAATGAAATGA 1245
Db 20 CACTTCATGCAATGAAATGA 1

RESULT 788
AAZ37676/c
ID AAZ37676 standard; DNA; 20 BP.
XX
XX AAZ37676;
AC
XX
DT 07-JAN-2000 (first entry)
DE
XX Human mdm2 phosphorothioate oligodeoxynucleotide #206.
XX
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1787 GTTGACCTGTCTATAAGAGA 1806
 Db |||||
 20 GTTGACCTGTCTATAAGAGA 1

RESULT 789

AAZ37679/c

ID AAZ37679 standard; DNA; 20 BP.

XX

AC AAZ37679;

XX

DT 07-JAN-2000 (first entry)

XX

XX Human mdm2 phosphorothioate oligodeoxynucleotide #209.

DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
 KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1808 TTATATATTTCTTAACATAT 1827

Db |||||
 20 TTATATATTTCTTAACATAT 1

RESULT 790

AAZ37706/c

ID AAZ37706 standard; DNA; 20 BP.

XX

AC AAZ37706;

XX

DT 07-JAN-2000 (first entry)

XX

XX Human mdm2 phosphorothioate oligodeoxynucleotide #236.

DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
 KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2020 TCTGTCTTAAATGAGAAGTA 2039

Db |||||
 20 TCTGTCTTAAATGAGAAGTA 1

RESULT 791

AAZ37734/c

ID AAZ37734 standard; DNA; 20 BP.

XX

AC AAZ37734;

XX

DT 07-JAN-2000 (first entry)

XX

XX Human mdm2 phosphorothioate oligodeoxynucleotide #264.

DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
 KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2319 TGATCCGCCACCTCGGCCT 2338

Db |||||
 20 TGATCCGCCACCTCGGCCT 1

RESULT 792

AAZ37523/c

ID AAZ37523 standard; DNA; 20 BP.

XX

AC AAZ37523;

XX

DT 07-JAN-2000 (first entry)

XX

XX Human mdm2 phosphorothioate oligodeoxynucleotide #53.

DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
 KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 AGGAAACTGGGAGTCTTGA 261

Db |||||
 20 AGGAAACTGGGAGTCTTGA 1

RESULT 793

AAZ37525/c

ID AAZ37525 standard; DNA; 20 BP.

XX

AC AAZ37525;

XX

DT 07-JAN-2000 (first entry)

XX

XX Human mdm2 phosphorothioate oligodeoxynucleotide #55.

DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
 KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 GATGGTGAGGAGCAGGCAAA 312

Db |||||
 20 GATGGTGAGGAGCAGGCAAA 1

RESULT 794

AAZ37549/c

ID AAZ37549 standard; DNA; 20 BP.

XX

AC AAZ37549;

XX

DT 07-JAN-2000 (first entry)

XX

XX Human mdm2 phosphorothioate oligodeoxynucleotide #79.

DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
 KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 GCTTCGGAACAGAGACCCT 391

Db |||||
 20 GCTTCGGAACAGAGACCCT 1

RESULT 795

AAZ37568/c

ID AAZ37568 standard; DNA; 20 BP.

XX

AC AAZ37568;

XX

DT 07-JAN-2000 (first entry)

XX

XX Human mdm2 phosphorothioate oligodeoxynucleotide #98.

```
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 593 AGAGCACAGGAAATATATATA 612
DB 20 AGAGCACAGGAAATATATATA 1

RESULT 796
AAZ37585/c
ID AAZ37585 standard; DNA; 20 BP.
XX AC AAZ37585;
XX DT 07-JAN-2000 (first entry)
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #115.
XX DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 787 CATCTAGAGGAGCAATT 806
DB 20 CATCTAGAGGAGCAATT 1

RESULT 797
AAZ37588/c
ID AAZ37588 standard; DNA; 20 BP.
XX AC AAZ37588;
XX DT 07-JAN-2000 (first entry)
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #118.
XX DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 824 TTCAGATGAATTATCTGCTG 843
DB 20 TTCAGATGAATTATCTGCTG 1

RESULT 798
AAZ37589/c
ID AAZ37589 standard; DNA; 20 BP.
XX AC AAZ37589;
XX DT 07-JAN-2000 (first entry)
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #119.
XX DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 833 ATTATCTGGTGAACGACAAA 852
DB 20 ATTATCTGGTGAACGACAAA 1

RESULT 799
AAZ37602/c
ID AAZ37602 standard; DNA; 20 BP.
XX AC AAZ37602;
XX DT 07-JAN-2000 (first entry)
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #132.
XX DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 983 TGATGCTGGTGAAGTGAAC 1002
DB 20 TGATGCTGGTGAAGTGAAC 1

RESULT 800
AAZ37637/c
ID AAZ37637 standard; DNA; 20 BP.
XX AC AAZ37637;
XX DT 07-JAN-2000 (first entry)
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #167.
XX DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1346 CAAACTGGAAACTCAACAC 1365
DB 20 CAAACTGGAAACTCAACAC 1

RESULT 801
AAZ37638/c
ID AAZ37638 standard; DNA; 20 BP.
XX AC AAZ37638;
XX DT 07-JAN-2000 (first entry)
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #168.
XX DE Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1358 CTCACACACAGCTGAAGAGG 1377
DB 20 CTCACACACAGCTGAAGAGG 1

RESULT 802
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AAZ37659/c
ID  AAZ37659 standard; DNA; 20 BP.
XX
AC  AAZ37659;
XX
DT  07-JAN-2000 (first entry)
XX
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #189.
XX
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
    Query Match      0.8%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.8e+03;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1580 AGAGAGTGTGGATCTAGTT 1599
    |||||
    20 AGAGAGTGTGGATCTAGTT 1

Db

RESULT 803
AAZ37665/c
ID  AAZ37665 standard; DNA; 20 BP.
XX
AC  AAZ37665;
XX
DT  07-JAN-2000 (first entry)
XX
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #195.
XX
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
    Query Match      0.8%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.8e+03;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1667 TGGCAAAACAGGACATCTTA 1686
    |||||
    20 TGGCAAAACAGGACATCTTA 1

Db

RESULT 804
AAZ37673/c
ID  AAZ37673 standard; DNA; 20 BP.
XX
AC  AAZ37673;
XX
DT  07-JAN-2000 (first entry)
XX
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #203.
XX
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
    Query Match      0.8%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.8e+03;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1736 CCCAGTATGTAGACAACAA 1755
    |||||
    20 CCCAGTATGTAGACAACAA 1

Db

RESULT 805
AAZ37690/c
ID  AAZ37690 standard; DNA; 20 BP.
XX
AC  AAZ37690;
XX
DT  07-JAN-2000 (first entry)
XX
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #220.
XX
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
    Query Match      0.8%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.8e+03;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1898 AGATTTCTCTCTTTAGTAT 1917
    |||||
    20 AGATTTCTCTCTTTAGTAT 1

Db

RESULT 806
AAZ37705/c
ID  AAZ37705 standard; DNA; 20 BP.
XX
AC  AAZ37705;
XX
DT  07-JAN-2000 (first entry)
XX
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #235.
XX
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
    Query Match      0.8%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.8e+03;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2015 TCTACTCTGTCTTAAATGAG 2034
    |||||
    20 TCTACTCTGTCTTAAATGAG 1

Db

RESULT 807
AAZ37733/c
ID  AAZ37733 standard; DNA; 20 BP.
XX
AC  AAZ37733;
XX
DT  07-JAN-2000 (first entry)
XX
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #263.
XX
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
    Query Match      0.8%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.8e+03;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2307 CTCCTGACCTCGTGATCCGC 2326
    |||||
    20 CTCCTGACCTCGTGATCCGC 1

Db

RESULT 808
AAZ37560/c
ID  AAZ37560 standard; DNA; 20 BP.
XX
AC  AAZ37560;
XX
DT  07-JAN-2000 (first entry)
XX
DE  Human mdm2 phosphorothioate oligodeoxynucleotide #90.
XX
KW  Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
    antisense; modulation; oligonucleotide; expression; inhibition;
    Query Match      0.8%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.8e+03;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 525 CAACATATTGTATATTGTTTC 544
DB 20 CAACATATTGTATATTGTTTC 1

RESULT 809
AAZ37593/c
ID AAZ37593 standard; DNA; 20 BP.
XX
XX
AC AAZ37593;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #123.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 880 CCTTTCTCTTGTGATGAAGC 899
DB 20 CCTTTCTCTTGTGATGAAGC 1

RESULT 810
AAZ37601/c
ID AAZ37601 standard; DNA; 20 BP.
XX
XX
AC AAZ37601;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #131.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 971 GAATCCGGATCTTGATGCTG 990
DB 20 GAATCCGGATCTTGATGCTG 1

RESULT 811
AAZ37666/c
ID AAZ37666 standard; DNA; 20 BP.
XX
XX
AC AAZ37666;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #196.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1675 CAGGACATCTTATGGCCTGC 1694
DB 20 CAGGACATCTTATGGCCTGC 1
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RESULT 812
AAZ37667/c
ID AAZ37667 standard; DNA; 20 BP.
XX
XX
AC AAZ37667;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #197.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1684 TTATGGCCTGCTTTACATGT 1703
DB 20 TTATGGCCTGCTTTACATGT 1

RESULT 813
AAZ37683/c
ID AAZ37683 standard; DNA; 20 BP.
XX
XX
AC AAZ37683;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #213.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1840 TTAGACAACCTGAAATTTAT 1859
DB 20 TTAGACAACCTGAAATTTAT 1

RESULT 814
AAZ37691/c
ID AAZ37691 standard; DNA; 20 BP.
XX
XX
AC AAZ37691;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #221.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1905 TTCTCTTTAGTATAATTGAC 1924
DB 20 TTCTCTTTAGTATAATTGAC 1

RESULT 815
AAZ37724/c
ID AAZ37724 standard; DNA; 20 BP.
XX
XX
AC AAZ37724;
XX
DT 07-JAN-2000 (first entry)
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XX Human mdm2 phosphorothioate oligodeoxynucleotide #254.
DE
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2213 GCTTGGCCTACAGTCATCTG 2232
DB 20 GCTTGGCCTACAGTCATCTG 1

RESULT 816
AAZ37736/c
ID AAZ37736 standard; DNA; 20 BP.
XX
AC AAZ37736;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #266.
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2334 GGCCTCCCAAGTGTGGGA 2353
DB 20 GGCCTCCCAAGTGTGGGA 1

RESULT 817
AAZ37490/c
ID AAZ37490 standard; DNA; 20 BP.
XX
AC AAZ37490;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #20.
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2132 AGTGCAAGTGGTGATCTTG 2151
DB 20 AGTGCAAGTGGTGATCTTG 1

RESULT 818
AAZ37541/c
ID AAZ37541 standard; DNA; 20 BP.
XX
AC AAZ37541;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #71.
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;

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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 311 AATGTGCAATACCAACATGT 330
DB 20 AATGTGCAATACCAACATGT 1

RESULT 819
AAZ37544/c
ID AAZ37544 standard; DNA; 20 BP.
XX
AC AAZ37544;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #74.
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 314 GTGCAATACCAACATGTCTG 333
DB 20 GTGCAATACCAACATGTCTG 1

RESULT 820
AAZ37548/c
ID AAZ37548 standard; DNA; 20 BP.
XX
AC AAZ37548;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #78.
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 361 CACAGATTCAGCTTCGGAA 380
DB 20 CACAGATTCAGCTTCGGAA 1

RESULT 821
AAZ37576/c
ID AAZ37576 standard; DNA; 20 BP.
XX
AC AAZ37576;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #106.
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 682 AGAACAGGTGTCACTTGAA 701
DB 20 AGAACAGGTGTCACTTGAA 1

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RESULT 822
AAZ37580/c
ID AAZ37580 standard; DNA; 20 BP.
XX
AC AAZ37580;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #110.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
  antisense; modulation; oligonucleotide; expression; inhibition;
  Query Match 0.8%; Score 20; DB 1; Length 20;
  Best Local Similarity 100.0%; Pred. No. 1.8e+03;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 727 TACAAGAGCTTCAGGAAGAG 746
Db 20 TACAAGAGCTTCAGGAAGAG 1

RESULT 823
AAZ37600/c
ID AAZ37600 standard; DNA; 20 BP.
XX
AC AAZ37600;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #130.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
  antisense; modulation; oligonucleotide; expression; inhibition;
  Query Match 0.8%; Score 20; DB 1; Length 20;
  Best Local Similarity 100.0%; Pred. No. 1.8e+03;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 964 CGCCATCGAATCCGGATCTT 983
Db 20 CGCCATCGAATCCGGATCTT 1

RESULT 824
AAZ37625/c
ID AAZ37625 standard; DNA; 20 BP.
XX
AC AAZ37625;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #155.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
  antisense; modulation; oligonucleotide; expression; inhibition;
  Query Match 0.8%; Score 20; DB 1; Length 20;
  Best Local Similarity 100.0%; Pred. No. 1.8e+03;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1207 TAGCTGACTATTGGAATGC 1226
Db 20 TAGCTGACTATTGGAATGC 1

RESULT 825
AAZ37634/c
ID AAZ37634 standard; DNA; 20 BP.
XX
AC AAZ37634;
XX

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DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #164.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
  antisense; modulation; oligonucleotide; expression; inhibition;
  Query Match 0.8%; Score 20; DB 1; Length 20;
  Best Local Similarity 100.0%; Pred. No. 1.8e+03;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1311 AAAGGGAAGATAAAGGGGA 1330
Db 20 AAAGGGAAGATAAAGGGGA 1

RESULT 826
AAZ37687/c
ID AAZ37687 standard; DNA; 20 BP.
XX
AC AAZ37687;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #217.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
  antisense; modulation; oligonucleotide; expression; inhibition;
  Query Match 0.8%; Score 20; DB 1; Length 20;
  Best Local Similarity 100.0%; Pred. No. 1.8e+03;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1872 AAGTGAGAAAATCCCTCAAT 1891
Db 20 AAGTGAGAAAATCCCTCAAT 1

RESULT 827
AAZ37689/c
ID AAZ37689 standard; DNA; 20 BP.
XX
AC AAZ37689;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #219.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
  antisense; modulation; oligonucleotide; expression; inhibition;
  Query Match 0.8%; Score 20; DB 1; Length 20;
  Best Local Similarity 100.0%; Pred. No. 1.8e+03;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1889 AATTCACATAGATTCTTCT 1908
Db 20 AATTCACATAGATTCTTCT 1

RESULT 828
AAZ37704/c
ID AAZ37704 standard; DNA; 20 BP.
XX
AC AAZ37704;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #234.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
  antisense; modulation; oligonucleotide; expression; inhibition;

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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2004 TTTAAATAAATTTCTACTCTG 2023
Db 20 TTTAAATAAATTTCTACTCTG 1

RESULT 829
AAZ37712/c
ID AAZ37712 standard; DNA; 20 BP.
XX
AC AAZ37712;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #242.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2116 CTGTTACCCAGGCTGGAGTG 2135
Db 20 CTGTTACCCAGGCTGGAGTG 1

RESULT 830
AAZ37486/c
ID AAZ37486 standard; DNA; 20 BP.
XX
AC AAZ37486;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #16.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1776 TATTTCCCTAGTTGACCTG 1795
Db 20 TATTTCCCTAGTTGACCTG 1

RESULT 831
AAZ37513/c
ID AAZ37513 standard; DNA; 20 BP.
XX
AC AAZ37513;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #43.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 GATCCTGCTGCTTCGAGC 124
Db 20 GATCCTGCTGCTTCGAGC 1
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RESULT 832
AAZ37535/c
ID AAZ37535 standard; DNA; 20 BP.
XX
AC AAZ37535;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #65.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 305 CAGGCAAAATGTGCAATACCA 324
Db 20 CAGGCAAAATGTGCAATACCA 1

RESULT 833
AAZ37554/c
ID AAZ37554 standard; DNA; 20 BP.
XX
AC AAZ37554;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #84.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 450 ACTTATCTACTATGAAGAGGT 469
Db 20 ACTTATCTACTATGAAGAGGT 1

RESULT 834
AAZ37575/c
ID AAZ37575 standard; DNA; 20 BP.
XX
AC AAZ37575;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #105.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 669 ACATCTGTGAGTGAGAACAG 688
Db 20 ACATCTGTGAGTGAGAACAG 1

RESULT 835
AAZ37591/c
ID AAZ37591 standard; DNA; 20 BP.
XX
AC AAZ37591;
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XX 07-JAN-2000 (first entry)
DT
XX Human mdm2 phosphorothioate oligodeoxynucleotide #121.
DE
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 857 ACGCCACAAATCTGATAGTA 876
DB 20 ACGCCACAAATCTGATAGTA 1

RESULT 836
AAZ37595/c
ID AAZ37595 standard; DNA; 20 BP.
XX
AC AAZ37595;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #125.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 904 CTCGTGTGTAATAAGGAG 923
DB 20 CTCGTGTGTAATAAGGAG 1

RESULT 837
AAZ37605/c
ID AAZ37605 standard; DNA; 20 BP.
XX
AC AAZ37605;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #135.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1017 TTGGATCAGGATTCAGTTTC 1036
DB 20 TTGGATCAGGATTCAGTTTC 1

RESULT 838
AAZ37629/c
ID AAZ37629 standard; DNA; 20 BP.
XX
AC AAZ37629;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #159.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1268 CAACAGATGTTGGCCCTTC 1287
DB 20 CAACAGATGTTGGCCCTTC 1

RESULT 839
AAZ37631/c
ID AAZ37631 standard; DNA; 20 BP.
XX
AC AAZ37631;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #161.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1283 CCTTCGTGAGATTTGGCTTC 1302
DB 20 CCTTCGTGAGATTTGGCTTC 1

RESULT 840
AAZ37641/c
ID AAZ37641 standard; DNA; 20 BP.
XX
AC AAZ37641;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #171.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1412 GAATGATTCAGAGATCAT 1431
DB 20 GAATGATTCAGAGATCAT 1

RESULT 841
AAZ37684/c
ID AAZ37684 standard; DNA; 20 BP.
XX
AC AAZ37684;
XX
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #214.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1850 TGAATTTTATTCATATAT 1869
DB 20 TGAATTTTATTCATATAT 1

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KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 GGCCCTGTGTGCGGAAGA 56
ID AAZ37503/c
XX |||||
AC AAZ37503;
XX |||||
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #33.
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCGCGCAGCTTGGCTGCTT 23
ID AAZ37514/c
XX |||||
AC AAZ37514;
XX |||||
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #44.
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 TGCTTTCGACCCAGGACA 132
ID AAZ37518/c
XX |||||
AC AAZ37518;
XX |||||
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #48.
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 CCAGTGCCTGGCCGGAGA 184
ID AAZ37532/c
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DB 20 CCAGTGCCTGGCCGGAGA 1
ID AAZ37520/c
XX |||||
AC AAZ37520;
XX |||||
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #50.
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 GCCCAGGCGTGTGCTTCC 221
ID AAZ37521/c
XX |||||
AC AAZ37521;
XX |||||
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #51.
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 208 GCGCTGCTGCTTCCGAGTA 227
ID AAZ37531/c
XX |||||
AC AAZ37531;
XX |||||
DT 07-JAN-2000 (first entry)
DE Human mdm2 phosphorothioate oligodeoxynucleotide #61.
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 AGGAGCAGCAATGTGCAA 319
ID AAZ37532/c
XX |||||
DB 20 AGGAGCAGCAATGTGCAA 1
ID AAZ37532 standard; DNA; 20 BP.
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XX AC AA237532;
XX DT 07-JAN-2000 (first entry)
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #62.
XX KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 GGAGCAGCGCAAAATGTGCAAT 320
DB 20 GGAGCAGCGCAAAATGTGCAAT 1

RESULT 856
AAZ37543/C
ID AAZ37543 standard; DNA; 20 BP.
XX AC AA237543;
XX DT 07-JAN-2000 (first entry)
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #73.
XX KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 313 TGTGCAATACCAATGCTCT 332
DB 20 TGTGCAATACCAATGCTCT 1

RESULT 857
AAZ37555/C
ID AAZ37555 standard; DNA; 20 BP.
XX AC AA237555;
XX DT 07-JAN-2000 (first entry)
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #85.
XX KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 477 TATCTTGGCCAGTATATTAT 496
DB 20 TATCTTGGCCAGTATATTAT 1

RESULT 858
AAZ37557/C
ID AAZ37557 standard; DNA; 20 BP.
XX AC AA237557;
XX DT 07-JAN-2000 (first entry)
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #87.
XX KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;

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KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 496 TGACTAAACGATTATATGAT 515
DB 20 TGACTAAACGATTATATGAT 1

RESULT 859
AAZ37562/C
ID AAZ37562 standard; DNA; 20 BP.
XX AC AA237562;
XX DT 07-JAN-2000 (first entry)
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #92.
XX KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 538 ATTGTTCAAATGATCTTCTA 557
DB 20 ATTGTTCAAATGATCTTCTA 1

RESULT 860
AAZ37564/C
ID AAZ37564 standard; DNA; 20 BP.
XX AC AA237564;
XX DT 07-JAN-2000 (first entry)
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #94.
XX KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 559 GAGATTGTTCGCGTGCCA 578
DB 20 GAGATTGTTCGCGTGCCA 1

RESULT 861
AAZ37567/C
ID AAZ37567 standard; DNA; 20 BP.
XX AC AA237567;
XX DT 07-JAN-2000 (first entry)
XX DE Human mdm2 phosphorothioate oligodeoxynucleotide #97.
XX KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisease; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 587 TGTGAAAGAGCAGACAGAAA 606
Db 20 TGTGAAAGAGCAGACAGAAA 1

RESULT 862
AAZ37613/c
ID AAZ37613 standard; DNA; 20 BP.
XX
AC AAZ37613;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #143.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 ATTATAGCCTTAGTGAAGAA 1103
Db 20 ATTATAGCCTTAGTGAAGAA 1

RESULT 863
AAZ37626/c
ID AAZ37626 standard; DNA; 20 BP.
XX
AC AAZ37626;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #156.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1220 GAAATGCACCTTCATGCAATG 1239
Db 20 GAAATGCACCTTCATGCAATG 1

RESULT 864
AAZ37628/c
ID AAZ37628 standard; DNA; 20 BP.
XX
AC AAZ37628;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #158.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1257 CCATCAGATTCACAGATG 1276
Db 20 CCATCAGATTCACAGATG 1

RESULT 865
AAZ37644/c

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ID AAZ37644 standard; DNA; 20 BP.
XX
AC AAZ37644;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #174.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1439 GGAATAATGATGATAAAATTA 1458
Db 20 GGAATAATGATGATAAAATTA 1

RESULT 866
AAZ37646/c
ID AAZ37646 standard; DNA; 20 BP.
XX
AC AAZ37646;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #176.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1456 TTACACAAGCTTCACAATCA 1475
Db 20 TTACACAAGCTTCACAATCA 1

RESULT 867
AAZ37698/c
ID AAZ37698 standard; DNA; 20 BP.
XX
AC AAZ37698;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #228.
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1956 TATAATTTGACTTGAATATG 1975
Db 20 TATAATTTGACTTGAATATG 1

RESULT 868
AAZ37711/c
ID AAZ37711 standard; DNA; 20 BP.
XX
AC AAZ37711;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #241.

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```
XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2111 TTGCTCTGTTACCCAGGCTG 2130
DB 20 TTGCTCTGTTACCCAGGCTG 1

RESULT 869
AAZ37718/c
ID AAZ37718 standard; DNA; 20 BP.
XX
AC AAZ37718;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #248.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2176 GGGTTCGCACCATTCCTCTG 2195
DB 20 GGGTTCGCACCATTCCTCTG 1

RESULT 870
AAZ37725/c
ID AAZ37725 standard; DNA; 20 BP.
XX
AC AAZ37725;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #255.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2218 GCCTACAGTCATCTGCCACC 2237
DB 20 GCCTACAGTCATCTGCCACC 1

RESULT 871
AAZ37732/c
ID AAZ37732 standard; DNA; 20 BP.
XX
AC AAZ37732;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #262.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2298 GGTCTCGATCTCTGACCTC 2317
DB 20 GGTCTCGATCTCTGACCTC 1

RESULT 872
AAZ37504/c
ID AAZ37504 standard; DNA; 20 BP.
XX
AC AAZ37504;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #34.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TTGGCTGCTTCTGGGCGCTG 33
DB 20 TTGGCTGCTTCTGGGCGCTG 1

RESULT 873
AAZ37561/c
ID AAZ37561 standard; DNA; 20 BP.
XX
AC AAZ37561;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #91.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 531 ATTGTATATTTTCAAAATGA 550
DB 20 ATTGTATATTTTCAAAATGA 1

RESULT 874
AAZ37563/c
ID AAZ37563 standard; DNA; 20 BP.
XX
AC AAZ37563;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #93.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 549 GATCTTCTAGGAGATTGTT 568
DB 20 GATCTTCTAGGAGATTGTT 1

RESULT 875
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AAZ37578/c
ID AAZ37578 standard; DNA; 20 BP.
XX
AC AAZ37578;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #108.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 704 TGGGAGTGATCAAAAGGACC 723
DB 20 TGGGAGTGATCAAAAGGACC 1

RESULT 876
AAZ37590/c
ID AAZ37590 standard; DNA; 20 BP.
XX
AC AAZ37590;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #120.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 844 AACGACAAAGAAAGCCAC 863
DB 20 AACGACAAAGAAAGCCAC 1

RESULT 877
AAZ37594/c
ID AAZ37594 standard; DNA; 20 BP.
XX
AC AAZ37594;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #124.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 895 AAAGCTGGCTCTGTGTGTA 914
DB 20 AAAGCTGGCTCTGTGTGTA 1

RESULT 878
AAZ37618/c
ID AAZ37618 standard; DNA; 20 BP.
XX
AC AAZ37618;
XX
DT 07-JAN-2000 (first entry)
XX

DE Human mdm2 phosphorothioate oligodeoxynucleotide #148.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1124 AGATGATGAGGTATATCAAG 1143
DB 20 AGATGATGAGGTATATCAAG 1

RESULT 879
AAZ37655/c
ID AAZ37655 standard; DNA; 20 BP.
XX
AC AAZ37655;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #185.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1541 TGTGAAGAGTTTGAAGGG 1560
DB 20 TGTGAAGAGTTTGAAGGG 1

RESULT 880
AAZ37688/c
ID AAZ37688 standard; DNA; 20 BP.
XX
AC AAZ37688;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #218.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1883 TGCCTCAATTTCACATAGATT 1902
DB 20 TGCCTCAATTTCACATAGATT 1

RESULT 881
AAZ37692/c
ID AAZ37692 standard; DNA; 20 BP.
XX
AC AAZ37692;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #222.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
antisense; modulation; oligonucleotide; expression; inhibition;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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XX Antisense oligonucleotide S5-6 directed against MDM2 encoding RNA.
DE
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 709 GTGATCAAAAGGACCTTGTA 728
Db 1 GTGATCAAAAGGACCTTGTA 20

RESULT 889
AAAX35113
ID AAX35113 standard; DNA; 20 BP.
XX
AC AAX35113;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide S7-2 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1003 ATTGAGGTGATTGGTGGAT 1022
Db 1 ATTGAGGTGATTGGTGGAT 20

RESULT 890
AAAX35132/c
ID AAX35132 standard; DNA; 20 BP.
XX
AC AAX35132;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide AS5-6 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 709 GTGATCAAAAGGACCTTGTA 728
Db 20 GTGATCAAAAGGACCTTGTA 1

RESULT 891
AAAX35100
ID AAX35100 standard; DNA; 20 BP.
XX
AC AAX35100;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide S2 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 369 CCAGCTTCGGAACAAGAGAC 388
Db 1 CCAGCTTCGGAACAAGAGAC 20

RESULT 892
AAAX35101
ID AAX35101 standard; DNA; 20 BP.
XX
AC AAX35101;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide S3 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 780 TCTACCTCATCTAGAGGAG 799
Db 1 TCTACCTCATCTAGAGGAG 20

RESULT 893
AAAX35103
ID AAX35103 standard; DNA; 20 BP.
XX
AC AAX35103;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide S8 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1230 TCATGCAATGAATGAATCC 1249
Db 1 TCATGCAATGAATGAATCC 20

RESULT 894
AAAX35137/c
ID AAX35137 standard; DNA; 20 BP.
XX
AC AAX35137;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide AS7-4 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1027 ATTGAGTTTCAGATCAGTTT 1046
Db 20 ATTGAGTTTCAGATCAGTTT 1
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RESULT 895
AAX35139/c
ID AAX35139 standard; DNA; 20 BP.
XX
XX
AC AAX35139;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide ASS-2H directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTCAGAACACGGTGTCA 694
Db 20 GTGAGTCAGAACACGGTGTCA 1

RESULT 896
AAX35122/c
ID AAX35122 standard; DNA; 20 BP.
XX
XX
AC AAX35122;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide AS1 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 ACCTCACAGATTCACGCTTC 376
Db 20 ACCTCACAGATTCACGCTTC 1

RESULT 897
AAX35134/c
ID AAX35134 standard; DNA; 20 BP.
XX
XX
AC AAX35134;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide AS7-1 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 998 TGAACATTCAGGTGATTGGT 1017
Db 20 TGAACATTCAGGTGATTGGT 1

RESULT 898
AAX35094
ID AAX35094 standard; DNA; 20 BP.
XX
AC AAX35094;
XX

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DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide S4 directed against MDM2 encoding RNA.
XX
XX
AC AAX35139;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide S1 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 481 TTGGCCAGTATATATGACT 500
Db 1 TTGGCCAGTATATATGACT 20

RESULT 899
AAX35099
ID AAX35099 standard; DNA; 20 BP.
XX
XX
AC AAX35099;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide S1 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 ACCTCACAGATTCACGCTTC 376
Db 1 ACCTCACAGATTCACGCTTC 20

RESULT 900
AAX35116
ID AAX35116 standard; DNA; 20 BP.
XX
XX
AC AAX35116;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide S7-5 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1038 GATCAGTTTAGTGTAGAATT 1057
Db 1 GATCAGTTTAGTGTAGAATT 20

RESULT 901
AAX35121/c
ID AAX35121 standard; DNA; 20 BP.
XX
XX
AC AAX35121;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide AS7 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1018 TGGATCAGGATTCAGTTTCA 1037
Db      20 TGGATCAGGATTCAGTTTCA 1

RESULT 902
AAX35126/c
ID AAX35126 standard; DNA; 20 BP.
XX
AC AAX35126;
XX
DT 01-JUL-1999 (first entry)
DE Antisense oligonucleotide AS8 directed against MDM2 encoding RNA.
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1230 TCATGCAATGAATGAATCC 1249
Db      20 TCATGCAATGAATGAATCC 1

RESULT 903
AAX35096
ID AAX35096 standard; DNA; 20 BP.
XX
AC AAX35096;
XX
DT 01-JUL-1999 (first entry)
DE Antisense oligonucleotide S7 directed against MDM2 encoding RNA.
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1018 TGGATCAGGATTCAGTTTCA 1037
Db      1 TGGATCAGGATTCAGTTTCA 20

RESULT 904
AAX35127/c
ID AAX35127 standard; DNA; 20 BP.
XX
AC AAX35127;
XX
DT 01-JUL-1999 (first entry)
DE Antisense oligonucleotide AS5-1 directed against MDM2 encoding RNA.
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 669 ACATCTGTGAGTGAACAG 688
Db      20 ACATCTGTGAGTGAACAG 1
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```
RESULT 905
AAX35111
ID AAX35111 standard; DNA; 20 BP.
XX
AC AAX35111;
XX
DT 01-JUL-1999 (first entry)
DE Antisense oligonucleotide SS-7 directed against MDM2 encoding RNA.
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 717 AAGGACCTTGTACAGAGCT 736
Db      1 AAGGACCTTGTACAGAGCT 20

RESULT 906
AAX35123/c
ID AAX35123 standard; DNA; 20 BP.
XX
AC AAX35123;
XX
DT 01-JUL-1999 (first entry)
DE Antisense oligonucleotide AS2 directed against MDM2 encoding RNA.
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 369 CCAGCTTCGGAACAAGAGAC 388
Db      20 CCAGCTTCGGAACAAGAGAC 1

RESULT 907
AAX35095
ID AAX35095 standard; DNA; 20 BP.
XX
AC AAX35095;
XX
DT 01-JUL-1999 (first entry)
DE Antisense oligonucleotide S5 directed against MDM2 encoding RNA.
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 695 CCTTGAAGGTGGAGTGATC 714
Db      1 CCTTGAAGGTGGAGTGATC 20

RESULT 908
AAX35119/c
ID AAX35119 standard; DNA; 20 BP.
XX
AC AAX35119;
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XX 01-JUL-1999 (first entry)
XX Antisense oligonucleotide AS4 directed against MDM2 encoding RNA.
DE MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
XX inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 481 TTGCCAGTATATTATGACT 500
DB 20 TTGCCAGTATATTATGACT 1
XX
RESULT 909
AAX35138/c
ID AAX35138 standard; DNA; 20 BP.
XX
AC AAX35138;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide AS7-5 directed against MDM2 encoding RNA.
XX MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
XX inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1038 GATCAGTTTGTAGTATT 1057
DB 20 GATCAGTTTGTAGTATT 1
XX
RESULT 910
AAX35102
ID AAX35102 standard; DNA; 20 BP.
XX
AC AAX35102;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide S6 directed against MDM2 encoding RNA.
XX MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
XX inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1203 TCCTTAGCTGACTATTGGAA 1222
DB 1 TCCTTAGCTGACTATTGGAA 20
XX
RESULT 911
AAX35106
ID AAX35106 standard; DNA; 20 BP.
XX
AC AAX35106;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide S5-2 directed against MDM2 encoding RNA.
XX MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
XX inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.
XX
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```
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 675 GTGAGTGAGAACAGGTGTCA 694
DB 1 GTGAGTGAGAACAGGTGTCA 20
XX
RESULT 912
AAX35112
ID AAX35112 standard; DNA; 20 BP.
XX
AC AAX35112;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide S7-1 directed against MDM2 encoding RNA.
XX MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
XX inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 998 TGAACATTTCAGGTGATTGGT 1017
DB 1 TGAACATTTCAGGTGATTGGT 20
XX
RESULT 913
AAX35131/c
ID AAX35131 standard; DNA; 20 BP.
XX
AC AAX35131;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide AS5-5 directed against MDM2 encoding RNA.
XX MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
XX inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 704 TGGGAGTGATCAAAAGGACC 723
DB 20 TGGGAGTGATCAAAAGGACC 1
XX
RESULT 914
AAX35115
ID AAX35115 standard; DNA; 20 BP.
XX
AC AAX35115;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide S7-4 directed against MDM2 encoding RNA.
XX MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
XX inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1027 ATTCACTTTTCAGATCAGTTT 1046
DB 1 ATTCACTTTTCAGATCAGTTT 1046
XX
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Db      1 ATTCAGTTTCAGATCAGTTT 20

RESULT 915
AAK35107
ID AAK35107 standard; DNA; 20 BP.
XX
AC AAK35107;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide S5-3 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      680 TGAGAACAGGTGTCACCTTG 699
Db      1 TGAGAACAGGTGTCACCTTG 20

RESULT 916
AAK35124/c
ID AAK35124 standard; DNA; 20 BP.
XX
AC AAK35124;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide AS3 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      780 TCTACCTCATCTAGAGGAG 799
Db      20 TCTACCTCATCTAGAGGAG 1

RESULT 917
AAK35133/c
ID AAK35133 standard; DNA; 20 BP.
XX
AC AAK35133;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide AS5-7 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      717 AAGGACCTTGTCAGAGCT 736
Db      20 AAGGACCTTGTCAGAGCT 1

RESULT 918
AAK35109
ID AAK35109 standard; DNA; 20 BP.
XX
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AC AAK35109;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide S5-5 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      704 TGGGAGTGATCAAAAGGACC 723
Db      1 TGGGAGTGATCAAAAGGACC 20

RESULT 919
AAK35105
ID AAK35105 standard; DNA; 20 BP.
XX
AC AAK35105;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide S5-1 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      669 ACATCTGTGAGTCAGAACAG 688
Db      1 ACATCTGTGAGTCAGAACAG 20

RESULT 920
AAK35108
ID AAK35108 standard; DNA; 20 BP.
XX
AC AAK35108;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide S5-4 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      685 ACAGGTGTTCACCTTGAAGGT 704
Db      1 ACAGGTGTTCACCTTGAAGGT 20

RESULT 921
AAK35128/c
ID AAK35128 standard; DNA; 20 BP.
XX
AC AAK35128;
XX
DT 01-JUL-1999 (first entry)
XX
DE Antisense oligonucleotide AS5-2 directed against MDM2 encoding RNA.
XX
KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
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```
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTGAGAACAGGTGTCA 694
DB 20 GTGAGTGAGAACAGGTGTCA 1
|||||
DB 20 TAGTAGAGACAGGGTTTCAC 1
|||||

RESULT 925
AAZ96410/c
ID AAA96410 standard; DNA; 20 BP.
XX AC AAA96410;
XX DT 08-FEB-2001 (first entry)
XX DE Primer used to amplify a sara43/44 polymorphic microsatellite repeat.
XX KW Autoimmune disease; polymorphic microsatellite repeat; PMR; CD28 gene;
ICOS gene; CTLA4 gene; costimulatory receptor gene locus; CGRL; lupus;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2122 CCCAGGCTGGAGTGCAGTGG 2141
DB 20 CCCAGGCTGGAGTGCAGTGG 1
|||||

RESULT 926
AAZ89373
ID AAZ89373 standard; DNA; 20 BP.
XX AC AAZ89373;
XX DT 15-JUN-2000 (first entry)
XX DE Human mdm-2 PCR primer MDM2PR1.
XX KW Human; mdm-2; PCR primer; reaction container; quantitation; diagnosis;
KW food analysis; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1531 GCCAAGAAGATGTGAAGAG 1550
DB 1 GCCAAGAAGATGTGAAGAG 20
|||||

RESULT 927
AAZ28013
ID AAA28013 standard; DNA; 20 BP.
XX AC AAA28013;
XX DT 29-AUG-2000 (first entry)
XX DE Uncoupling protein isoform UCP5SI nucleotide sequence PCR primer.
XX KW Uncoupling protein 5; UCP5; metabolism; chromosome 10q23-25; H+ leak;
KW metabolic rate; obesity; stroke; trauma; burn trauma; sepsis; infection;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2349 TGGGATTACAGGCATGAGCC 2368
DB 1 TGGGATTACAGGCATGAGCC 20
|||||

RESULT 928
AAZ14945/c
ID AAA14945 standard; DNA; 20 BP.
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KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTGAGAACAGGTGTCA 694
DB 20 GTGAGTGAGAACAGGTGTCA 1
|||||
DB 20 TAGTAGAGACAGGGTTTCAC 1
|||||

RESULT 922
AAZ35129/c
ID AAZ35129 standard; DNA; 20 BP.
XX AC AAZ35129;
XX DT 01-JUL-1999 (first entry)
XX DE Antisense oligonucleotide AS5-3 directed against MDM2 encoding RNA.
XX KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 680 TGAGAACAGGTGTCACTTG 699
DB 20 TGAGAACAGGTGTCACTTG 1
|||||

RESULT 923
AAZ35135/c
ID AAZ35135 standard; DNA; 20 BP.
XX AC AAZ35135;
XX DT 01-JUL-1999 (first entry)
XX DE Antisense oligonucleotide AS7-2 directed against MDM2 encoding RNA.
XX KW MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1003 ATTACAGGTGATTGGTTGGAT 1022
DB 20 ATTACAGGTGATTGGTTGGAT 1
|||||

RESULT 924
AAZ43583/c
ID AAZ43583 standard; DNA; 20 BP.
XX AC AAZ43583;
XX DT 21-FEB-2000 (first entry)
XX DE Alzheimer's disease detecting primer #10.
XX KW Alzheimer's disease; primer; dihydrolipoamidossuccinyl transferase;
KW mitochondria; alpha-ketoglutarate dehydrogenase; detection; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2263 TAGTAGAGACAGGGTTTCAC 2282
|||||
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XX AAA14945;
AC
XX 08-AUG-2000 (first entry)
DT PCR primer SR1 used to amplify the repeated DNA sequences Alu.
DE Chromosomal labelling; chromosomal band; IRS-PCR; Alu; LINE; karyotype;
XX interspersed repeat sequence-polymerase chain reaction; probe;
KW

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2122 CCAGGCTGGAGTGCAGTGG 2141
Db 20 CCCAGGCTGGAGTGCAGTGG 1

RESULT 929
AAA97667/c
ID AAA97667 standard; DNA; 20 BP.
XX
AC AAA97667;
XX
DT 15-FEB-2001 (first entry)
DE Human MDM2 PCR primer 4.
XX
KW Pseudocyclic oligonucleotide; functional segment; protective segment;
KW nucleic acid detection; mRNA cleavage; antisense therapy; PCO;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 676 TGAGTGAGAACACAGGTGTAC 695
Db 20 TGAGTGAGAACACAGGTGTAC 1

RESULT 930
AAA97654/c
ID AAA97654 standard; DNA; 20 BP.
XX
AC AAA97654;
XX
DT 15-FEB-2001 (first entry)
DE Human MDM2-targetted pseudocyclic oligonucleotide 12.
XX
KW Pseudocyclic oligonucleotide; functional segment; protective segment;
KW nucleic acid detection; mRNA cleavage; antisense therapy;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTGAGAACACAGGTGTCA 694
Db 20 GTGAGTGAGAACACAGGTGTCA 1

RESULT 931
AAA97657/c
ID AAA97657 standard; DNA; 20 BP.
XX
AC AAA97657;
XX
DT 15-FEB-2001 (first entry)
DE Human MDM2-targetted pseudocyclic oligonucleotide 1.
XX

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KW Pseudocyclic oligonucleotide; functional segment; protective segment;
KW nucleic acid detection; mRNA cleavage; antisense therapy;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTGAGAACACAGGTGTCA 694
Db 20 GTGAGTGAGAACACAGGTGTCA 1

RESULT 932
AAA97656/c
ID AAA97656 standard; DNA; 20 BP.
XX
AC AAA97656;
XX
DT 15-FEB-2001 (first entry)
DE Human MDM2-targetted pseudocyclic oligonucleotide 14.
XX
KW Pseudocyclic oligonucleotide; functional segment; protective segment;
KW nucleic acid detection; mRNA cleavage; antisense therapy;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTGAGAACACAGGTGTCA 694
Db 20 GTGAGTGAGAACACAGGTGTCA 1

RESULT 933
AAA97665/c
ID AAA97665 standard; DNA; 20 BP.
XX
AC AAA97665;
XX
DT 15-FEB-2001 (first entry)
DE Human MDM2 PCR primer 2.
XX
KW Pseudocyclic oligonucleotide; functional segment; protective segment;
KW nucleic acid detection; mRNA cleavage; antisense therapy; PCO;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTGAGAACACAGGTGTCA 694
Db 20 GTGAGTGAGAACACAGGTGTCA 1

RESULT 934
AAA97669/c
ID AAA97669 standard; DNA; 20 BP.
XX
AC AAA97669;
XX
DT 15-FEB-2001 (first entry)
DE Human MDM2 PCR primer 6.
XX
KW Pseudocyclic oligonucleotide; functional segment; protective segment;
KW nucleic acid detection; mRNA cleavage; antisense therapy; PCO;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTGAGAACACAGGTGTCA 694
Db 20 GTGAGTGAGAACACAGGTGTCA 1

RESULT 934
AAA97669/c
ID AAA97669 standard; DNA; 20 BP.
XX
AC AAA97669;
XX
DT 15-FEB-2001 (first entry)
DE Human MDM2 PCR primer 6.
XX
KW Pseudocyclic oligonucleotide; functional segment; protective segment;
KW nucleic acid detection; mRNA cleavage; antisense therapy; PCO;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 672 TCTGTGAGTGAGAACAGGTG 691
 DB 20 TCTGTGAGTGAGAACAGGTG 1

RESULT 935

AA97655/c
 ID AAA97655 standard; DNA; 20 BP.

XX AC AAA97655;
 XX DT 15-FEB-2001 (first entry)
 XX DE Human MDM2-targeted pseudocyclic oligonucleotide 13.
 XX KW Pseudocyclic oligonucleotide; functional segment; protective segment;
 XX KW nucleic acid detection; mRNA cleavage; antisense therapy;

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTGAGACAGGTGTCA 694
 DB 20 GTGAGTGAGACAGGTGTCA 1

RESULT 936

AA97666/c
 ID AAA97666 standard; DNA; 20 BP.

XX AC AAA97666;
 XX DT 15-FEB-2001 (first entry)
 XX DE Human MDM2 PCR primer 3.
 XX KW Pseudocyclic oligonucleotide; functional segment; protective segment;
 XX KW nucleic acid detection; mRNA cleavage; antisense therapy; PCO;

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 677 GAGTGAGACAGGTGTCA 696
 DB 20 GAGTGAGACAGGTGTCA 1

RESULT 937

AA97668/c
 ID AAA97668 standard; DNA; 20 BP.

XX AC AAA97668;
 XX DT 15-FEB-2001 (first entry)
 XX DE Human MDM2 PCR primer 5.
 XX KW Pseudocyclic oligonucleotide; functional segment; protective segment;
 XX KW nucleic acid detection; mRNA cleavage; antisense therapy; PCO;

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 674 TGTGAGTGAGACAGGTGTC 693
 DB 20 TGTGAGTGAGACAGGTGTC 1

RESULT 938

AAD14808

ID AAD14808 standard; DNA; 20 BP.
 XX AC AAD14808;
 XX DT 01-NOV-2001 (first entry)
 XX DE Human glycogen synthase kinase 3 alpha antisense oligo ISIS #116649.
 XX KW Human; glycogen synthase kinase 3 alpha; antidiabetic; cytostatic;
 XX KW antisense therapy; diabetes; hyperproliferative disorder; inflammation;

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2338 TCCCAAGTCTGGGATTAC 2357
 DB 1 TCCCAAGTCTGGGATTAC 20

RESULT 939

AAK95176/c
 ID AAK95176 standard; DNA; 20 BP.

XX AC AAK95176;
 XX DT 06-NOV-2001 (first entry)
 XX DE Human cDNA clone-specific primer, SEQ ID NO: 4421.
 XX KW Human; full length cDNA; cDNA synthesis; oligo-capping; PCR primer; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2341 CAAAGTCTGGGATTACAGG 2360
 DB 20 CAAAGTCTGGGATTACAGG 1

RESULT 940

AAF23807/c
 ID AAF23807 standard; DNA; 20 BP.

XX AC AAF23807;
 XX DT 22-MAR-2001 (first entry)
 XX DE Oligo #7 used to produce ligand-conjugated oligomeric compounds.
 XX KW Ligand-conjugated oligomeric compound; aryl propionic acid;
 XX KW nucleic acid delivery; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1695 TTTCATGTGCAAGAAGCT 1714
 DB 20 TTTCATGTGCAAGAAGCT 1

RESULT 941

AAF80627/c
 ID AAF80627 standard; DNA; 20 BP.

XX AC AAF80627;
 XX DT 02-MAY-2001 (first entry)
 XX DE Human mdm2 phosphorothioate oligonucleotide #1.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
KW
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGGAGCTTGGCTG 20
DB 20 GCACCGCGGAGCTTGGCTG 1

RESULT 942
AAF80629/c
ID AAF80629 standard; DNA; 20 BP.

XX AAF80629;

DT 02-MAY-2001 (first entry)

DE Human mdm2 phosphorothioate oligonucleotide #3.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 CTCTGACCGAGATCTCTGCTG 114
DB 20 CTCTGACCGAGATCTCTGCTG 1

RESULT 943
AAF80643/c
ID AAF80643 standard; DNA; 20 BP.

XX AAF80643;

DT 02-MAY-2001 (first entry)

DE Human mdm2 phosphorothioate oligonucleotide #17.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1934 TAGTGGAAATAGTAATCTT 1953
DB 20 TAGTGGAAATAGTAATCTT 1

RESULT 944
AAF80681/c
ID AAF80681 standard; DNA; 20 BP.

XX AAF80681;

DT 02-MAY-2001 (first entry)

DE Human mdm2 phosphorothioate oligonucleotide #55.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 296 GGTGAGGAGCAGCAATGT 315
DB 20 GGTGAGGAGCAGCAATGT 1

RESULT 945
AAF80687/c
ID AAF80687 standard; DNA; 20 BP.

XX AAF80687;

DT 02-MAY-2001 (first entry)

DE Human mdm2 phosphorothioate oligonucleotide #61.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 GAGCAGGCAATGTGCAATA 321
DB 20 GAGCAGGCAATGTGCAATA 1

RESULT 946
AAF80688/c
ID AAF80688 standard; DNA; 20 BP.

XX AAF80688;

DT 02-MAY-2001 (first entry)

DE Human mdm2 phosphorothioate oligonucleotide #62.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 GCAGGCAATGTGCAATACC 323
DB 20 GCAGGCAATGTGCAATACC 1

RESULT 947
AAF80700/c
ID AAF80700 standard; DNA; 20 BP.

XX AAF80700;

DT 02-MAY-2001 (first entry)

DE Human mdm2 phosphorothioate oligonucleotide #74.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 TACCTACTGATGTGCTGTA 353
DB 20 TACCTACTGATGTGCTGTA 1

RESULT 948

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1412 GAATGATCCAGAGTGCAT 1431
 Db 20 GAATGATCCAGAGTGCAT 1

RESULT 955
 AAF80798/c
 ID AAF80798 standard; DNA; 20 BP.

XX AAF80798;
 XX
 DT 02-MAY-2001 (first entry)

DE Human mdm2 phosphorothioate oligonucleotide #172.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
 XX
 Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1439 GGAAATGATGATAAAATTA 1458
 Db 20 GGAAATGATGATAAAATTA 1

RESULT 956

AAF80888/c
 ID AAF80888 standard; DNA; 20 BP.

XX AAF80888;
 XX
 DT 02-MAY-2001 (first entry)

DE Human mdm2 phosphorothioate oligonucleotide #262.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
 XX
 Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2319 TGATCCGCCACCTGGCCT 2338
 Db 20 TGATCCGCCACCTGGCCT 1

RESULT 957

AAF80641/c
 ID AAF80641 standard; DNA; 20 BP.

XX AAF80641;
 XX
 DT 02-MAY-2001 (first entry)

DE Human mdm2 phosphorothioate oligonucleotide #15.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
 XX
 Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1785 TAGTTGACCTGTCTATAGA 1804
 Db 20 TAGTTGACCTGTCTATAGA 1

RESULT 958
 AAF80689/c
 ID AAF80689 standard; DNA; 20 BP.

XX AAF80689;
 XX
 DT 02-MAY-2001 (first entry)

DE Human mdm2 phosphorothioate oligonucleotide #63.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
 XX
 Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 305 CAGGCAAAATGTGCAATACCA 324
 Db 20 CAGGCAAAATGTGCAATACCA 1

RESULT 959

AAF80718/c
 ID AAF80718 standard; DNA; 20 BP.

XX AAF80718;
 XX
 DT 02-MAY-2001 (first entry)

DE Human mdm2 phosphorothioate oligonucleotide #92.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
 XX
 Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 559 GAGATTGTTGGCGTGCCA 578
 Db 20 GAGATTGTTGGCGTGCCA 1

RESULT 960

AAF80735/c
 ID AAF80735 standard; DNA; 20 BP.

XX AAF80735;
 XX
 DT 02-MAY-2001 (first entry)

DE Human mdm2 phosphorothioate oligonucleotide #109.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
 XX
 Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 740 GGAAGAGAAACCTTCATCTT 759
 Db 20 GGAAGAGAAACCTTCATCTT 1

RESULT 961

AAF80778/c
 ID AAF80778 standard; DNA; 20 BP.

XX AAF80778;
 XX
 DT 02-MAY-2001 (first entry)


```
XX Human mdm2 phosphorothioate oligonucleotide #152.
DE
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1196 TGAATTTCTTAGCTGACT 1215
DB 20 TGAATTTCTTAGCTGACT 1

RESULT 962
AAF80784/c
ID AAF80784 standard; DNA; 20 BP.
XX
AC AAF80784;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #158.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1275 TGTGGGCCCTTCGTGAGAA 1294
DB 20 TGTGGGCCCTTCGTGAGAA 1

RESULT 963
AAF80788/c
ID AAF80788 standard; DNA; 20 BP.
XX
AC AAF80788;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #162.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1311 AAAGGGAAGATAAAGGGGA 1330
DB 20 AAAGGGAAGATAAAGGGGA 1

RESULT 964
AAF80789/c
ID AAF80789 standard; DNA; 20 BP.
XX
AC AAF80789;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #163.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1325 AGGGGAATCTCTGAGAAAG 1344
DB 20 AGGGGAATCTCTGAGAAAG 1

RESULT 965
AAF80791/c
ID AAF80791 standard; DNA; 20 BP.
XX
AC AAF80791;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #165.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1346 CAAACTGGAAACTCAACAC 1365
DB 20 CAAACTGGAAACTCAACAC 1

RESULT 966
AAF80801/c
ID AAF80801 standard; DNA; 20 BP.
XX
AC AAF80801;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #175.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1466 TTCACAATCACAAGAAAGTG 1485
DB 20 TTCACAATCACAAGAAAGTG 1

RESULT 967
AAF80817/c
ID AAF80817 standard; DNA; 20 BP.
XX
AC AAF80817;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #191.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1648 AAAATGGTTGCATTGTCCAT 1667
DB 20 AAAATGGTTGCATTGTCCAT 1
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RESULT 968
AAF80826/c
ID AAF80826 standard; DNA; 20 BP.
XX
XX AAF80826;
XX
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #200.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1726 ATAAGCCCTGCCAGTATGT 1745
Db 20 ATAAGCCCTGCCAGTATGT 1

RESULT 969
AAF80836/c
ID AAF80836 standard; DNA; 20 BP.
XX
XX AAF80836;
XX
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #210.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1832 CTAGGAATTTAGACAACCTG 1851
Db 20 CTAGGAATTTAGACAACCTG 1

RESULT 970
AAF80839/c
ID AAF80839 standard; DNA; 20 BP.
XX
XX AAF80839;
XX
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #213.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1855 TTTATTTCATATATCAAG 1874
Db 20 TTTATTTCATATATCAAG 1

RESULT 971
AAF80842/c
ID AAF80842 standard; DNA; 20 BP.
XX
XX AAF80842;
XX
XX

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DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #216.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1883 TGCCTCAATTCACATAGATT 1902
Db 20 TGCCTCAATTCACATAGATT 1

RESULT 972
AAF80845/c
ID AAF80845 standard; DNA; 20 BP.
XX
XX AAF80845;
XX
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #219.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1905 TTCTCTTTAGTATAATTGAC 1924
Db 20 TTCTCTTTAGTATAATTGAC 1

RESULT 973
AAF80848/c
ID AAF80848 standard; DNA; 20 BP.
XX
XX AAF80848;
XX
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #222.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1920 TTGACCTACTTTGGTAGTGG 1939
Db 20 TTGACCTACTTTGGTAGTGG 1

RESULT 974
AAF80860/c
ID AAF80860 standard; DNA; 20 BP.
XX
XX AAF80860;
XX
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #234.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2020 TCTGCTTAAATGAGAAGTA 2039
DB 20 TCTGCTTAAATGAGAAGTA 1

RESULT 975
AAF80892/c
ID AAF80892 standard; DNA; 20 BP.
XX
AC AAF80892;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #266.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2351 GGATTACAGGCGATGAGCCAC 2370
DB 20 GGATTACAGGCGATGAGCCAC 1

RESULT 976
AAF80638/c
ID AAF80638 standard; DNA; 20 BP.
XX
AC AAF80638;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #12.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1381 TTGATGTTCTGATGTTGAAA 1400
DB 20 TTGATGTTCTGATGTTGAAA 1

RESULT 977
AAF80674/c
ID AAF80674 standard; DNA; 20 BP.
XX
AC AAF80674;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #48.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 GCCCAGGGCGTGTGCTTCC 221
DB 20 GCCCAGGGCGTGTGCTTCC 1

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 978
AAF80745/c
ID AAF80745 standard; DNA; 20 BP.
XX
AC AAF80745;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #119.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 857 ACGCCACAAATCTGATAGTA 876
DB 20 ACGCCACAAATCTGATAGTA 1

RESULT 979
AAF80755/c
ID AAF80755 standard; DNA; 20 BP.
XX
AC AAF80755;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #129.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 971 GAATCCGGATCTTGATGCTG 990
DB 20 GAATCCGGATCTTGATGCTG 1

RESULT 980
AAF80763/c
ID AAF80763 standard; DNA; 20 BP.
XX
AC AAF80763;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #137.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1051 TAGAATTTGAAGTTGAATCT 1070
DB 20 TAGAATTTGAAGTTGAATCT 1

RESULT 981
AAF80767/c
ID AAF80767 standard; DNA; 20 BP.
XX
AC AAF80767;

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XX 02-MAY-2001 (first entry)
DT Human mdm2 phosphorothioate oligonucleotide #141.
DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
KW
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1084 ATTATAGCCTTAGTGAAGAA 1103
DB 20 ATTATAGCCTTAGTGAAGAA 1

RESULT 982
AAF80785/c
ID AAF80785 standard; DNA; 20 BP.
XX
AC AAF80785;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #159.
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1283 CCTTCGTGAGAAATGGCTTC 1302
DB 20 CCTTCGTGAGAAATGGCTTC 1

RESULT 983
AAF80820/c
ID AAF80820 standard; DNA; 20 BP.
XX
AC AAF80820;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #194.
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1675 CAGGACATCTTATGGCCTGC 1694
DB 20 CAGGACATCTTATGGCCTGC 1

RESULT 984
AAF80840/c
ID AAF80840 standard; DNA; 20 BP.
XX
AC AAF80840;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #214.
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1865 TATATCAAAAGTGAGAAAATG 1884
DB 20 TATATCAAAAGTGAGAAAATG 1

RESULT 985
AAF80850/c
ID AAF80850 standard; DNA; 20 BP.
XX
AC AAF80850;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #224.
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1940 AATAGTGAATACTTACTATA 1959
DB 20 AATAGTGAATACTTACTATA 1

RESULT 986
AAF80859/c
ID AAF80859 standard; DNA; 20 BP.
XX
AC AAF80859;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #233.
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2015 TCTACTCTGCTTAAATGAG 2034
DB 20 TCTACTCTGCTTAAATGAG 1

RESULT 987
AAF80861/c
ID AAF80861 standard; DNA; 20 BP.
XX
AC AAF80861;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #235.
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2051 TTTTCTTAAATATGTATATG 2070
DB 20 TTTTCTTAAATATGTATATG 1

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Db      20 TTTTCTTAATAATATGATATG 1

RESULT 988
AAF80883/c
ID AAF80883 standard; DNA; 20 BP.
XX
XX AAF80883;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #257.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2274 GGGTTTCACCGTGTAGCCA 2293
      |||||
      20 GGGTTTCACCGTGTAGCCA 1

Db

RESULT 989
AAF80889/c
ID AAF80889 standard; DNA; 20 BP.
XX
XX AAF80889;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #263.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2274 GGGTTTCACCGTGTAGCCA 2293
      |||||
      20 GGGTTTCACCGTGTAGCCA 1

Db

RESULT 990
AAF80634/c
ID AAF80634 standard; DNA; 20 BP.
XX
XX AAF80634;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #8.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      303 AGCAGGCAATGTGCAATAC 322
      |||||
      20 AGCAGGCAATGTGCAATAC 1

Db

RESULT 991
AAF80646/c
ID AAF80646 standard; DNA; 20 BP.
XX
XX

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AC AAF80646;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #20.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2256 GTACTTTTAGTAGACAGG 2275
      |||||
      20 GTACTTTTAGTAGACAGG 1

Db

RESULT 992
AAF80671/c
ID AAF80671 standard; DNA; 20 BP.
XX
XX AAF80671;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #45.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      158 CGAGCGCCCGTGCCTGGC 177
      |||||
      20 CGAGCGCCCGTGCCTGGC 1

Db

RESULT 993
AAF80715/c
ID AAF80715 standard; DNA; 20 BP.
XX
XX AAF80715;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #89.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      531 ATTGTATATTGTCAAATGA 550
      |||||
      20 ATTGTATATTGTCAAATGA 1

Db

RESULT 994
AAF80719/c
ID AAF80719 standard; DNA; 20 BP.
XX
XX AAF80719;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #93.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

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XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 566 GTTTGGCGTGCACAGCTTCT 585
DB 20 GTTTGGCGTGCACAGCTTCT 1

RESULT 995
AAF80725/c
ID AAF80725 standard; DNA; 20 BP.
XX AC AAF80725;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #99.
XX DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 TCTACAGGAAGCTTGGTAGTA 638
DB 20 TCTACAGGAAGCTTGGTAGTA 1

RESULT 996
AAF80742/c
ID AAF80742 standard; DNA; 20 BP.
XX AC AAF80742;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #116.
XX DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 824 TTCAGATGAATATCTGGTG 843
DB 20 TTCAGATGAATATCTGGTG 1

RESULT 997
AAF80756/c
ID AAF80756 standard; DNA; 20 BP.
XX AC AAF80756;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #130.
XX DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 983 TGATGCTGGTGTAAAGTGAAC 1002

Db 20 TGATGCTGGTGTAAAGTGAAC 1

RESULT 998
AAF80765/c
ID AAF80765 standard; DNA; 20 BP.
XX AC AAF80765;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #139.
XX DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1068 TCTCTCGACTCAGAGATTA 1087
DB 20 TCTCTCGACTCAGAGATTA 1

RESULT 999
AAF80779/c
ID AAF80779 standard; DNA; 20 BP.
XX AC AAF80779;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #153.
XX DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1207 TAGCTGACTATTGGAATGC 1226
DB 20 TAGCTGACTATTGGAATGC 1

RESULT 1000
AAF80803/c
ID AAF80803 standard; DNA; 20 BP.
XX AC AAF80803;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #177.
XX DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1489 ACTATTCTCAGGCATCACT 1508
DB 20 ACTATTCTCAGGCATCACT 1

RESULT 1001
AAF80810/c
ID AAF80810 standard; DNA; 20 BP.

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XX AAF80810;
XX
XX DT 02-MAY-2001 (first entry)
XX
XX DE Human mdm2 phosphorothioate oligonucleotide #184.
XX
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
XX
XX Query Match 0.8%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1550 GTTTGAAGGGAAGAACCC 1569
DB 20 GTTTGAAGGGAAGAACCC 1

RESULT 1002
AAF80812/c
ID AAF80812 standard; DNA; 20 BP.
XX
XX AC AAF80812;
XX
XX DT 02-MAY-2001 (first entry)
XX
XX DE Human mdm2 phosphorothioate oligonucleotide #186.
XX
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
XX
XX Query Match 0.8%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1566 ACCCAAGACAAAGAGAG 1595
DB 20 ACCCAAGACAAAGAGAG 1

RESULT 1003
AAF80828/c
ID AAF80828 standard; DNA; 20 BP.
XX
XX AC AAF80828;
XX
XX DT 02-MAY-2001 (first entry)
XX
XX DE Human mdm2 phosphorothioate oligonucleotide #202.
XX
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
XX
XX Query Match 0.8%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1745 TAGACACCAATTCAAATGA 1764
DB 20 TAGACACCAATTCAAATGA 1

RESULT 1004
AAF80831/c
ID AAF80831 standard; DNA; 20 BP.
XX
XX AC AAF80831;
XX
XX DT 02-MAY-2001 (first entry)
XX
XX DE Human mdm2 phosphorothioate oligonucleotide #205.
XX
XX

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KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
XX
XX Query Match 0.8%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1798 TATAAGAGAATTATATTT 1817
DB 20 TATAAGAGAATTATATTT 1

RESULT 1005
AAF80834/c
ID AAF80834 standard; DNA; 20 BP.
XX
XX AC AAF80834;
XX
XX DT 02-MAY-2001 (first entry)
XX
XX DE Human mdm2 phosphorothioate oligonucleotide #208.
XX
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
XX
XX Query Match 0.8%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1816 TTCTAACTATATAACCCCTAG 1835
DB 20 TTCTAACTATATAACCCCTAG 1

RESULT 1006
AAF80846/c
ID AAF80846 standard; DNA; 20 BP.
XX
XX AC AAF80846;
XX
XX DT 02-MAY-2001 (first entry)
XX
XX DE Human mdm2 phosphorothioate oligonucleotide #220.
XX
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
XX
XX Query Match 0.8%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1908 TCCTTAGTATATTGACCTA 1927
DB 20 TCCTTAGTATATTGACCTA 1

RESULT 1007
AAF80866/c
ID AAF80866 standard; DNA; 20 BP.
XX
XX AC AAF80866;
XX
XX DT 02-MAY-2001 (first entry)
XX
XX DE Human mdm2 phosphorothioate oligonucleotide #240.
XX
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
XX
XX Query Match 0.8%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2116 CTGTTACCCAGGCTGGAGTG 2135
Db 20 CTGTTACCCAGGCTGGAGTG 1
RESULT 1008
AAF80878/c
ID AAF80878 standard; DNA; 20 BP.
XX
AC AAF80878;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #252.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2213 GCTTGGCCTACAGTCATCTG 2232
Db 20 GCTTGGCCTACAGTCATCTG 1
RESULT 1009
AAF80633/c
ID AAF80633 standard; DNA; 20 BP.
XX
AC AAF80633;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #7.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 295 TGGTGAGGAGCAGGCAATG 314
Db 20 TGGTGAGGAGCAGGCAATG 1
RESULT 1010
AAF80639/c
ID AAF80639 standard; DNA; 20 BP.
XX
AC AAF80639;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #13.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1695 TTTACATGTGCAAGAAGCT 1714
Db 20 TTTACATGTGCAAGAAGCT 1
RESULT 1011
AAF80676/c
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ID AAF80676 standard; DNA; 20 BP.
XX
AC AAF80676;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #50.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 217 CTTCCGCGAGTAGTCAGTCCC 236
Db 20 CTTCCGCGAGTAGTCAGTCCC 1
RESULT 1012
AAF80694/c
ID AAF80694 standard; DNA; 20 BP.
XX
AC AAF80694;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #68.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 310 AAATGTGCAATACCAACATG 329
Db 20 AAATGTGCAATACCAACATG 1
RESULT 1013
AAF80695/c
ID AAF80695 standard; DNA; 20 BP.
XX
AC AAF80695;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #69.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 311 AATGTGCAATACCAACATGT 330
Db 20 AATGTGCAATACCAACATGT 1
RESULT 1014
AAF80708/c
ID AAF80708 standard; DNA; 20 BP.
XX
AC AAF80708;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #82.
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XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
XX
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 450 ACTTATCTATGAAAGAGGT 469
Db 20 ACTTATCTATGAAAGAGGT 1

RESULT 1015
AAF80743/c
ID AAF80743 standard; DNA; 20 BP.
XX
XX AAF80743;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #117.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 833 ATTATCTGTTGAACGACAAA 852
Db 20 ATTATCTGTTGAACGACAAA 1

RESULT 1016
AAF80751/c
ID AAF80751 standard; DNA; 20 BP.
XX
XX AAF80751;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #125.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 927 TGTGTGAAAGACAGTAG 946
Db 20 TGTGTGAAAGACAGTAG 1

RESULT 1017
AAF80752/c
ID AAF80752 standard; DNA; 20 BP.
XX
XX AAF80752;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #126.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 936 AGAAGCAGTAGCAGTGAATC 955
Db 20 AGAAGCAGTAGCAGTGAATC 1

RESULT 1018
AAF80781/c
ID AAF80781 standard; DNA; 20 BP.
XX
XX AAF80781;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #155.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1226 CACTTCATGCAATGAAATGA 1245
Db 20 CACTTCATGCAATGAAATGA 1

RESULT 1019
AAF80815/c
ID AAF80815 standard; DNA; 20 BP.
XX
XX AAF80815;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #189.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1617 GAACCTTGTGTGATTGTGCA 1636
Db 20 GAACCTTGTGTGATTGTGCA 1

RESULT 1020
AAF80822/c
ID AAF80822 standard; DNA; 20 BP.
XX
XX AAF80822;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #196.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 CCTGCTTTACATGTGCAAG 1709
Db 20 CCTGCTTTACATGTGCAAG 1

RESULT 1021

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AAF80824/c
ID AAF80824 standard; DNA; 20 BP.
XX
AC AAF80824;

DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #198.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1710 AAGCTAAAGAAAGGAATAA 1729
DB 20 AAGCTAAAGAAAGGAATAA 1

RESULT 1022
AAF80825/c
ID AAF80825 standard; DNA; 20 BP.
XX
AC AAF80825;

DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #199.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1720 AAAGGAATAAGCCTGCCCA 1739
DB 20 AAAGGAATAAGCCTGCCCA 1

RESULT 1023
AAF80841/c
ID AAF80841 standard; DNA; 20 BP.
XX
AC AAF80841;

DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #215.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1872 AAGTGAGAAATGCCTCAAT 1891
DB 20 AAGTGAGAAATGCCTCAAT 1

RESULT 1024
AAF80844/c
ID AAF80844 standard; DNA; 20 BP.
XX
AC AAF80844;

DT 02-MAY-2001 (first entry)
XX

DE Human mdm2 phosphorothioate oligonucleotide #218.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1898 AGATTCTTCTCTTTAGTAT 1917
DB 20 AGATTCTTCTCTTTAGTAT 1

RESULT 1025
AAF80854/c
ID AAF80854 standard; DNA; 20 BP.
XX
AC AAF80854;

DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #228.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1973 ATGTAGCTCATCCTTTACAC 1992
DB 20 ATGTAGCTCATCCTTTACAC 1

RESULT 1026
AAF80857/c
ID AAF80857 standard; DNA; 20 BP.
XX
AC AAF80857;

DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #231.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1997 TCCTAATTTTAAATAATTC 2016
DB 20 TCCTAATTTTAAATAATTC 1

RESULT 1027
AAF80667/c
ID AAF80667 standard; DNA; 20 BP.
XX
AC AAF80667;

DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #41.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 GATCCTGCTGCTTTTCGAGC 124
Db 20 GATCCTGCTGCTTTTCGAGC 1

RESULT 1028
AAF80670/c
ID AAF80670 standard; DNA; 20 BP.
XX AC AAF80670;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #44.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 AGTGGGTACGAGCGCCCGAGT 169
Db 20 AGTGGGTACGAGCGCCCGAGT 1

RESULT 1029
AAF80672/c
ID AAF80672 standard; DNA; 20 BP.
XX AC AAF80672;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #46.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 CCAGTGCCTGCGCCCGAGA 184
Db 20 CCAGTGCCTGCGCCCGAGA 1

RESULT 1030
AAF80675/c
ID AAF80675 standard; DNA; 20 BP.
XX AC AAF80675;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #49.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 208 GGGGTGCTGCTTCGCGAGTA 227
Db 20 GGGGTGCTGCTTCGCGAGTA 1

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RESULT 1031
AAF80682/c
ID AAF80682 standard; DNA; 20 BP.
XX AC AAF80682;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #56.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 297 GTGAGGAGCAGGCAAAATGTG 316
Db 20 GTGAGGAGCAGGCAAAATGTG 1

RESULT 1032
AAF80683/c
ID AAF80683 standard; DNA; 20 BP.
XX AC AAF80683;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #57.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 298 TGAGGAGCAGGCAAAATGTG 317
Db 20 TGAGGAGCAGGCAAAATGTG 1

RESULT 1033
AAF80704/c
ID AAF80704 standard; DNA; 20 BP.
XX AC AAF80704;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #78.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 386 GACCTGCTTAGACCAAGC 405
Db 20 GACCTGCTTAGACCAAGC 1

RESULT 1034
AAF80706/c
ID AAF80706 standard; DNA; 20 BP.
XX AC AAF80706;
XX DT 02-MAY-2001 (first entry)

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XX Human mdm2 phosphorothioate oligonucleotide #80.
DE
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
KW
XX
XX
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 AGCCATTGCTTTTGAAGTTA 422
DB 20 AGCCATTGCTTTTGAAGTTA 1

RESULT 1035
AAF80734/c
ID AAF80734 standard; DNA; 20 BP.
XX
AC AAF80734;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #108.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 727 TACAAGAGCTTCAGAGAG 746
DB 20 TACAAGAGCTTCAGAGAG 1

RESULT 1036
AAF80736/c
ID AAF80736 standard; DNA; 20 BP.
XX
AC AAF80736;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #110.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 752 TTCATCTTCACATTTGGTTT 771
DB 20 TTCATCTTCACATTTGGTTT 1

RESULT 1037
AAF80741/c
ID AAF80741 standard; DNA; 20 BP.
XX
AC AAF80741;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #115.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 810 GAGACAGAGAAAATTCAGA 829
DB 20 GAGACAGAGAAAATTCAGA 1

RESULT 1038
AAF80747/c
ID AAF80747 standard; DNA; 20 BP.
XX
AC AAF80747;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #121.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 880 CCCTTTCCTTTGATGAAAGC 899
DB 20 CCCTTTCCTTTGATGAAAGC 1

RESULT 1039
AAF80772/c
ID AAF80772 standard; DNA; 20 BP.
XX
AC AAF80772;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #146.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1124 AGATGATGAGGTATATCAAG 1143
DB 20 AGATGATGAGGTATATCAAG 1

RESULT 1040
AAF80797/c
ID AAF80797 standard; DNA; 20 BP.
XX
AC AAF80797;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #171.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1434 GTTGAGGAAAATGATGATAA 1453
DB 20 GTTGAGGAAAATGATGATAA 1
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RESULT 1041
AAF80811/c
ID AAF80811 standard; DNA; 20 BP.
XX
XX AAF80811;
AC AAF80811;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #185.
DE
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1560 GAAGAAACCCCAAGCAAGA 1579
Db 20 GAAGAAACCCCAAGCAAGA 1

RESULT 1042
AAF80814/c
ID AAF80814 standard; DNA; 20 BP.
XX
XX AAF80814;
AC AAF80814;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #188.
DE
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1605 CTTAATGCCATTGAACCTTG 1624
Db 20 CTTAATGCCATTGAACCTTG 1

RESULT 1043
AAF80816/c
ID AAF80816 standard; DNA; 20 BP.
XX
XX AAF80816;
AC AAF80816;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #190.
DE
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1624 GTGTGATTGTCAAGGTCGA 1643
Db 20 GTGTGATTGTCAAGGTCGA 1

RESULT 1044
AAF80853/c
ID AAF80853 standard; DNA; 20 BP.
XX
XX AAF80853;
AC AAF80853;
XX

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DT 02-MAY-2001 (first entry)
XX
XX Human mdm2 phosphorothioate oligonucleotide #227.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1969 GAATATGTAGCTCATCCTTT 1988
Db 20 GAATATGTAGCTCATCCTTT 1

RESULT 1045
AAF80869/c
ID AAF80869 standard; DNA; 20 BP.
XX
XX AAF80869;
AC AAF80869;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #243.
DE
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2140 GGGTGATCTGGCTCACTGC 2159
Db 20 GGGTGATCTGGCTCACTGC 1

RESULT 1046
AAF80875/c
ID AAF80875 standard; DNA; 20 BP.
XX
XX AAF80875;
AC AAF80875;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #249.
DE
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2198 TCAGCCTCCCAATTAGCTTG 2217
Db 20 TCAGCCTCCCAATTAGCTTG 1

RESULT 1047
AAF80632/c
ID AAF80632 standard; DNA; 20 BP.
XX
XX AAF80632;
AC AAF80632;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #6.
DE
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

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Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 CTCCAAGCGCGAAACCCCG 292
DB 20 CTCCAAGCGCGAAACCCCG 1

RESULT 1048
AAF80637/c
ID AAF80637 standard; DNA; 20 BP.

XX AAF80637;
XX

DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #11.
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1047 AGTGTAGAAATTGAAGTTGA 1066
DB 20 AGTGTAGAAATTGAAGTTGA 1

RESULT 1049
AAF80657/c
ID AAF80657 standard; DNA; 20 BP.

XX AAF80657;
XX

DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #31.
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCGCGCGAGCTGGCTGCTT 23
DB 20 CCGCGCGAGCTGGCTGCTT 1

RESULT 1050
AAF80679/c
ID AAF80679 standard; DNA; 20 BP.

XX AAF80679;
XX

DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #53.
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 GATGCTGAGGACGAGGCAAA 312
DB 20 GATGCTGAGGACGAGGCAAA 1

RESULT 1051
AAF80686/c
ID AAF80686 standard; DNA; 20 BP.
XX AAF80686;
XX

DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #60.
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 GGAGCAGGCAAAATGTGCAAT 320
DB 20 GGAGCAGGCAAAATGTGCAAT 1

RESULT 1052
AAF80732/c
ID AAF80732 standard; DNA; 20 BP.

XX AAF80732;
XX

DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #106.
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 704 TGGGAGTGATCAAAAGGACC 723
DB 20 TGGGAGTGATCAAAAGGACC 1

RESULT 1053
AAF80739/c
ID AAF80739 standard; DNA; 20 BP.

XX AAF80739;
XX

DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #113.
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 787 CATCTAGAAGGAGAGCAATT 806
DB 20 CATCTAGAAGGAGAGCAATT 1

RESULT 1054
AAF80761/c
ID AAF80761 standard; DNA; 20 BP.

XX AAF80761;
AC AAF80761;

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XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #135.
XX DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1034 TTCAGATCAGTTTAGTGTAG 1053
DB 20 TTCAGATCAGTTTAGTGTAG 1

RESULT 1055
AAF80764/c
ID AAF80764 standard; DNA; 20 BP.
XX AC AAF80764;
XX
DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #138.
XX DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1059 GAAGTTGAATCTCTCGACTC 1078
DB 20 GAAGTTGAATCTCTCGACTC 1

RESULT 1056
AAF80809/c
ID AAF80809 standard; DNA; 20 BP.
XX AC AAF80809;
XX
DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #183.
XX DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1541 TGTGAAAGAGTTTGAAAGGG 1560
DB 20 TGTGAAAGAGTTTGAAAGGG 1

RESULT 1057
AAF80849/c
ID AAF80849 standard; DNA; 20 BP.
XX AC AAF80849;
XX
DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #223.
XX DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #135.
XX DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1933 GTAGTGAATAGTAATACT 1952
DB 20 GTAGTGAATAGTAATACT 1

RESULT 1058
AAF80879/c
ID AAF80879 standard; DNA; 20 BP.
XX AC AAF80879;
XX
DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #253.
XX DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2218 GCCTACAGTCATCTGCCACC 2237
DB 20 GCCTACAGTCATCTGCCACC 1

RESULT 1059
AAF80658/c
ID AAF80658 standard; DNA; 20 BP.
XX AC AAF80658;
XX
DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #32.
XX DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TTGGCTGCTTCTGGGGCCCTG 33
DB 20 TTGGCTGCTTCTGGGGCCCTG 1

RESULT 1060
AAF80660/c
ID AAF80660 standard; DNA; 20 BP.
XX AC AAF80660;
XX
DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #34.
XX DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GCCTGTGTGGCCCTGTGTGT 48
DB 20 GCCTGTGTGGCCCTGTGTGT 48

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Db      20 GCCTGTGTGGCCCTGTGTGT 1

RESULT 1061
AAF8068/c
ID AAF80668 standard; DNA; 20 BP.
XX
XX AAF80668;
AC
XX
XX
DT 02-MAY-2001 (first entry)
XX
XX Human mdm2 phosphorothioate oligonucleotide #42.
DE
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      113 TGCCTTCCGAGCAGGAGCA 132
Db      20 TGCCTTCCGAGCAGGAGCA 1

RESULT 1062
AAF80678/c
ID AAF80678 standard; DNA; 20 BP.
XX
XX AAF80678;
AC
XX
XX
DT 02-MAY-2001 (first entry)
XX
XX Human mdm2 phosphorothioate oligonucleotide #52.
DE
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      289 CCCGATGCTGAGGAGCAGG 308
Db      20 CCCGATGCTGAGGAGCAGG 1

RESULT 1063
AAF80709/c
ID AAF80709 standard; DNA; 20 BP.
XX
XX AAF80709;
AC
XX
XX
DT 02-MAY-2001 (first entry)
XX
XX Human mdm2 phosphorothioate oligonucleotide #83.
DE
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      477 TATCTTGGCCAGTATATTAT 496
Db      20 TATCTTGGCCAGTATATTAT 1

RESULT 1064
AAF80714/c
ID AAF80714 standard; DNA; 20 BP.
XX

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AC AAF80714;
XX
XX 02-MAY-2001 (first entry)
XX
XX Human mdm2 phosphorothioate oligonucleotide #88.
DE
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      525 CAACATATTGTATATTGTTTC 544
Db      20 CAACATATTGTATATTGTTTC 1

RESULT 1065
AAF80723/c
ID AAF80723 standard; DNA; 20 BP.
XX
XX AAF80723;
AC
XX
XX
DT 02-MAY-2001 (first entry)
XX
XX Human mdm2 phosphorothioate oligonucleotide #97.
DE
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      600 AGGAAATATATACCATGAT 619
Db      20 AGGAAATATATACCATGAT 1

RESULT 1066
AAF80724/c
ID AAF80724 standard; DNA; 20 BP.
XX
XX AAF80724;
AC
XX
XX
DT 02-MAY-2001 (first entry)
XX
XX Human mdm2 phosphorothioate oligonucleotide #98.
DE
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      609 TATACCATGATCTTACAGGAA 628
Db      20 TATACCATGATCTTACAGGAA 1

RESULT 1067
AAF80750/c
ID AAF80750 standard; DNA; 20 BP.
XX
XX AAF80750;
AC
XX
XX
DT 02-MAY-2001 (first entry)
XX
XX Human mdm2 phosphorothioate oligonucleotide #124.
DE
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

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XX
Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 915 ATAAGGGAGATATGTTGTGA 934
DB 20 ATAAGGGAGATATGTTGTGA 1

RESULT 1068
AAF80768/c
ID AAF80768 standard; DNA; 20 BP.
XX
AC AAF80768;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #142.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1092 CTTAGTGAAGAGGCAAGA 1111
DB 20 CTTAGTGAAGAGGCAAGA 1

RESULT 1069
AAF80771/c
ID AAF80771 standard; DNA; 20 BP.
XX
AC AAF80771;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #145.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1115 CTCAGATGAAGATGATGAGG 1134
DB 20 CTCAGATGAAGATGATGAGG 1

RESULT 1070
AAF80813/c
ID AAF80813 standard; DNA; 20 BP.
XX
AC AAF80813;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #187.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1580 AGAGAGTGTGGAATCTAGTT 1599

XX
Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 915 ATAAGGGAGATATGTTGTGA 934
DB 20 ATAAGGGAGATATGTTGTGA 1

RESULT 1071
AAF80874/c
ID AAF80874 standard; DNA; 20 BP.
XX
AC AAF80874;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #248.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2191 TCCTGCCTCAGCTCCCAAT 2210
DB 20 TCCTGCCTCAGCTCCCAAT 1

RESULT 1072
AAF80881/c
ID AAF80881 standard; DNA; 20 BP.
XX
AC AAF80881;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #255.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2253 TTTGTACTTTTGTAGTAGAGAC 2272
DB 20 TTTGTACTTTTGTAGTAGAGAC 1

RESULT 1073
AAF80885/c
ID AAF80885 standard; DNA; 20 BP.
XX
AC AAF80885;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #259.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2290 GCCAGGATGCTTCGATCTC 2309
DB 20 GCCAGGATGCTTCGATCTC 1

RESULT 1074
AAF80887/c
ID AAF80887 standard; DNA; 20 BP.
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XX AAF80887;
AC
XX
DT 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #261.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2307 CTCCTGACCTCGTGATCCGC 2326
Db 20 CTCCTGACCTCGTGATCCGC 1

RESULT 1075
AAF80663/c
ID AAF80663 standard; DNA; 20 BP.
XX
AC AAF80663;
XX
DT 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #37.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 GGAAGAATGGAGCAAGAGC 69
Db 20 GGAAGAATGGAGCAAGAGC 1

RESULT 1076
AAF80665/c
ID AAF80665 standard; DNA; 20 BP.
XX
AC AAF80665;
XX
DT 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #39.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 CGAGCCCGAGGGCGGCGGC 89
Db 20 CGAGCCCGAGGGCGGCGGC 1

RESULT 1077
AAF80669/c
ID AAF80669 standard; DNA; 20 BP.
XX
AC AAF80669;
XX
DT 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #43.
XX

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KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 GCAGCCGAGGACCGTCCC 139
Db 20 GCAGCCGAGGACCGTCCC 1

RESULT 1078
AAF80717/c
ID AAF80717 standard; DNA; 20 BP.
XX
AC AAF80717;
XX
DT 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #91.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 549 GATCTTCTAGGAGATTGTT 568
Db 20 GATCTTCTAGGAGATTGTT 1

RESULT 1079
AAF80738/c
ID AAF80738 standard; DNA; 20 BP.
XX
AC AAF80738;
XX
DT 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #112.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 774 AGACCATCTACCTCATCTAG 793
Db 20 AGACCATCTACCTCATCTAG 1

RESULT 1080
AAF80754/c
ID AAF80754 standard; DNA; 20 BP.
XX
AC AAF80754;
XX
DT 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #128.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 774 AGACCATCTACCTCATCTAG 793
Db 20 AGACCATCTACCTCATCTAG 1

RESULT 1080
AAF80754/c
ID AAF80754 standard; DNA; 20 BP.
XX
AC AAF80754;
XX
DT 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #128.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 964 CGCCATCGAATCCGATCTT 983
 DB 20 CGCCATCGAATCCGATCTT 1

RESULT 1081

AAF80775/c

ID AAF80775 standard; DNA; 20 BP.

XX AC AAF80775;

XX 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #149.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1161 GGGGAGAGTGATACAGATTC 1180

DB 20 GGGGAGAGTGATACAGATTC 1

RESULT 1082

AAF80780/c

ID AAF80780 standard; DNA; 20 BP.

XX AC AAF80780;

XX 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #154.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1220 GAAATGCATTCATGCAATG 1239

DB 20 GAAATGCATTCATGCAATG 1

RESULT 1083

AAF80806/c

ID AAF80806 standard; DNA; 20 BP.

XX AC AAF80806;

XX 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #180.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1517 CATTATTATAGCAGCCAAG 1536

DB 20 CATTATTATAGCAGCCAAG 1

RESULT 1084

AAF80829/c

ID AAF80829 standard; DNA; 20 BP.

XX AC AAF80829;

XX 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #203.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1757 TCAAATGATTGTGCTAACTT 1776

DB 20 TCAAATGATTGTGCTAACTT 1

RESULT 1085

AAF80851/c

ID AAF80851 standard; DNA; 20 BP.

XX AC AAF80851;

XX 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #225.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1948 ATACTTACTATAATTGACT 1967

DB 20 ATACTTACTATAATTGACT 1

RESULT 1086

AAF80864/c

ID AAF80864 standard; DNA; 20 BP.

XX AC AAF80864;

XX 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #238.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2103 ACCGAGTCTTGTCTCTTAC 2122

DB 20 ACCGAGTCTTGTCTCTTAC 1

RESULT 1087

AAF80867/c

ID AAF80867 standard; DNA; 20 BP.

XX AC AAF80867;

XX 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #241.

XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
KW
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2123 CCAGGCTGGAGTGCAGTGGG 2142
DB 20 CCAGGCTGGAGTGCAGTGGG 1

RESULT 1088
AAF80677/c
ID AAF80677 standard; DNA; 20 BP.
XX
AC AAF80677;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #51.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 AGGAACTGGGAGTCTTGA 261
DB 20 AGGAACTGGGAGTCTTGA 1

RESULT 1089
AAF80707/c
ID AAF80707 standard; DNA; 20 BP.
XX
AC AAF80707;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #81.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 422 ATTAAGTCTGTGTGCAC 441
DB 20 ATTAAGTCTGTGTGCAC 1

RESULT 1090
AAF80722/c
ID AAF80722 standard; DNA; 20 BP.
XX
AC AAF80722;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #96.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 593 AGAGCACAGGAAATATATA 612
DB 20 AGAGCACAGGAAATATATA 1

RESULT 1091
AAF80731/c
ID AAF80731 standard; DNA; 20 BP.
XX
AC AAF80731;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #105.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 691 GTCACCTTGAAGTGGGAGT 710
DB 20 GTCACCTTGAAGTGGGAGT 1

RESULT 1092
AAF80737/c
ID AAF80737 standard; DNA; 20 BP.
XX
AC AAF80737;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #111.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 761 ACATTGGTTTCTAGACCAT 780
DB 20 ACATTGGTTTCTAGACCAT 1

RESULT 1093
AAF80757/c
ID AAF80757 standard; DNA; 20 BP.
XX
AC AAF80757;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #131.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 996 AGTGAACATTTCAGGTGATTG 1015
DB 20 AGTGAACATTTCAGGTGATTG 1

RESULT 1094

DE Human mdm2 phosphorothioate oligonucleotide #195.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1684 TTATGCCCTGCTTACATGT 1703
DB 20 TTATGCCCTGCTTACATGT 1

RESULT 1098
AAF80838/c
ID AAF80838 standard; DNA; 20 BP.
XX
AC AAF80838;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #212.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1850 TGAATAATTTCACATATAT 1869
DB 20 TGAATAATTTCACATATAT 1

RESULT 1099
AAF80843/c
ID AAF80843 standard; DNA; 20 BP.
XX
AC AAF80843;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #217.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1889 AATTCACATAGATTCTTCT 1908
DB 20 AATTCACATAGATTCTTCT 1

RESULT 1100
AAF80872/c
ID AAF80872 standard; DNA; 20 BP.
XX
AC AAF80872;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #246.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1333 TCTCTGAGAAGCCAAACTG 1352
DB 20 TCTCTGAGAAGCCAAACTG 1

RESULT 1097
AAF80821/c
ID AAF80821 standard; DNA; 20 BP.
XX
AC AAF80821;
XX
DT 02-MAY-2001 (first entry)
XX

DE Human mdm2 phosphorothioate oligonucleotide #151.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1184 TGAAGAAGATCCTGAAAATT 1203
DB 20 TGAAGAAGATCCTGAAAATT 1

RESULT 1095
AAF80782/c
ID AAF80782 standard; DNA; 20 BP.
XX
AC AAF80782;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #156.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1257 CCATCATTTGCACAGATG 1276
DB 20 CCATCATTTGCACAGATG 1

RESULT 1096
AAF80790/c
ID AAF80790 standard; DNA; 20 BP.
XX
AC AAF80790;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #164.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1333 TCTCTGAGAAGCCAAACTG 1352
DB 20 TCTCTGAGAAGCCAAACTG 1

RESULT 1097
AAF80821/c
ID AAF80821 standard; DNA; 20 BP.
XX
AC AAF80821;
XX
DT 02-MAY-2001 (first entry)
XX

DE Human mdm2 phosphorothioate oligonucleotide #195.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1684 TTATGCCCTGCTTACATGT 1703
DB 20 TTATGCCCTGCTTACATGT 1

RESULT 1098
AAF80838/c
ID AAF80838 standard; DNA; 20 BP.
XX
AC AAF80838;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #212.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1850 TGAATAATTTCACATATAT 1869
DB 20 TGAATAATTTCACATATAT 1

RESULT 1099
AAF80843/c
ID AAF80843 standard; DNA; 20 BP.
XX
AC AAF80843;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #217.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1889 AATTCACATAGATTCTTCT 1908
DB 20 AATTCACATAGATTCTTCT 1

RESULT 1100
AAF80872/c
ID AAF80872 standard; DNA; 20 BP.
XX
AC AAF80872;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #246.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1333 TCTCTGAGAAGCCAAACTG 1352
DB 20 TCTCTGAGAAGCCAAACTG 1

RESULT 1097
AAF80821/c
ID AAF80821 standard; DNA; 20 BP.
XX
AC AAF80821;
XX
DT 02-MAY-2001 (first entry)
XX

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2176 GGGTTGCGACCAATTCCTCG 2195
Db 20 GGGTTGCGACCAATTCCTCG 1

RESULT 1101
AAF80876/c
ID AAF80876 standard; DNA; 20 BP.
XX
AC AAF80876;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #250.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2202 CCTCCCAATTAGCTTGGCCT 2221
Db 20 CCTCCCAATTAGCTTGGCCT 1

RESULT 1102
AAF80882/c
ID AAF80882 standard; DNA; 20 BP.
XX
AC AAF80882;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #256.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2265 GTAGAGACAGGGTTTCACCG 2284
Db 20 GTAGAGACAGGGTTTCACCG 1

RESULT 1103
AAF80691/c
ID AAF80691 standard; DNA; 20 BP.
XX
AC AAF80691;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #65.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 307 GGCAAAATGTGCAATACCAAC 326
Db 20 GGCAAAATGTGCAATACCAAC 1
```

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RESULT 1104
AAF80692/c
ID AAF80692 standard; DNA; 20 BP.
XX
AC AAF80692;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #66.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 308 GCAAATGTGCAATACCAACA 327
Db 20 GCAAATGTGCAATACCAACA 1

RESULT 1105
AAF80730/c
ID AAF80730 standard; DNA; 20 BP.
XX
AC AAF80730;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #104.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 682 AGAACAGGTGTTCACCTTGAA 701
Db 20 AGAACAGGTGTTCACCTTGAA 1

RESULT 1106
AAF80759/c
ID AAF80759 standard; DNA; 20 BP.
XX
AC AAF80759;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #133.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1017 TTGGATCAGGATTCAGTTTC 1036
Db 20 TTGGATCAGGATTCAGTTTC 1

RESULT 1107
AAF80766/c
ID AAF80766 standard; DNA; 20 BP.
XX
AC AAF80766;
XX
DT 02-MAY-2001 (first entry)
```

XX Human mdm2 phosphorothioate oligonucleotide #140.
 XX Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1077 TCAGAAGATTATAGCCTTAG 1096
 DB 20 TCAGAAGATTATAGCCTTAG 1

RESULT 1108
 AAF80792/c
 ID AAF80792 standard; DNA; 20 BP.

XX AAF80792;
 XX 02-MAY-2001 (first entry)
 XX Human mdm2 phosphorothioate oligonucleotide #166.
 XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1358 CTCAACACACAGCTGAAGAGG 1377
 DB 20 CTCAACACACAGCTGAAGAGG 1

RESULT 1109
 AAF80796/c
 ID AAF80796 standard; DNA; 20 BP.

XX AAF80796;
 XX 02-MAY-2001 (first entry)
 XX Human mdm2 phosphorothioate oligonucleotide #170.
 XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1421 CAGAGACTCATGTGTTGAGG 1440
 DB 20 CAGAGACTCATGTGTTGAGG 1

RESULT 1110
 AAF80818/c
 ID AAF80818 standard; DNA; 20 BP.

XX AAF80818;
 XX 02-MAY-2001 (first entry)
 XX Human mdm2 phosphorothioate oligonucleotide #192.
 XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1657 GCATTGTCCATGGCAAAACA 1676
 DB 20 GCATTGTCCATGGCAAAACA 1

RESULT 1111
 AAF80835/c
 ID AAF80835 standard; DNA; 20 BP.

XX AAF80835;
 XX 02-MAY-2001 (first entry)
 XX Human mdm2 phosphorothioate oligonucleotide #209.
 XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1823 TATATAACCCCTAGGAATTTA 1842
 DB 20 TATATAACCCCTAGGAATTTA 1

RESULT 1112
 AAF80858/c
 ID AAF80858 standard; DNA; 20 BP.

XX AAF80858;
 XX 02-MAY-2001 (first entry)
 XX Human mdm2 phosphorothioate oligonucleotide #232.
 XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2004 TTTAAATAATTTCTACTCTG 2023
 DB 20 TTTAAATAATTTCTACTCTG 1

RESULT 1113
 AAF80865/c
 ID AAF80865 standard; DNA; 20 BP.

XX AAF80865;
 XX 02-MAY-2001 (first entry)
 XX Human mdm2 phosphorothioate oligonucleotide #239.
 XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2111 TTGCTCTGTATCCAGGCTG 2130
 DB 20 TTGCTCTGTATCCAGGCTG 1

```

RESULT 1114
AAF80870/c
ID AAF80870 standard; DNA; 20 BP.
XX
XX AAF80870;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #244.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX

QY 2146 TCTTGGCTCACTGCAAGCTC 2165
DB 20 TCTTGGCTCACTGCAAGCTC 1

RESULT 1115
AAF80891/c
ID AAF80891 standard; DNA; 20 BP.
XX
XX AAF80891;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #265.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX

QY 2341 CAAAGTGCTGGGATTACAGG 2360
DB 20 CAAAGTGCTGGGATTACAGG 1

RESULT 1116
AAF80630/c
ID AAF80630 standard; DNA; 20 BP.
XX
XX AAF80630;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #4.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX

QY 147 ATTAGTGGCTAGGAGCGCC 166
DB 20 ATTAGTGGCTAGGAGCGCC 1

RESULT 1117
AAF80631/c
ID AAF80631 standard; DNA; 20 BP.
XX
XX AAF80631;
XX

RESULT 1118
AAF80661/c
ID AAF80661 standard; DNA; 20 BP.
XX
XX AAF80661;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #35.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX

QY 181 GAGAGTGGGAATGATCCCCGA 200
DB 20 GAGAGTGGGAATGATCCCCGA 1

RESULT 1119
AAF80662/c
ID AAF80662 standard; DNA; 20 BP.
XX
XX AAF80662;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #36.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX

QY 34 TGTGGCCCTGTGTTCGGA 53
DB 20 TGTGGCCCTGTGTTCGGA 1

RESULT 1120
AAF80684/c
ID AAF80684 standard; DNA; 20 BP.
XX
XX AAF80684;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #58.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX

QY 43 GTGTGTCGGAAGATGGAGC 62
DB 20 GTGTGTCGGAAGATGGAGC 1

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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 299 GAGGAGCAGGCAATGTGCA 318
Db 20 GAGGAGCAGGCAATGTGCA 1

RESULT 1121
AAF80685/c
ID AAF80685 standard; DNA; 20 BP.
XX
AC AAF80685;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #59.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 AGGAGCAGGCAATGTGCAA 319
Db 20 AGGAGCAGGCAATGTGCAA 1

RESULT 1122
AAF80726/c
ID AAF80726 standard; DNA; 20 BP.
XX
AC AAF80726;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #100.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 634 TAGTAGTCAATCAGCAGAA 653
Db 20 TAGTAGTCAATCAGCAGAA 1

RESULT 1123
AAF80749/c
ID AAF80749 standard; DNA; 20 BP.
XX
AC AAF80749;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #123.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 904 CTCTGTGTGTAATAAGGAG 923
Db 20 CTCTGTGTGTAATAAGGAG 1

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 1124
AAF80753/c
ID AAF80753 standard; DNA; 20 BP.
XX
AC AAF80753;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #127.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 949 GTGAATCTACAGGACGCCA 968
Db 20 GTGAATCTACAGGACGCCA 1

RESULT 1125
AAF80783/c
ID AAF80783 standard; DNA; 20 BP.
XX
AC AAF80783;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #157.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1268 CAACAGATGTTGGCCCTTC 1287
Db 20 CAACAGATGTTGGCCCTTC 1

RESULT 1126
AAF80793/c
ID AAF80793 standard; DNA; 20 BP.
XX
AC AAF80793;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #167.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1368 GCTGAAGAGGGCTTTGATGT 1387
Db 20 GCTGAAGAGGGCTTTGATGT 1

RESULT 1127
AAF80799/c
ID AAF80799 standard; DNA; 20 BP.
XX
AC AAF80799;
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XX 02-MAY-2001 (first entry)
DT Human mdm2 phosphorothioate oligonucleotide #173.
DE Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1449 GATAAAATTACACAGCTTC 1468
DB 20 GATAAAATTACACAGCTTC 1

RESULT 1128
AAF80832/c
ID AAF80832 standard; DNA; 20 BP.
XX
AC AAF80832;
XX
DT 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #206.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1804 AGAATTATATATTTCTAACT 1823
DB 20 AGAATTATATATTTCTAACT 1

RESULT 1129
AAF80833/c
ID AAF80833 standard; DNA; 20 BP.
XX
AC AAF80833;
XX
DT 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #207.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1808 TTATATATTTCTAACTATAT 1827
DB 20 TTATATATTTCTAACTATAT 1

RESULT 1130
AAF80847/c
ID AAF80847 standard; DNA; 20 BP.
XX
AC AAF80847;
XX
DT 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #221.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1913 AGTATAATTGACCTACTTTG 1932
DB 20 AGTATAATTGACCTACTTTG 1

RESULT 1131
AAF80873/c
ID AAF80873 standard; DNA; 20 BP.
XX
AC AAF80873;
XX
DT 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #247.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2185 CCATTCTCTGCTCAGCCT 2204
DB 20 CCATTCTCTGCTCAGCCT 1

RESULT 1132
AAF80642/c
ID AAF80642 standard; DNA; 20 BP.
XX
AC AAF80642;
XX
DT 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #16.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1818 CTAATATATATACCTAGGA 1837
DB 20 CTAATATATATACCTAGGA 1

RESULT 1133
AAF80664/c
ID AAF80664 standard; DNA; 20 BP.
XX
AC AAF80664;
XX
DT 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #38.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 CAAAGAGCCGAGCCGAGGG 81
DB 62 CAAAGAGCCGAGCCGAGGG 81
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Db      20 CAAGAGCCGAGCCGAGGG 1

RESULT 1134
AAF80673/c
ID AAF80673 standard; DNA; 20 BP.
XX
AC AAF80673;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #47.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      174 TGGCCCGAGAGTGAATGA 193
      |||||
Db      20 TGGCCCGAGAGTGAATGA 1

RESULT 1135
AAF80697/c
ID AAF80697 standard; DNA; 20 BP.
XX
AC AAF80697;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #71.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      313 TGTGCAATACCAACATGCT 332
      |||||
Db      20 TGTGCAATACCAACATGCT 1

RESULT 1136
AAF80703/c
ID AAF80703 standard; DNA; 20 BP.
XX
AC AAF80703;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #77.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      372 GCTTCGGAAACAGACCCT 391
      |||||
Db      20 GCTTCGGAAACAGACCCT 1

RESULT 1137
AAF80716/c
ID AAF80716 standard; DNA; 20 BP.
XX

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AC AAF80716;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #90.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      538 ATTGTTCAAATGATCTTCTA 557
      |||||
Db      20 ATTGTTCAAATGATCTTCTA 1

RESULT 1138
AAF80746/c
ID AAF80746 standard; DNA; 20 BP.
XX
AC AAF80746;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #120.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      867 TCTGATAGTATTCCCTTTC 886
      |||||
Db      20 TCTGATAGTATTCCCTTTC 1

RESULT 1139
AAF80760/c
ID AAF80760 standard; DNA; 20 BP.
XX
AC AAF80760;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #134.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1023 CAGGATTCAGTTTCAGATCA 1042
      |||||
Db      20 CAGGATTCAGTTTCAGATCA 1

RESULT 1140
AAF80773/c
ID AAF80773 standard; DNA; 20 BP.
XX
AC AAF80773;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #147.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

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XX
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1135 TATATCAAGTTACTGTGTAT 1154
    |||||
Db 20 TATATCAAGTTACTGTGTAT 1

RESULT 1141
AAF80774/c
ID AAF80774 standard; DNA; 20 BP.
XX
AC AAF80774;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #148.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 GTGTATCAGCGAGGGGAGAG 1168
    |||||
Db 20 GTGTATCAGCGAGGGGAGAG 1

RESULT 1142
AAF80776/c
ID AAF80776 standard; DNA; 20 BP.
XX
AC AAF80776;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #150.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1170 GATACAGATTTCATTGGAAGA 1189
    |||||
Db 20 GATACAGATTTCATTGGAAGA 1

RESULT 1143
AAF80804/c
ID AAF80804 standard; DNA; 20 BP.
XX
AC AAF80804;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #178.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1499 GCCATCAACTTCTAGTAGCA 1518
    |||||
Db 20 GCCATCAACTTCTAGTAGCA 1

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 CCCAGTATGTAGACAACCAA 1755
    |||||
Db 20 CCCAGTATGTAGACAACCAA 1

RESULT 1145
AAF80830/c
ID AAF80830 standard; DNA; 20 BP.
XX
AC AAF80830;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #204.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1787 GTTGACCTGTCTATAAGAGA 1806
    |||||
Db 20 GTTGACCTGTCTATAAGAGA 1

RESULT 1146
AAF80856/c
ID AAF80856 standard; DNA; 20 BP.
XX
AC AAF80856;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #230.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1990 CACCAACTCTCTAATTTTAAA 2009
    |||||
Db 20 CACCAACTCTCTAATTTTAAA 1

RESULT 1147
AAF80863/c
ID AAF80863 standard; DNA; 20 BP.
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XX AAF80863;
AC
XX
DT
XX
XX 02-MAY-2001 (first entry)
DE Human mdm2 phosphorothioate oligonucleotide #237.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2072 CATTAAATGTAACCTATTATTA 2091
Db 20 CATTAAATGTAACCTATTATTA 1

RESULT 1148
AAF80890/c
ID AAF80890 standard; DNA; 20 BP.
XX
AC AAF80890;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #264.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2334 GGCCTCCCAAAGTCTGGGA 2353
Db 20 GGCCTCCCAAAGTCTGGGA 1

RESULT 1149
AAF80644/c
ID AAF80644 standard; DNA; 20 BP.
XX
AC AAF80644;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #18.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2132 AGTGCAGTGGGTGATCTTGG 2151
Db 20 AGTGCAGTGGGTGATCTTGG 1

RESULT 1150
AAF80645/c
ID AAF80645 standard; DNA; 20 BP.
XX
AC AAF80645;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #19.
XX

KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2224 AGTCATCTGCCACACACCT 2243
Db 20 AGTCATCTGCCACACACCT 1

RESULT 1151
AAF80666/c
ID AAF80666 standard; DNA; 20 BP.
XX
AC AAF80666;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #40.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 98 TGACCGAGATCTCTGCTGCTT 117
Db 20 TGACCGAGATCTCTGCTGCTT 1

RESULT 1152
AAF80680/c
ID AAF80680 standard; DNA; 20 BP.
XX
AC AAF80680;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #54.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 294 ATGCTGAGGAGCAGGCAAAAT 313
Db 20 ATGCTGAGGAGCAGGCAAAAT 1

RESULT 1153
AAF80693/c
ID AAF80693 standard; DNA; 20 BP.
XX
AC AAF80693;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #67.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 309 CAAATGTGCAATACCAACAT 328
Db 20 CAAATGTGCAATACCAACAT 1

RESULT 1154
AAF80696/c
ID AAF80696 standard; DNA; 20 BP.
XX
AC AAF80696;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #70.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 ATGTGCAATACCAACATGTC 331
Db 20 ATGTGCAATACCAACATGTC 1

RESULT 1155
AAF80699/c
ID AAF80699 standard; DNA; 20 BP.
XX
AC AAF80699;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #73.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 CAACATGCTGTACTACTG 342
Db 20 CAACATGCTGTACTACTG 1

RESULT 1156
AAF80701/c
ID AAF80701 standard; DNA; 20 BP.
XX
AC AAF80701;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #75.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 351 GTAACCACTCACAGATTCC 370
Db 20 GTAACCACTCACAGATTCC 1

RESULT 1157
AAF80713/c

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ID AAF80713 standard; DNA; 20 BP.
XX
AC AAF80713;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #87.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 515 TGAGAGCAACAACATATTG 534
Db 20 TGAGAGCAACAACATATTG 1

RESULT 1158
AAF80744/c
ID AAF80744 standard; DNA; 20 BP.
XX
AC AAF80744;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #118.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 844 AACGACAAAGAAAACGCCAC 863
Db 20 AACGACAAAGAAAACGCCAC 1

RESULT 1159
AAF80748/c
ID AAF80748 standard; DNA; 20 BP.
XX
AC AAF80748;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #122.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 895 AAAGCCTGGCTCTGTGTGTA 914
Db 20 AAAGCCTGGCTCTGTGTGTA 1

RESULT 1160
AAF80769/c
ID AAF80769 standard; DNA; 20 BP.
XX
AC AAF80769;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #143.

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XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
 KW
 XX

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1100 AGAAGGACAAGAACTCTCAG 1119
 ID AAF80770/c
 XX
 AC AAF80770;
 XX

RESULT 1161
 AAF80770/c
 ID AAF80770 standard; DNA; 20 BP.
 XX
 AC AAF80770;
 XX

DT 02-MAY-2001 (first entry)
 XX
 XX Human mdm2 phosphorothioate oligonucleotide #144.
 XX
 KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
 XX

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1105 GACAAGAACTCTCAGATGAA 1124
 ID AAF80800/c
 XX
 AC AAF80800;
 XX

RESULT 1162
 AAF80800/c
 ID AAF80800 standard; DNA; 20 BP.
 XX
 AC AAF80800;
 XX

DT 02-MAY-2001 (first entry)
 XX
 XX Human mdm2 phosphorothioate oligonucleotide #174.
 XX
 KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
 XX

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1456 TTACACAAGCTTCAATCA 1475
 ID AAF80855/c
 XX
 AC AAF80855;
 XX

RESULT 1163
 AAF80855/c
 ID AAF80855 standard; DNA; 20 BP.
 XX
 AC AAF80855;
 XX

DT 02-MAY-2001 (first entry)
 XX
 XX Human mdm2 phosphorothioate oligonucleotide #229.
 XX
 KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
 XX

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1982 ATCCTTTACCAACTCCTA 2001
 ID AAF80862/c
 XX
 AC AAF80862;
 XX

RESULT 1164
 AAF80862/c
 ID AAF80862 standard; DNA; 20 BP.
 XX
 AC AAF80862;
 XX

DT 02-MAY-2001 (first entry)
 XX
 XX Human mdm2 phosphorothioate oligonucleotide #236.
 XX
 KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
 XX

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2059 AATATCTATATGACATTTAA 2078
 ID AAF80871/c
 XX
 AC AAF80871;
 XX

RESULT 1165
 AAF80871/c
 ID AAF80871 standard; DNA; 20 BP.
 XX
 AC AAF80871;
 XX

DT 02-MAY-2001 (first entry)
 XX
 XX Human mdm2 phosphorothioate oligonucleotide #245.
 XX
 KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
 XX

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 TCACTGCAAGCTCTGCCCTC 2172
 ID AAF80877/c
 XX
 AC AAF80877;
 XX

RESULT 1166
 AAF80877/c
 ID AAF80877 standard; DNA; 20 BP.
 XX
 AC AAF80877;
 XX

DT 02-MAY-2001 (first entry)
 XX
 XX Human mdm2 phosphorothioate oligonucleotide #251.
 XX
 KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
 XX

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2210 TTAGCTTGGCCTACAGTCAT 2229
 ID AAF80885/c
 XX
 AC AAF80885;
 XX

RESULT 1167
 AAF80885/c
 ID AAF80885 standard; DNA; 20 BP.
 XX
 AC AAF80885;
 XX

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AAF80884/c
ID AAF80884 standard; DNA; 20 BP.
XX
AC AAF80884;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #258.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2283 CGTGTAGCCAGGATGGTCT 2302
DB 20 CGTGTAGCCAGGATGGTCT 1

RESULT 1168
AAF80628/c
ID AAF80628 standard; DNA; 20 BP.
XX
AC AAF80628;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #2.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 GGCCTGTGTGTCGGAAGA 56
DB 20 GGCCTGTGTGTCGGAAGA 1

RESULT 1169
AAF80698/c
ID AAF80698 standard; DNA; 20 BP.
XX
AC AAF80698;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #72.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 314 GTGCAATACCAACATGCTG 333
DB 20 GTGCAATACCAACATGCTG 1

RESULT 1170
AAF80711/c
ID AAF80711 standard; DNA; 20 BP.
XX
AC AAF80711;
XX
DT 02-MAY-2001 (first entry)
XX

DE Human mdm2 phosphorothioate oligonucleotide #85.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 496 TGACTAAACGATTATATGAT 515
DB 20 TGACTAAACGATTATATGAT 1

RESULT 1171
AAF80729/c
ID AAF80729 standard; DNA; 20 BP.
XX
AC AAF80729;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #103.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 669 ACATCTGTGAGTGAGAACAG 688
DB 20 ACATCTGTGAGTGAGAACAG 1

RESULT 1172
AAF80762/c
ID AAF80762 standard; DNA; 20 BP.
XX
AC AAF80762;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #136.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1046 TAGGTAGAAATTGAAAGTTG 1065
DB 20 TAGGTAGAAATTGAAAGTTG 1

RESULT 1173
AAF80787/c
ID AAF80787 standard; DNA; 20 BP.
XX
AC AAF80787;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #161.
XX
KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1301 TCCTGAAGATAAAGGGAAG 1320
DB 20 TCCTGAAGATAAAGGGAAG 1

RESULT 1174
AAF80794/c
ID AAF80794 standard; DNA; 20 BP.
XX AC AAF80794;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #168.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1401 AAACTATAGTGAATGATTC 1420
DB 20 AAACTATAGTGAATGATTC 1

RESULT 1175
AAF80805/c
ID AAF80805 standard; DNA; 20 BP.
XX AC AAF80805;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #179.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1506 ACTTCTAGTAGCATTATTTA 1525
DB 20 ACTTCTAGTAGCATTATTTA 1

RESULT 1176
AAF80807/c
ID AAF80807 standard; DNA; 20 BP.
XX AC AAF80807;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #181.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 TTTATAGCAGCCAGAGAT 1541
DB 20 TTTATAGCAGCCAGAGAT 1
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RESULT 1177
AAF80886/c
ID AAF80886 standard; DNA; 20 BP.
XX AC AAF80886;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #260.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2298 GGTCTCGATCTCTGACCTC 2317
DB 20 GGTCTCGATCTCTGACCTC 1

RESULT 1178
AAF80635/c
ID AAF80635 standard; DNA; 20 BP.
XX AC AAF80635;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #9.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 331 CTGTACCTACTGATGGTGCT 350
DB 20 CTGTACCTACTGATGGTGCT 1

RESULT 1179
AAF80636/c
ID AAF80636 standard; DNA; 20 BP.
XX AC AAF80636;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #10.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 617 GATCTACAGGAACCTTGGTAG 636
DB 20 GATCTACAGGAACCTTGGTAG 1

RESULT 1180
AAF80640/c
ID AAF80640 standard; DNA; 20 BP.
XX AC AAF80640;
XX DT 02-MAY-2001 (first entry)
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XX DE Human mdm2 phosphorothioate oligonucleotide #14.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1776 TATTTCCCTAGTTGACCTG 1795
Db 20 TATTTCCCTAGTTGACCTG 1

RESULT 1181
AAF80649/c
ID AAF80649 standard; DNA; 20 BP.
XX
AC AAF80649;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #23.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 GGCCCTGTGTGCGAAGA 56
Db 20 GGCCCTGTGTGCGAAGA 1

RESULT 1182
AAF80659/c
ID AAF80659 standard; DNA; 20 BP.
XX
AC AAF80659;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #33.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 GCTTCTGGGGCTGTGTGGC 39
Db 20 GCTTCTGGGGCTGTGTGGC 1

RESULT 1183
AAF80690/c
ID AAF80690 standard; DNA; 20 BP.
XX
AC AAF80690;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #64.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match      0.8%; Score 20; DB 1; Length 20;

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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 AGCAAAATGTGCAATACCAA 325
Db 20 AGCAAAATGTGCAATACCAA 1

RESULT 1184
AAF80702/c
ID AAF80702 standard; DNA; 20 BP.
XX
AC AAF80702;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #76.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 361 CACAGATTCAGCTTCGAA 380
Db 20 CACAGATTCAGCTTCGAA 1

RESULT 1185
AAF80712/c
ID AAF80712 standard; DNA; 20 BP.
XX
AC AAF80712;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #86.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 503 ACGATTATATGATGAGAAGC 522
Db 20 ACGATTATATGATGAGAAGC 1

RESULT 1186
AAF80721/c
ID AAF80721 standard; DNA; 20 BP.
XX
AC AAF80721;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human mdm2 phosphorothioate oligonucleotide #95.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 587 TGTGAAAGAGCACAGGAAAA 606
Db 20 TGTGAAAGAGCACAGGAAAA 1

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RESULT 1187
AAF80740/c
ID   AAF80740 standard; DNA; 20 BP.
XX
XX
AC   AAF80740;
XX
DT   02-MAY-2001 (first entry)
XX
DE   Human mdm2 phosphorothioate oligonucleotide #114.
XX
KW   Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   798 AGAGCAATTAGTGAGACAGA 817
Db   20 AGAGCAATTAGTGAGACAGA 1

RESULT 1188
AAF80758/c
ID   AAF80758 standard; DNA; 20 BP.
XX
XX
AC   AAF80758;
XX
DT   02-MAY-2001 (first entry)
XX
DE   Human mdm2 phosphorothioate oligonucleotide #132.
XX
KW   Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1006 CAGGTGATTGGTTGGATCAG 1025
Db   20 CAGGTGATTGGTTGGATCAG 1

RESULT 1189
AAF80786/c
ID   AAF80786 standard; DNA; 20 BP.
XX
XX
AC   AAF80786;
XX
DT   02-MAY-2001 (first entry)
XX
DE   Human mdm2 phosphorothioate oligonucleotide #160.
XX
KW   Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1292 GAATTGGCTTCCTGAAGATA 1311
Db   20 GAATTGGCTTCCTGAAGATA 1

RESULT 1190
AAF80802/c
ID   AAF80802 standard; DNA; 20 BP.
XX
XX
AC   AAF80802;
XX

RESULT 1187
XX
DE   Human mdm2 phosphorothioate oligonucleotide #176.
XX
KW   Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1481 AAGTGAAGACTATTCTCAGC 1500
Db   20 AAGTGAAGACTATTCTCAGC 1

RESULT 1191
AAF80808/c
ID   AAF80808 standard; DNA; 20 BP.
XX
XX
AC   AAF80808;
XX
DT   02-MAY-2001 (first entry)
XX
DE   Human mdm2 phosphorothioate oligonucleotide #182.
XX
KW   Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1533 CAAGAAGATGTGAAGAGTT 1552
Db   20 CAAGAAGATGTGAAGAGTT 1

RESULT 1192
AAF80819/c
ID   AAF80819 standard; DNA; 20 BP.
XX
XX
AC   AAF80819;
XX
DT   02-MAY-2001 (first entry)
XX
DE   Human mdm2 phosphorothioate oligonucleotide #193.
XX
KW   Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1667 TGGCAAAACAGGACATCTTA 1686
Db   20 TGGCAAAACAGGACATCTTA 1

RESULT 1193
AAF80823/c
ID   AAF80823 standard; DNA; 20 BP.
XX
XX
AC   AAF80823;
XX
DT   02-MAY-2001 (first entry)
XX
DE   Human mdm2 phosphorothioate oligonucleotide #197.
XX
KW   Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
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Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1702 GTGCAAGAAGCTAAAGAA 1721
| | | | | | | | | | | | | | | | | | | | | |
Db 20 GTGCAAGAAGCTAAAGAA 1

RESULT 1194
AAF80837/c
ID AAF80837 standard; DNA; 20 BP.

XX AAF80837;

DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #211.
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1840 TTAGACACCTGAAATTTAT 1859
| | | | | | | | | | | | | | | | | | | | | |
Db 20 TTAGACACCTGAAATTTAT 1

RESULT 1195
AAF80852/c
ID AAF80852 standard; DNA; 20 BP.

XX AAF80852;

DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #226.
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1956 TATATTTGACTTGAATATG 1975
| | | | | | | | | | | | | | | | | | | | | |
Db 20 TATATTTGACTTGAATATG 1

RESULT 1196
AAF80868/c
ID AAF80868 standard; DNA; 20 BP.

XX AAF80868;

DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #242.
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2133 GTGCAGTGGTGATCTTGGC 2152
| | | | | | | | | | | | | | | | | | | | | |
Db 20 GTGCAGTGGTGATCTTGGC 1

RESULT 1197
AAF80880/c
ID AAF80880 standard; DNA; 20 BP.

XX AAF80880;

DT 02-MAY-2001 (first entry)

XX Human mdm2 phosphorothioate oligonucleotide #254.
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2232 GCCACCACCTGGCTAATT 2251
| | | | | | | | | | | | | | | | | | | | | |
Db 20 GCCACCACCTGGCTAATT 1

RESULT 1198
AAD07540/c
ID AAD07540 standard; DNA; 20 BP.

XX AAD07540;

DT 10-AUG-2001 (first entry)

XX Human mdm2 antisense oligonucleotide (ISIS #16514).

XX Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
KW tumour; prophylaxis; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 331 CTGTACTACTGATGTGCT 350
| | | | | | | | | | | | | | | | | | | | | |
Db 20 CTGTACTACTGATGTGCT 1

RESULT 1199
AAD07542/c
ID AAD07542 standard; DNA; 20 BP.

XX AAD07542;

DT 10-AUG-2001 (first entry)

XX Human mdm2 antisense oligonucleotide (ISIS #16516).

XX Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
KW tumour; prophylaxis; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1047 AGTGTAGAATTTGAAGTTGA 1066
| | | | | | | | | | | | | | | | | | | | | |
Db 20 AGTGTAGAATTTGAAGTTGA 1

RESULT 1200
AAD07543/c
ID AAD07543 standard; DNA; 20 BP.

XX AAD07543;

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XX 10-AUG-2001 (first entry)
XX Human mdm2 antisense oligonucleotide (ISIS #16517).
XX Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
XX tumour; prophylaxis; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1381 TTGATGTTCTGATGTAATA 1400
DB 20 TTGATGTTCTGATGTAATA 1

RESULT 1201
AAD07537/c
ID AAD07537 standard; DNA; 20 BP.
XX AC
XX AAD07537;
XX
DT 10-AUG-2001 (first entry)
XX Human mdm2 antisense oligonucleotide (ISIS #16511).
XX Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
XX tumour; prophylaxis; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 CTCACGCGGAAACCCCG 292
DB 20 CTCACGCGGAAACCCCG 1

RESULT 1202
AAD07539/c
ID AAD07539 standard; DNA; 20 BP.
XX AC
XX AAD07539;
XX
DT 10-AUG-2001 (first entry)
XX Human mdm2 antisense oligonucleotide (ISIS #16513).
XX Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
XX tumour; prophylaxis; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 AGCAGGCAATGTGCAATAC 322
DB 20 AGCAGGCAATGTGCAATAC 1

RESULT 1203
AAD07549/c
ID AAD07549 standard; DNA; 20 BP.
XX AC
XX AAD07549;
XX
DT 10-AUG-2001 (first entry)
XX Human mdm2 antisense oligonucleotide (ISIS #16523).
XX Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
XX tumour; prophylaxis; antisense; ss.

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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2132 AGTCAGTGGGTGATCTTGG 2151
DB 20 AGTCAGTGGGTGATCTTGG 1

RESULT 1204
AAD07554/c
ID AAD07554 standard; DNA; 20 BP.
XX AC
XX AAD07554;
XX
DT 10-AUG-2001 (first entry)
XX Human mdm2 antisense oligonucleotide (ISIS #17615).
XX Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
XX tumour; prophylaxis; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 GGCCCTGTGTGCGGAAGA 56
DB 20 GGCCCTGTGTGCGGAAGA 1

RESULT 1205
AAD07532/c
ID AAD07532 standard; DNA; 20 BP.
XX AC
XX AAD07532;
XX
DT 10-AUG-2001 (first entry)
XX Human mdm2 antisense oligonucleotide (ISIS #16506).
XX Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
XX tumour; prophylaxis; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGGAGCTTGGCTG 20
DB 20 GCACCGCGGAGCTTGGCTG 1

RESULT 1206
AAD07533/c
ID AAD07533 standard; DNA; 20 BP.
XX AC
XX AAD07533;
XX
DT 10-AUG-2001 (first entry)
XX Human mdm2 antisense oligonucleotide (ISIS #16507).
XX Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
XX tumour; prophylaxis; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 GGCCCTGTGTGCGGAAGA 56
DB 20 GGCCCTGTGTGCGGAAGA 1

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Db 20 GGCCCTGTGTGTCGGAAGA 1

RESULT 1207
AAD07541/c
ID AAD07541 standard; DNA; 20 BP.
XX
AC AAD07541;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide (ISIS #16515).
XX
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
KW tumour; prophylaxis; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 617 GATCTACAGGACTTGGTAG 636
Db 20 GATCTACAGGACTTGGTAG 1

RESULT 1208
AAD07546/c
ID AAD07546 standard; DNA; 20 BP.
XX
AC AAD07546;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide (ISIS #16520).
XX
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
KW tumour; prophylaxis; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1785 TAGTTGACCTGTCTATAAGA 1804
Db 20 TAGTTGACCTGTCTATAAGA 1

RESULT 1209
AAD07547/c
ID AAD07547 standard; DNA; 20 BP.
XX
AC AAD07547;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide (ISIS #16521).
XX
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
KW tumour; prophylaxis; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1818 CTAACCTATATACCCCTAGGA 1837
Db 20 CTAACCTATATACCCCTAGGA 1

RESULT 1210
AAD07535/c
ID AAD07535 standard; DNA; 20 BP.
XX

AC AAD07535;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide (ISIS #16509).
XX
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
KW tumour; prophylaxis; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 147 ATTAGTGGTACGAGCGCCC 166
Db 20 ATTAGTGGTACGAGCGCCC 1

RESULT 1211
AAD07538/c
ID AAD07538 standard; DNA; 20 BP.
XX
AC AAD07538;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide (ISIS #16512).
XX
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
KW tumour; prophylaxis; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 295 TGGTGAGGACGAGCAATG 314
Db 20 TGGTGAGGACGAGCAATG 1

RESULT 1212
AAD07550/c
ID AAD07550 standard; DNA; 20 BP.
XX
AC AAD07550;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide (ISIS #16524).
XX
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
KW tumour; prophylaxis; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2224 AGTCATCTGCCACACACCT 2243
Db 20 AGTCATCTGCCACACACCT 1

RESULT 1213
AAD07545/c
ID AAD07545 standard; DNA; 20 BP.
XX
AC AAD07545;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide (ISIS #16519).
XX
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;

KW tumour; prophylaxis; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1776 TATTCCCTAGTTGACCTG 1795
ID AAD07536 standard; DNA; 20 BP.
XX
AC AAD07536;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide (ISIS #16522).
XX
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
KW tumour; prophylaxis; antisense; ss.

RESULT 1214
AAD07548/c
ID AAD07548 standard; DNA; 20 BP.
XX
AC AAD07548;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide (ISIS #16522).
XX
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
KW tumour; prophylaxis; antisense; ss.

QY 1934 TAGTGGATAGTGAATCTT 1953
ID AAD07544 standard; DNA; 20 BP.
XX
AC AAD07544;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide (ISIS #16518).
XX
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
KW tumour; prophylaxis; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1934 TAGTGGATAGTGAATCTT 1953
ID AAD07544 standard; DNA; 20 BP.
XX
AC AAD07544;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide (ISIS #16518).
XX
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
KW tumour; prophylaxis; antisense; ss.

RESULT 1215

AAD07544/c
ID AAD07544 standard; DNA; 20 BP.
XX
AC AAD07544;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide (ISIS #16518).
XX
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
KW tumour; prophylaxis; antisense; ss.

QY 1695 TTTACATGTGCAAGAAGCT 1714
ID AAD07534 standard; DNA; 20 BP.
XX
AC AAD07534;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide (ISIS #16508).
XX
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
KW tumour; prophylaxis; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1695 TTTACATGTGCAAGAAGCT 1714
ID AAD07534 standard; DNA; 20 BP.
XX
AC AAD07534;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide (ISIS #16508).
XX
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
KW tumour; prophylaxis; antisense; ss.

RESULT 1216

AAD07534/c
ID AAD07534 standard; DNA; 20 BP.
XX
AC AAD07534;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide (ISIS #16508).
XX
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
KW tumour; prophylaxis; antisense; ss.

QY 95 CTCTGACCGAGATCCTGCTG 114

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 CTCTGACCGAGATCCTGCTG 114

Db 20 CTCTGACCGAGATCCTGCTG 1

RESULT 1217

AAD07536/c
ID AAD07536 standard; DNA; 20 BP.
XX
AC AAD07536;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide (ISIS #16510).
XX
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
KW tumour; prophylaxis; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 GAGAGTGAATGATCCCCGA 200
ID AAD07551 standard; DNA; 20 BP.
XX
AC AAD07551;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide (ISIS #16525).
XX
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
KW tumour; prophylaxis; antisense; ss.

RESULT 1218

AAD07551/c
ID AAD07551 standard; DNA; 20 BP.
XX
AC AAD07551;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide (ISIS #16525).
XX
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
KW tumour; prophylaxis; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2256 GTACTTTTGTAGTAGACAGG 2275
ID AAD07551 standard; DNA; 20 BP.
XX
AC AAD07551;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide (ISIS #16525).
XX
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
KW tumour; prophylaxis; antisense; ss.

RESULT 1219

AAD07551/c
ID AAD07551 standard; DNA; 20 BP.
XX
AC AAD07551;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide (ISIS #16525).
XX
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
KW tumour; prophylaxis; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTCAGTGAGAACAGGTGCTCA 694
ID AAD07551 standard; DNA; 20 BP.
XX
AC AAD07551;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide (ISIS #16525).
XX
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
KW tumour; prophylaxis; antisense; ss.

RESULT 1220

AAD07551/c
ID AAD07551 standard; DNA; 20 BP.
XX
AC AAD07551;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide (ISIS #16525).
XX
KW Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;
KW tumour; prophylaxis; antisense; ss.

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XX AAH38246;
AC
XX 14-AUG-2001 (first entry)
DT
DE SNP specific lower PCR primer SEQ ID 1042.
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2338 TCCCAAGTGTGGGATTAC 2357
Db 1 TCCCAAGTGTGGGATTAC 20

RESULT 1221
AAH38602
ID AAH38602 standard; DNA; 20 BP.
XX
XX AAH38602;
AC
XX 14-AUG-2001 (first entry)
DT
DE SNP specific lower PCR primer SEQ ID 1398.
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2352 GATTACAGGCATGAGCCACC 2371
Db 1 GATTACAGGCATGAGCCACC 20

RESULT 1222
AAF28586/c
ID AAF28586 standard; DNA; 20 BP.
XX
XX AAF28586;
AC
XX 02-APR-2001 (first entry)
DT
DE Epo-R PCR primer #1.
XX
XX Human; myeloid progenitor cell; transplantation; PCR primer; c-kit;
KW CD117; IL-7Ralpha; interleukin-7 receptor alpha; Epo-R; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2344 AGTGTCTGGGATTACAGGCAT 2363
Db 20 AGTGTCTGGGATTACAGGCAT 1

RESULT 1223
AAH20702/c
ID AAH20702 standard; DNA; 20 BP.
XX
XX AAH20702;
AC
XX 13-AUG-2001 (first entry)
DT
DE Human telomeric repeat binding factor 2 oligonucleotide 111430.
XX

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KW Antisense; phosphorothioate; human; telomeric repeat binding factor 2;
KW inhibitor; premature aging; hyperproliferative disorder; cancer;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2292 CAGGATGGTCTCGATCTCCT 2311
Db 20 CAGGATGGTCTCGATCTCCT 1

RESULT 1224
AAH20704/c
ID AAH20704 standard; DNA; 20 BP.
XX
XX AAH20704;
AC
XX 13-AUG-2001 (first entry)
DT
DE Human telomeric repeat binding factor 2 oligonucleotide 111432.
XX
XX Antisense; phosphorothioate; human; telomeric repeat binding factor 2;
KW inhibitor; premature aging; hyperproliferative disorder; cancer;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2346 TGCTGGGATTACAGGCATGA 2365
Db 20 TGCTGGGATTACAGGCATGA 1

RESULT 1225
AAS29242/c
ID AAS29242 standard; DNA; 20 BP.
XX
XX AAS29242;
AC
XX 21-NOV-2001 (first entry)
DT
DE Human mdm2 antisense oligonucleotide 16506.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGCGAGCTTGCGTG 20
Db 20 GCACCGCGCGAGCTTGCGTG 1

RESULT 1226
AAS29245/c
ID AAS29245 standard; DNA; 20 BP.
XX
XX AAS29245;
AC
XX 21-NOV-2001 (first entry)
DT
DE Human mdm2 antisense oligonucleotide 16509.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 147 ATTAGTGGTACGAGCGCCC 166
 Db 20 ATTAGTGGTACGAGCGCCC 1

RESULT 1227

AAS29257/c

ID AAS29257 standard; DNA; 20 BP.

XX AC

XX AAS29257;

DT 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 16521.

DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match

Best Local Similarity 0.8%; Score 20; DB 1; Length 20;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1818 CTAACCTATATACCCCTAGGA 1837

Db 20 CTAACCTATATACCCCTAGGA 1

RESULT 1228

AAS29276/c

ID AAS29276 standard; DNA; 20 BP.

XX AC

XX AAS29276;

DT 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31714.

DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match

Best Local Similarity 0.8%; Score 20; DB 1; Length 20;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 TGTGGCCCTGTGTGTCGAA 53

Db 20 TGTGGCCCTGTGTGTCGAA 1

RESULT 1229

AAS29279/c

ID AAS29279 standard; DNA; 20 BP.

XX AC

XX AAS29279;

DT 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31395.

DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match

Best Local Similarity 0.8%; Score 20; DB 1; Length 20;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 62 CAAGAAGCCGAGCCCGAGGG 81

Db 20 CAAGAAGCCGAGCCCGAGGG 1

RESULT 1230

AAS29324/c

ID AAS29324 standard; DNA; 20 BP.

XX AC

XX AAS29324;

DT 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31726.

DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match

Best Local Similarity 0.8%; Score 20; DB 1; Length 20;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 477 TATCTTGGCCAGTATATTAT 496

Db 20 TATCTTGGCCAGTATATTAT 1

RESULT 1231

AAS29344/c

ID AAS29344 standard; DNA; 20 BP.

XX AC

XX AAS29344;

DT 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31429.

DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match

Best Local Similarity 0.8%; Score 20; DB 1; Length 20;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 669 ACATCTGTGAGTGAGAACAG 688

Db 20 ACATCTGTGAGTGAGAACAG 1

RESULT 1232

AAS29353/c

ID AAS29353 standard; DNA; 20 BP.

XX AC

XX AAS29353;

DT 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31432.

DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match

Best Local Similarity 0.8%; Score 20; DB 1; Length 20;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 774 AGACCATCTACCTCATCTAG 793

Db 20 AGACCATCTACCTCATCTAG 1

RESULT 1233

AAS29421/c

ID AAS29421 standard; DNA; 20 BP.

XX AC

XX AAS29421;

DT 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31589.

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XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1517 CATTATTATTATAGCAGCCCAAG 1536
Db 20 CATTATTATTATAGCAGCCCAAG 1

RESULT 1234
AAS29425/c
ID AAS29425 standard; DNA; 20 BP.
XX AC
XX AAS29425;
XX 21-NOV-2001 (first entry)
DT
DE Human mdm2 antisense oligonucleotide 31591.
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1550 GTTGAAGGGAAGAAACCC 1569
Db 20 GTTGAAGGGAAGAAACCC 1

RESULT 1235
AAS29440/c
ID AAS29440 standard; DNA; 20 BP.
XX AC
XX AAS29440;
XX 21-NOV-2001 (first entry)
DT
DE Human mdm2 antisense oligonucleotide 31598.
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1720 AAAGGAATAAGCCTTGCCCA 1739
Db 20 AAAGGAATAAGCCTTGCCCA 1

RESULT 1236
AAS29453/c
ID AAS29453 standard; DNA; 20 BP.
XX AC
XX AAS29453;
XX 21-NOV-2001 (first entry)
DT
DE Human mdm2 antisense oligonucleotide 31605.
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1850 TGAATTTATTACATATAT 1869
Db 20 TGAATTTATTACATATAT 1

RESULT 1237
AAS29458/c
ID AAS29458 standard; DNA; 20 BP.
XX AC
XX AAS29458;
XX 21-NOV-2001 (first entry)
DT
DE Human mdm2 antisense oligonucleotide 31609.
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1889 AATTCACATAGATTCTTCT 1908
Db 20 AATTCACATAGATTCTTCT 1

RESULT 1238
AAS29467/c
ID AAS29467 standard; DNA; 20 BP.
XX AC
XX AAS29467;
XX 21-NOV-2001 (first entry)
DT
DE Human mdm2 antisense oligonucleotide 31777.
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1956 TATAATTTGACTTGAATATG 1975
Db 20 TATAATTTGACTTGAATATG 1

RESULT 1239
AAS29471/c
ID AAS29471 standard; DNA; 20 BP.
XX AC
XX AAS29471;
XX 21-NOV-2001 (first entry)
DT
DE Human mdm2 antisense oligonucleotide 31779.
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1990 CACCAACTCTCTAATTTTAA 2009
Db 20 CACCAACTCTCTAATTTTAA 1

RESULT 1240

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AAS29475/c
ID AAS29475 standard; DNA; 20 BP.
XX
AC AAS29475;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31780.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2020 TCTGCTCTTAATGAGAGTA 2039
Db 20 TCTGCTCTTAATGAGAGTA 1

RESULT 1241
AAS29487/c
ID AAS29487 standard; DNA; 20 BP.
XX
AC AAS29487;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31622.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2176 GGGTTCGCACCATCTCTCG 2195
Db 20 GGGTTCGCACCATCTCTCG 1

RESULT 1242
AAS29500/c
ID AAS29500 standard; DNA; 20 BP.
XX
AC AAS29500;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31788.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2290 GCCAGGATGGTCTCGATCTC 2309
Db 20 GCCAGGATGGTCTCGATCTC 1

RESULT 1243
AAS29274/c
ID AAS29274 standard; DNA; 20 BP.
XX
AC AAS29274;
XX
DT 21-NOV-2001 (first entry)
XX

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DE Human mdm2 antisense oligonucleotide 31713.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 GCTTCTGGGGCCTGTGTGGC 39
Db 20 GCTTCTGGGGCCTGTGTGGC 1

RESULT 1244
AAS29288/c
ID AAS29288 standard; DNA; 20 BP.
XX
AC AAS29288;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31720.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 174 TGGCCCGGAGAGTGGATGA 193
Db 20 TGGCCCGGAGAGTGGATGA 1

RESULT 1245
AAS29320/c
ID AAS29320 standard; DNA; 20 BP.
XX
AC AAS29320;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31560.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 392 GGTAGACCAAGCCATTGC 411
Db 20 GGTAGACCAAGCCATTGC 1

RESULT 1246
AAS29338/c
ID AAS29338 standard; DNA; 20 BP.
XX
AC AAS29338;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31733.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 600 AGGAAATATATACCATGAT 619
DB 20 AGGAAATATATACCATGAT 1

RESULT 1247
AAS29339/c
ID AAS29339 standard; DNA; 20 BP.
XX
AC AAS29339;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31565.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 609 TATACATGATCTACAGGAA 628
DB 20 TATACATGATCTACAGGAA 1

RESULT 1248
AAS29358/c
ID AAS29358 standard; DNA; 20 BP.
XX
AC AAS29358;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31740.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 833 ATTATCTGGTGAACGACAAA 852
DB 20 ATTATCTGGTGAACGACAAA 1

RESULT 1249
AAS29372/c
ID AAS29372 standard; DNA; 20 BP.
XX
AC AAS29372;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31576.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 996 AGTGAACATTGAGGTATTG 1015
DB 20 AGTGAACATTGAGGTATTG 1

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RESULT 1250
AAS29401/c
ID AAS29401 standard; DNA; 20 BP.
XX
AC AAS29401;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31583.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1292 GAATTGGCTTCCTGAAGATA 1311
DB 20 GAATTGGCTTCCTGAAGATA 1

RESULT 1251
AAS29432/c
ID AAS29432 standard; DNA; 20 BP.
XX
AC AAS29432;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31594.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1648 AAAATGGTTGCATTGTCCAT 1667
DB 20 AAAATGGTTGCATTGTCCAT 1

RESULT 1252
AAS29450/c
ID AAS29450 standard; DNA; 20 BP.
XX
AC AAS29450;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31774.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1823 TATATAACCCCTAGGAATTTA 1842
DB 20 TATATAACCCCTAGGAATTTA 1

RESULT 1253
AAS29251/c
ID AAS29251 standard; DNA; 20 BP.
XX
AC AAS29251;
XX
DT 21-NOV-2001 (first entry)

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XX Human mdm2 antisense oligonucleotide 16515.
DE
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 617 GATCTACAGGAACTTGCTAG 636
DB 20 GATCTACAGGAACTTGCTAG 1

RESULT 1254
AAS29258/c
ID AAS29258 standard; DNA; 20 BP.
XX
AC AAS29258;
XX
XX 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 16522.
DE
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1934 TAGTGGAAATAGTGAATACCTT 1953
DB 20 TAGTGGAAATAGTGAATACCTT 1

RESULT 1255
AAS29285/c
ID AAS29285 standard; DNA; 20 BP.
XX
AC AAS29285;
XX
XX 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31555.
DE
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 AGTGCCTACGAGCGCCAGT 169
DB 20 AGTGCCTACGAGCGCCAGT 1

RESULT 1256
AAS29299/c
ID AAS29299 standard; DNA; 20 BP.
XX
AC AAS29299;
XX
XX 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31405.
DE
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 299 GAGGACGAGCAAAATGTGCA 318
DB 20 GAGGACGAGCAAAATGTGCA 1

RESULT 1257
AAS29325/c
ID AAS29325 standard; DNA; 20 BP.
XX
AC AAS29325;
XX
XX 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31424.
DE
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 ATATTATGACTAAACGATTA 509
DB 20 ATATTATGACTAAACGATTA 1

RESULT 1258
AAS29333/c
ID AAS29333 standard; DNA; 20 BP.
XX
AC AAS29333;
XX
XX 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31426.
DE
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 559 GAGATTGTGTGCGTGCCA 578
DB 20 GAGATTGTGTGCGTGCCA 1

RESULT 1259
AAS29362/c
ID AAS29362 standard; DNA; 20 BP.
XX
AC AAS29362;
XX
XX 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31435.
DE
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 880 CCTTTTCCTTTGATGAAGC 899
DB 20 CCTTTTCCTTTGATGAAGC 1
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RESULT 1260
AAS29383/C
ID AAS29383 standard; DNA; 20 BP.
XX
XX
AC AAS29383;
XX
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31750.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1092 CTTAGTGAAGAGGACAAGA 1111
DB 20 CTTAGTGAAGAGGACAAGA 1

RESULT 1261
AAS29384/C
ID AAS29384 standard; DNA; 20 BP.
XX
XX
AC AAS29384;
XX
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31579.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1100 AGAAGGACAAGAACTCTCAG 1119
DB 20 AGAAGGACAAGAACTCTCAG 1

RESULT 1262
AAS29393/C
ID AAS29393 standard; DNA; 20 BP.
XX
XX
AC AAS29393;
XX
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31581.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1196 TGAATTTCTTCTAGTCTGACT 1215
DB 20 TGAATTTCTTCTAGTCTGACT 1

RESULT 1263
AAS29418/C
ID AAS29418 standard; DNA; 20 BP.
XX
XX
AC AAS29418;
XX
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31765.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1489 ACTATTCTCAGCCATCAACT 1508
DB 20 ACTATTCTCAGCCATCAACT 1

RESULT 1264
AAS29424/C
ID AAS29424 standard; DNA; 20 BP.
XX
XX
AC AAS29424;
XX
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31767.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1541 TGTCAAAGAGTTTGAAGGG 1560
DB 20 TGTCAAAGAGTTTGAAGGG 1

RESULT 1265
AAS29433/C
ID AAS29433 standard; DNA; 20 BP.
XX
XX
AC AAS29433;
XX
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31770.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1657 GCATTGTCCATGCAAAACA 1676
DB 20 GCATTGTCCATGCAAAACA 1

RESULT 1266
AAS29491/C
ID AAS29491 standard; DNA; 20 BP.
XX
XX
AC AAS29491;
XX
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31624.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
XX
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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2202 CCTCCCAATTAGCTTGCCCT 2221
DB 20 CCTCCCAATTAGCTTGCCCT 1

RESULT 1267
AAS29281/c
ID AAS29281 standard; DNA; 20 BP.
XX
AC AAS29281;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31554.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 TGACCGAGATCCTGCTGCTT 117
DB 20 TGACCGAGATCCTGCTGCTT 1

RESULT 1268
AAS29293/c
ID AAS29293 standard; DNA; 20 BP.
XX
AC AAS29293;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31557.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 289 CCCGGATGGTGAGGAGCAGG 308
DB 20 CCCGGATGGTGAGGAGCAGG 1

RESULT 1269
AAS29306/c
ID AAS29306 standard; DNA; 20 BP.
XX
AC AAS29306;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31413.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 307 GGCAAAATGTGCAATACCAAC 326
DB 20 GGCAAAATGTGCAATACCAAC 1

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RESULT 1270
AAS29313/c
ID AAS29313 standard; DNA; 20 BP.
XX
AC AAS29313;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31420.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 314 GTGCAATACCAACATGCTG 333
DB 20 GTGCAATACCAACATGCTG 1

RESULT 1271
AAS29318/c
ID AAS29318 standard; DNA; 20 BP.
XX
AC AAS29318;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31724.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 GCTTCGGAACAAGAGACCCT 391
DB 20 GCTTCGGAACAAGAGACCCT 1

RESULT 1272
AAS29331/c
ID AAS29331 standard; DNA; 20 BP.
XX
AC AAS29331;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31563.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 538 ATGTTCAATGATCTTCTA 557
DB 20 ATGTTCAATGATCTTCTA 1

RESULT 1273
AAS29335/c
ID AAS29335 standard; DNA; 20 BP.
XX
AC AAS29335;

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XX 21-NOV-2001 (first entry)
DT Human mdm2 antisense oligonucleotide 31564.
XX
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 575 GCCAAGCTTCTCTGTGAAG 594
Db 20 GCCAAGCTTCTCTGTGAAG 1
RESULT 1274
AAS29346/c
ID AAS29346 standard; DNA; 20 BP.
XX
AC AAS29346;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31736.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 691 GTCACCTTGAAGTGGGAGT 710
Db 20 GTCACCTTGAAGTGGGAGT 1
RESULT 1275
AAS29359/c
ID AAS29359 standard; DNA; 20 BP.
XX
AC AAS29359;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31434.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 844 AACGACAAAGAAAGCCAC 863
Db 20 AACGACAAAGAAAGCCAC 1
RESULT 1276
AAS29361/c
ID AAS29361 standard; DNA; 20 BP.
XX
AC AAS29361;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31741.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW

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Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 867 TCTGATAGTATTTCCCTTTC 886
Db 20 TCTGATAGTATTTCCCTTTC 1
RESULT 1277
AAS29365/c
ID AAS29365 standard; DNA; 20 BP.
XX
AC AAS29365;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31436.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 915 ATAAGGAGATATGTTGTGA 934
Db 20 ATAAGGAGATATGTTGTGA 1
RESULT 1278
AAS29375/c
ID AAS29375 standard; DNA; 20 BP.
XX
AC AAS29375;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31746.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1023 CAGGATTCAGTTTCAGATCA 1042
Db 20 CAGGATTCAGTTTCAGATCA 1
RESULT 1279
AAS29377/c
ID AAS29377 standard; DNA; 20 BP.
XX
AC AAS29377;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31747.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1046 TAGTGTAGAAATTTGAAGTTG 1065
Db 20 TAGTGTAGAAATTTGAAGTTG 1

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Db      20 TAGGTAGAAATTGAAGTTG 1

RESULT 1280
AAS29395/c
ID AAS29395 standard; DNA; 20 BP.
XX
AC AAS29395;
XX
DT 21-NOV-2001 (first entry)
XX
XX Human mdm2 antisense oligonucleotide 31445.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1220 GAAATGCACCTTCATGCAATG 1239
      |||||
Db      20 GAAATGCACCTTCATGCAATG 1

RESULT 1281
AAS29405/c
ID AAS29405 standard; DNA; 20 BP.
XX
XX AAS29405;
AC
XX
DT 21-NOV-2001 (first entry)
XX
XX Human mdm2 antisense oligonucleotide 31760.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1333 TCTCTGAGAAAGCAAACTG 1352
      |||||
Db      20 TCTCTGAGAAAGCAAACTG 1

RESULT 1282
AAS29406/c
ID AAS29406 standard; DNA; 20 BP.
XX
XX AAS29406;
AC
XX
DT 21-NOV-2001 (first entry)
XX
XX Human mdm2 antisense oligonucleotide 31448.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1346 CAAACTGGAATACTCAACAC 1365
      |||||
Db      20 CAAACTGGAATACTCAACAC 1

RESULT 1283
AAS29411/c
ID AAS29411 standard; DNA; 20 BP.
XX

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AC AAS29411;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31762.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1421 CAGAGAGTCATGTTGAGG 1440
      |||||
Db      20 CAGAGAGTCATGTTGAGG 1

RESULT 1284
AAS29463/c
ID AAS29463 standard; DNA; 20 BP.
XX
XX AAS29463;
AC
XX
DT 21-NOV-2001 (first entry)
XX
XX Human mdm2 antisense oligonucleotide 31776.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1920 TTGACCTACTTTGTTAGTGG 1939
      |||||
Db      20 TTGACCTACTTTGTTAGTGG 1

RESULT 1285
AAS29465/c
ID AAS29465 standard; DNA; 20 BP.
XX
XX AAS29465;
AC
XX
DT 21-NOV-2001 (first entry)
XX
XX Human mdm2 antisense oligonucleotide 31612.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
XX

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1940 AATAGTGAATACTTACTATA 1959
      |||||
Db      20 AATAGTGAATACTTACTATA 1

RESULT 1286
AAS29483/c
ID AAS29483 standard; DNA; 20 BP.
XX
XX AAS29483;
AC
XX
DT 21-NOV-2001 (first entry)
XX
XX Human mdm2 antisense oligonucleotide 31782.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW

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KW atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2133 GTGAGTGGGTGATCTTGCC 2152
|||||
Db 20 GTGAGTGGGTGATCTTGCC 1

RESULT 1287
AAS29261/c
ID AAS29261 standard; DNA; 20 BP.
XX
AC AAS29261;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 16525.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2256 GTACTTTTAGTAGACAGG 2275
|||||
Db 20 GTACTTTTAGTAGACAGG 1

RESULT 1288
AAS29277/c
ID AAS29277 standard; DNA; 20 BP.
XX
AC AAS29277;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31553.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 GTGTGTCGGAAGATGGAGC 62
|||||
Db 20 GTGTGTCGGAAGATGGAGC 1

RESULT 1289
AAS29287/c
ID AAS29287 standard; DNA; 20 BP.
XX
AC AAS29287;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31397.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 CCAGTGCCCTGGCCCGGAGA 184
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Db 20 CCAGTGCCCTGGCCCGGAGA 1

RESULT 1290
AAS29291/c
ID AAS29291 standard; DNA; 20 BP.
XX
AC AAS29291;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31398.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 CTTCCGCGAGTAGTCAGTCCC 236
|||||
Db 20 CTTCCGCGAGTAGTCAGTCCC 1

RESULT 1291
AAS29298/c
ID AAS29298 standard; DNA; 20 BP.
XX
AC AAS29298;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31404.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 298 TGAGGAGCAGGCAAAATGTC 317
|||||
Db 20 TGAGGAGCAGGCAAAATGTC 1

RESULT 1292
AAS29303/c
ID AAS29303 standard; DNA; 20 BP.
XX
AC AAS29303;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31410.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 GCAGGCAAAATGCAATACC 323
|||||
Db 20 GCAGGCAAAATGCAATACC 1

RESULT 1293
AAS29307/c
ID AAS29307 standard; DNA; 20 BP.
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XX AAS29307;
XX 21-NOV-2001 (first entry)
XX Human mdm2 antisense oligonucleotide 31414.
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
XX atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 308 GCAATGTGCAATACCAACA 327
Db 20 GCAATGTGCAATACCAACA 1

RESULT 1294
AAS29315/c
ID AAS29315 standard; DNA; 20 BP.
XX
XX AAS29315;
XX
XX 21-NOV-2001 (first entry)
XX Human mdm2 antisense oligonucleotide 31723.
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
XX atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 334 TACCTACTGATGGTGCTGTA 353
Db 20 TACCTACTGATGGTGCTGTA 1

RESULT 1295
AAS29316/c
ID AAS29316 standard; DNA; 20 BP.
XX
XX AAS29316;
XX
XX 21-NOV-2001 (first entry)
XX Human mdm2 antisense oligonucleotide 31421.
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
XX atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 351 GTACACCTCAGATTC 370
Db 20 GTACACCTCAGATTC 1

RESULT 1296
AAS29349/c
ID AAS29349 standard; DNA; 20 BP.
XX
XX AAS29349;
XX
XX 21-NOV-2001 (first entry)
XX Human mdm2 antisense oligonucleotide 31737.
XX

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KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 727 TACAAGAGCTTCAGGAAG 746
Db 20 TACAAGAGCTTCAGGAAG 1

RESULT 1297
AAS29388/c
ID AAS29388 standard; DNA; 20 BP.
XX
XX AAS29388;
XX
XX 21-NOV-2001 (first entry)
XX Human mdm2 antisense oligonucleotide 31753.
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1135 TATATCAAGTTACTGTGTAT 1154
Db 20 TATATCAAGTTACTGTGTAT 1

RESULT 1298
AAS29404/c
ID AAS29404 standard; DNA; 20 BP.
XX
XX AAS29404;
XX
XX 21-NOV-2001 (first entry)
XX Human mdm2 antisense oligonucleotide 31584.
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1325 AGGGGAATCTCTGAGAAAG 1344
Db 20 AGGGGAATCTCTGAGAAAG 1

RESULT 1299
AAS29422/c
ID AAS29422 standard; DNA; 20 BP.
XX
XX AAS29422;
XX
XX 21-NOV-2001 (first entry)
XX Human mdm2 antisense oligonucleotide 31590.
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1522 TTTATAGCAGCCAGCAAGAT 1541
DB 20 TTTATAGCAGCCAGCAAGAT 1

RESULT 1300
AAS29430/c
ID AAS29430 standard; DNA; 20 BP.
XX
AC AAS29430;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31455.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1617 GAACCTTGTTGATTGTCA 1636
DB 20 GAACCTTGTTGATTGTCA 1

RESULT 1301
AAS29439/c
ID AAS29439 standard; DNA; 20 BP.
XX
AC AAS29439;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31597.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1710 AAGCTAAAGAAAGGAATAA 1729
DB 20 AAGCTAAAGAAAGGAATAA 1

RESULT 1302
AAS29476/c
ID AAS29476 standard; DNA; 20 BP.
XX
AC AAS29476;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31617.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2051 TTTCTTAAATATGTATATG 2070
DB 20 TTTCTTAAATATGTATATG 1

RESULT 1303
AAS29480/c
ID AAS29480 standard; DNA; 20 BP.
XX
AC AAS29480;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31467.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2111 TTGCTCTGTTTACCAGGCTG 2130
DB 20 TTGCTCTGTTTACCAGGCTG 1

RESULT 1304
AAS29486/c
ID AAS29486 standard; DNA; 20 BP.
XX
AC AAS29486;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31783.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 TCACTGCAAGCTCTGCCCTC 2172
DB 20 TCACTGCAAGCTCTGCCCTC 1

RESULT 1305
AAS29504/c
ID AAS29504 standard; DNA; 20 BP.
XX
AC AAS29504;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31790.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2325 GCCCACCCTGGCCTCCCAAA 2344
DB 20 GCCCACCCTGGCCTCCCAAA 1

RESULT 1306
AAS29247/c
ID AAS29247 standard; DNA; 20 BP.
XX
AC AAS29247;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 16511.

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XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 CTCCAAGCGGAAACCCCG 292
Db 20 CTCCAAGCGGAAACCCCG 1

RESULT 1307
AAS29252/c
ID AAS29252 standard; DNA; 20 BP.

XX
XX AAS29252;

XX 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 16516.

XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1047 AGTGTAGAATTGAAGTTGA 1066
Db 20 AGTGTAGAATTGAAGTTGA 1

RESULT 1308
AAS29264/c
ID AAS29264 standard; DNA; 20 BP.

XX
XX AAS29264;

XX 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 17615.

XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 GGCCCTGTGTTCGGAAGA 56
Db 20 GGCCCTGTGTTCGGAAGA 1

RESULT 1309
AAS29282/c
ID AAS29282 standard; DNA; 20 BP.

XX
XX AAS29282;

XX 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31717.

XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 GATCCTGCTGCTTTCGAGC 124
Db 20 GATCCTGCTGCTTTCGAGC 1

RESULT 1310
AAS29284/c
ID AAS29284 standard; DNA; 20 BP.

XX
XX AAS29284;

XX 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31718.

XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 120 GCAGCCAGGAGCACCGTCCC 139
Db 20 GCAGCCAGGAGCACCGTCCC 1

RESULT 1311
AAS29319/c
ID AAS29319 standard; DNA; 20 BP.

XX
XX AAS29319;

XX 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31422.

XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 386 GACCTGTGTAGACCAAGC 405
Db 20 GACCTGTGTAGACCAAGC 1

RESULT 1312
AAS29350/c
ID AAS29350 standard; DNA; 20 BP.

XX
XX AAS29350;

XX 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31431.

XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 740 GGAAGAGAAACCTTCATCTT 759
Db 20 GGAAGAGAAACCTTCATCTT 1

RESULT 1313

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1368 GCTGAAGAGGGCTTTGATGT 1387
|||||
Db 20 GCTGAAGAGGGCTTTGATGT 1

RESULT 1320

AAS29434/c
ID AAS29434 standard; DNA; 20 BP.

XX
AC AAS29434;
XX

DT 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31456.

DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytosstatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1667 TGGCAAAACAGGACATCTTA 1686

Db 20 TGGCAAAACAGGACATCTTA 1

RESULT 1321

AAS29437/c
ID AAS29437 standard; DNA; 20 BP.

XX
AC AAS29437;
XX

DT 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31771.

DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytosstatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 CCTGCTTTACATGTGCAAG 1709

Db 20 CCTGCTTTACATGTGCAAG 1

RESULT 1322

AAS29459/c
ID AAS29459 standard; DNA; 20 BP.

XX
AC AAS29459;
XX

DT 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31462.

DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytosstatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1898 AGATTTCTTCTCTTCTTCTAT 1917

Db 20 AGATTTCTTCTCTTCTTCTAT 1

RESULT 1323

AAS29482/c

ID AAS29482 standard; DNA; 20 BP.

XX
AC AAS29482;
XX

DT 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31620.

DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytosstatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2123 CCAGGCTGGAGTCAGTGGG 2142

Db 20 CCAGGCTGGAGTCAGTGGG 1

RESULT 1324

AAS29499/c

ID AAS29499 standard; DNA; 20 BP.

XX
AC AAS29499;
XX

DT 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31471.

DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytosstatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2283 CGTGTAGCCAGGATGGTCT 2302

Db 20 CGTGTAGCCAGGATGGTCT 1

RESULT 1325

AAS29506/c

ID AAS29506 standard; DNA; 20 BP.

XX
AC AAS29506;
XX

DT 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31791.

DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytosstatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2341 CAAAGTGCTGGGATTACAGG 2360

Db 20 CAAAGTGCTGGGATTACAGG 1

RESULT 1326

AAS29244/c

ID AAS29244 standard; DNA; 20 BP.

XX
AC AAS29244;
XX

DT 21-NOV-2001 (first entry)

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XX Human mdm2 antisense oligonucleotide 16508.
DE
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 CTCTGACCGAGATCTGCTG 114
DB 20 CTCTGACCGAGATCTGCTG 1

RESULT 1327
AAS29260/c
ID AAS29260 standard; DNA; 20 BP.
XX
AC AAS29260;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 16524.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2224 AGTCATCTGCCACACCT 2243
DB 20 AGTCATCTGCCACACCT 1

RESULT 1328
AAS29272/c
ID AAS29272 standard; DNA; 20 BP.
XX
AC AAS29272;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31712.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCGCGGAGCTTGCTGCTT 23
DB 20 CCGCGGAGCTTGCTGCTT 1

RESULT 1329
AAS29292/c
ID AAS29292 standard; DNA; 20 BP.
XX
AC AAS29292;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31722.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;

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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 AGGAACTGGGAGTCTTGA 261
DB 20 AGGAACTGGGAGTCTTGA 1

RESULT 1330
AAS29300/c
ID AAS29300 standard; DNA; 20 BP.
XX
AC AAS29300;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31406.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 AGGAGCAGGCAATGTGCAA 319
DB 20 AGGAGCAGGCAATGTGCAA 1

RESULT 1331
AAS29351/c
ID AAS29351 standard; DNA; 20 BP.
XX
AC AAS29351;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31569.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 752 TTCATCTTCACATTGGTTT 771
DB 20 TTCATCTTCACATTGGTTT 1

RESULT 1332
AAS29370/c
ID AAS29370 standard; DNA; 20 BP.
XX
AC AAS29370;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31744.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 971 GAATCCGATCTTGATGCTG 990
DB 20 GAATCCGATCTTGATGCTG 1

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RESULT 1333
AAS29394/c
ID AAS29394 standard; DNA; 20 BP.
XX
AC AAS29394;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31755.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1207 TAGCTGACTATTGGAATGC 1226
Db 20 TAGCTGACTATTGGAATGC 1

RESULT 1334
AAS29414/c
ID AAS29414 standard; DNA; 20 BP.
XX
AC AAS29414;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31587.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1449 GATAAAATTACACAGCTTC 1468
Db 20 GATAAAATTACACAGCTTC 1

RESULT 1335
AAS29416/c
ID AAS29416 standard; DNA; 20 BP.
XX
AC AAS29416;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31451.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1466 TTCACAATCACAGAAGTG 1485
Db 20 TTCACAATCACAGAAGTG 1

RESULT 1336
AAS29442/c
ID AAS29442 standard; DNA; 20 BP.
XX
AC AAS29442;
XX

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DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31458.
XX
AC AAS29394;
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 CCCAGTATGTAGACACCAA 1755
Db 20 CCCAGTATGTAGACACCAA 1

RESULT 1337
AAS29243/c
ID AAS29243 standard; DNA; 20 BP.
XX
AC AAS29243;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 16507.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 GGCCTGTGTGTCGGAAGA 56
Db 20 GGCCTGTGTGTCGGAAGA 1

RESULT 1338
AAS29301/c
ID AAS29301 standard; DNA; 20 BP.
XX
AC AAS29301;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31407.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 GGAGCAGCGCAAAATGTGCAAT 320
Db 20 GGAGCAGCGCAAAATGTGCAAT 1

RESULT 1339
AAS29329/c
ID AAS29329 standard; DNA; 20 BP.
XX
AC AAS29329;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31425.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 525 CAACATATTGTATTTGTTTC 544
DB 20 CAACATATTGTATTTGTTTC 1

RESULT 1340
AAS29334/c
ID AAS29334 standard; DNA; 20 BP.
XX
AC AAS29334;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31731.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 566 GTTGGCGTGCACAGCTTCT 585
DB 20 GTTGGCGTGCACAGCTTCT 1

RESULT 1341
AAS29336/c
ID AAS29336 standard; DNA; 20 BP.
XX
AC AAS29336;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31732.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 587 TGTGAAGACGACAGGAAA 606
DB 20 TGTGAAGACGACAGGAAA 1

RESULT 1342
AAS29345/c
ID AAS29345 standard; DNA; 20 BP.
XX
AC AAS29345;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31567.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 682 AGAACAGGTGTACCTTGAA 701
DB 20 AGAACAGGTGTACCTTGAA 1
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RESULT 1343
AAS29347/c
ID AAS29347 standard; DNA; 20 BP.
XX
AC AAS29347;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31430.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 704 TGGAGTGTATCAAAAGGACC 723
DB 20 TGGAGTGTATCAAAAGGACC 1

RESULT 1344
AAS29360/c
ID AAS29360 standard; DNA; 20 BP.
XX
AC AAS29360;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31572.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 857 ACGCCACAATCTGATAGTA 876
DB 20 ACGCCACAATCTGATAGTA 1

RESULT 1345
AAS29381/c
ID AAS29381 standard; DNA; 20 BP.
XX
AC AAS29381;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31749.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1077 TCAGAGATTATAGCCTTAG 1096
DB 20 TCAGAGATTATAGCCTTAG 1

RESULT 1346
AAS29385/c
ID AAS29385 standard; DNA; 20 BP.
XX
AC AAS29385;
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XX 21-NOV-2001 (first entry)
XX Human mdm2 antisense oligonucleotide 31751.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
XX atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1105 GACAAGAACTCTCAGATGAA 1124
DB 20 GACAAGAACTCTCAGATGAA 1

RESULT 1347
AAS29387/c
ID AAS29387 standard; DNA; 20 BP.
XX
XX AAS29387;
XX
XX 21-NOV-2001 (first entry)
XX Human mdm2 antisense oligonucleotide 31752.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
XX atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1124 AGATGATGAGGTATATCAAG 1143
DB 20 AGATGATGAGGTATATCAAG 1

RESULT 1348
AAS29397/c
ID AAS29397 standard; DNA; 20 BP.
XX
XX AAS29397;
XX
XX 21-NOV-2001 (first entry)
XX Human mdm2 antisense oligonucleotide 31582.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
XX atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1257 CCATCATTGCAACAGATG 1276
DB 20 CCATCATTGCAACAGATG 1

RESULT 1349
AAS29420/c
ID AAS29420 standard; DNA; 20 BP.
XX
XX AAS29420;
XX
XX 21-NOV-2001 (first entry)
XX Human mdm2 antisense oligonucleotide 31766.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
XX atherosclerosis; tumour; cytostatic; anti psoriatic;
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Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1506 ACTTCTAGTAGCATTATTTA 1525
DB 20 ACTTCTAGTAGCATTATTTA 1

RESULT 1350
AAS29460/c
ID AAS29460 standard; DNA; 20 BP.
XX
XX AAS29460;
XX
XX 21-NOV-2001 (first entry)
XX Human mdm2 antisense oligonucleotide 31610.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
XX atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1905 TTCTCTTTAGTATAATTGAC 1924
DB 20 TTCTCTTTAGTATAATTGAC 1

RESULT 1351
AAS29466/c
ID AAS29466 standard; DNA; 20 BP.
XX
XX AAS29466;
XX
XX 21-NOV-2001 (first entry)
XX Human mdm2 antisense oligonucleotide 31613.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
XX atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1948 ATACTTACTATATAATTGACT 1967
DB 20 ATACTTACTATATAATTGACT 1

RESULT 1352
AAS29470/c
ID AAS29470 standard; DNA; 20 BP.
XX
XX AAS29470;
XX
XX 21-NOV-2001 (first entry)
XX Human mdm2 antisense oligonucleotide 31614.
DE
DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
XX atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY - 1982 ATCCTTTACCAACTCCTTA 2001
DB 20 ATCCTTTACCAACTCCTTA 2001
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Db      20 ATCCTTTACCACTCCTA 1
RESULT 1353
AAS29477/c
ID AAS29477 standard; DNA; 20 BP.
XX
AC
AAS29477;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31466.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2059 AATATGTATATGACATTTAA 2078
Db      20 AATATGTATATGACATTTAA 1
RESULT 1354
AAS29495/c
ID AAS29495 standard; DNA; 20 BP.
XX
AC
AAS29495;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31470.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2232 GCCACACACCTGGCTAATT 2251
Db      20 GCCACACACCTGGCTAATT 1
RESULT 1355
AAS29278/c
ID AAS29278 standard; DNA; 20 BP.
XX
AC
AAS29278;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31715.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 50 GGAAGATGGAGCAAGAGC 69
Db      20 GGAAGATGGAGCAAGAGC 1
RESULT 1356
AAS29286/c
ID AAS29286 standard; DNA; 20 BP.
XX
AC
AAS29286;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31719.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 158 CGAGCGCCGAGTCCCTGGC 177
Db      20 CGAGCGCCGAGTCCCTGGC 1
RESULT 1357
AAS29296/c
ID AAS29296 standard; DNA; 20 BP.
XX
AC
AAS29296;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31402.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 296 GGTGAGGAGCAGCAATGT 315
Db      20 GGTGAGGAGCAGCAATGT 1
RESULT 1358
AAS29308/c
ID AAS29308 standard; DNA; 20 BP.
XX
AC
AAS29308;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31415.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 309 CAAATGTGCAATACCAACAT 328
Db      20 CAAATGTGCAATACCAACAT 1
RESULT 1359
AAS29310/c
ID AAS29310 standard; DNA; 20 BP.
XX
AC
AAS29310;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31417.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;

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KW atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 311 AATGTGCAATACCAACATGT 330
DB 20 AATGTGCAATACCAACATGT 1
|||||
RESULT 1360
AAS29321/c
ID AAS29321 standard; DNA; 20 BP.
XX AC
XX AAS29321;
XX AC
DT 21-NOV-2001 (first entry)
XX DE Human mdm2 antisense oligonucleotide 31725.
XX DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 AGCCATTGCTTTGAAGTTA 422
DB 20 AGCCATTGCTTTGAAGTTA 1
|||||
RESULT 1361
AAS29326/c
ID AAS29326 standard; DNA; 20 BP.
XX AC
XX AAS29326;
XX AC
DT 21-NOV-2001 (first entry)
XX DE Human mdm2 antisense oligonucleotide 31727.
XX DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 496 TGACTAACGATTATATGAT 515
DB 20 TGACTAACGATTATATGAT 1
|||||
RESULT 1362
AAS29348/c
ID AAS29348 standard; DNA; 20 BP.
XX AC
XX AAS29348;
XX AC
DT 21-NOV-2001 (first entry)
XX DE Human mdm2 antisense oligonucleotide 31568.
XX DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 718 AGGACCTTGTAAGAGCTT 737
DB 20 AGGACCTTGTAAGAGCTT 1
|||||
RESULT 1363
AAS29364/c
ID AAS29364 standard; DNA; 20 BP.
XX AC
XX AAS29364;
XX AC
DT 21-NOV-2001 (first entry)
XX DE Human mdm2 antisense oligonucleotide 31742.
XX DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 904 CTCTGTGTGTAATAAGGGAG 923
DB 20 CTCTGTGTGTAATAAGGGAG 1
|||||
RESULT 1364
AAS29379/c
ID AAS29379 standard; DNA; 20 BP.
XX AC
XX AAS29379;
XX AC
DT 21-NOV-2001 (first entry)
XX DE Human mdm2 antisense oligonucleotide 31748.
XX DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1059 GAAGTTGAATCTCTCGACTC 1078
DB 20 GAAGTTGAATCTCTCGACTC 1
|||||
RESULT 1365
AAS29399/c
ID AAS29399 standard; DNA; 20 BP.
XX AC
XX AAS29399;
XX AC
DT 21-NOV-2001 (first entry)
XX DE Human mdm2 antisense oligonucleotide 31446.
XX DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1275 TGTGGGCCCTTCGTGAGAA 1294
DB 20 TGTGGGCCCTTCGTGAGAA 1
|||||
RESULT 1366
AAS29435/c
ID AAS29435 standard; DNA; 20 BP.
DB 20 TGTGGGCCCTTCGTGAGAA 1
|||||
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XX AAS29435;
AC
XX
DT 21-NOV-2001 (first entry)
DE
XX Human mdm2 antisense oligonucleotide 31595.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1675 CAGGACATCTTATGCGCTGC 1694
Db 20 CAGGACATCTTATGCGCTGC 1

RESULT 1367
AAS29443/c
ID AAS29443 standard; DNA; 20 BP.
XX
AC AAS29443;
XX
DT 21-NOV-2001 (first entry)
DE
XX Human mdm2 antisense oligonucleotide 31599.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1745 TAGACAACCAATTCAAATGA 1764
Db 20 TAGACAACCAATTCAAATGA 1

RESULT 1368
AAS29447/c
ID AAS29447 standard; DNA; 20 BP.
XX
AC AAS29447;
XX
DT 21-NOV-2001 (first entry)
DE
XX Human mdm2 antisense oligonucleotide 31602.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1804 AGAATTATATTTCTACT 1823
Db 20 AGAATTATATTTCTACT 1

RESULT 1369
AAS29448/c
ID AAS29448 standard; DNA; 20 BP.
XX
AC AAS29448;
XX
DT 21-NOV-2001 (first entry)
DE
XX Human mdm2 antisense oligonucleotide 31773.
XX

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KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1808 TTATATATTTCTAATATAT 1827
Db 20 TTATATATTTCTAATATAT 1

RESULT 1370
AAS29456/c
ID AAS29456 standard; DNA; 20 BP.
XX
AC AAS29456;
XX
DT 21-NOV-2001 (first entry)
DE
XX Human mdm2 antisense oligonucleotide 31607.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1872 AAGTGAGAAAATGCCTCAAT 1891
Db 20 AAGTGAGAAAATGCCTCAAT 1

RESULT 1371
AAS29457/c
ID AAS29457 standard; DNA; 20 BP.
XX
AC AAS29457;
XX
DT 21-NOV-2001 (first entry)
DE
XX Human mdm2 antisense oligonucleotide 31608.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1883 TGCCTCAATTACATAGATT 1902
Db 20 TGCCTCAATTACATAGATT 1

RESULT 1372
AAS29461/c
ID AAS29461 standard; DNA; 20 BP.
XX
AC AAS29461;
XX
DT 21-NOV-2001 (first entry)
DE
XX Human mdm2 antisense oligonucleotide 31775.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1908 TCCTTAGTATAATTGACCTA 1927
 ID AAS29462 standard; DNA; 20 BP.
 DB 20 TCCTTAGTATAATTGACCTA 1

RESULT 1373

AAS29462/c
 ID AAS29462 standard; DNA; 20 BP.

XX AAS29462;
 XX 21-NOV-2001 (first entry)
 DT Human mdm2 antisense oligonucleotide 31611.
 DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;
 KW

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1913 AGTATAATTGACCTACTTTG 1932
 DB 20 AGTATAATTGACCTACTTTG 1

RESULT 1374

AAS29502/c
 ID AAS29502 standard; DNA; 20 BP.

XX AAS29502;
 XX 21-NOV-2001 (first entry)
 DT Human mdm2 antisense oligonucleotide 31789.
 DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;
 KW

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2307 CTCCTGACCTCGTGATCCGC 2326
 DB 20 CTCCTGACCTCGTGATCCGC 1

RESULT 1375

AAS29505/c
 ID AAS29505 standard; DNA; 20 BP.

XX AAS29505;
 XX 21-NOV-2001 (first entry)
 DT Human mdm2 antisense oligonucleotide 31630.
 DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;
 KW

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2334 GGCCTCCCAAGTGCTGGGA 2353
 DB 20 GGCCTCCCAAGTGCTGGGA 1

RESULT 1376

AAS29249/c

ID AAS29249 standard; DNA; 20 BP.
 XX AAS29249;
 XX 21-NOV-2001 (first entry)
 DT Human mdm2 antisense oligonucleotide 16513.

DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;
 KW

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 AGCAGGCAAAATGTGCAATAC 322
 DB 20 AGCAGGCAAAATGTGCAATAC 1

RESULT 1377

AAS29250/c
 ID AAS29250 standard; DNA; 20 BP.

XX AAS29250;
 XX 21-NOV-2001 (first entry)
 DT Human mdm2 antisense oligonucleotide 16514.
 DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;
 KW

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 331 CTGTACTACTGATGGTGCT 350
 DB 20 CTGTACTACTGATGGTGCT 1

RESULT 1378

AAS29253/c
 ID AAS29253 standard; DNA; 20 BP.

XX AAS29253;
 XX 21-NOV-2001 (first entry)
 DT Human mdm2 antisense oligonucleotide 16517.
 DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;
 KW

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1381 TTGATGTTCTGATTGTAAA 1400
 DB 20 TTGATGTTCTGATTGTAAA 1

RESULT 1379

AAS29259/c
 ID AAS29259 standard; DNA; 20 BP.

XX AAS29259;
 XX 21-NOV-2001 (first entry)
 DT Human mdm2 antisense oligonucleotide 16523.

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XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2132 AGTGCAGTGGGTGATCTTGG 2151
DB 20 AGTGCAGTGGGTGATCTTGG 1

RESULT 1380
AAS29294/c
ID AAS29294 standard; DNA; 20 BP.
XX
AC AAS29294;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31399.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 GATGGTGAGGAGCAGGCAAA 312
DB 20 GATGGTGAGGAGCAGGCAAA 1

RESULT 1381
AAS29352/c
ID AAS29352 standard; DNA; 20 BP.
XX
AC AAS29352;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31738.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 761 ACATTTGGTTTCTAGACCAT 780
DB 20 ACATTTGGTTTCTAGACCAT 1

RESULT 1382
AAS29355/c
ID AAS29355 standard; DNA; 20 BP.
XX
AC AAS29355;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31739.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 798 AGAGCAATTAGTGAGACAGA 817
DB 20 AGAGCAATTAGTGAGACAGA 1

RESULT 1383
AAS29398/c
ID AAS29398 standard; DNA; 20 BP.
XX
AC AAS29398;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31757.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1268 CAACAGATGTTGGGCCCTTC 1287
DB 20 CAACAGATGTTGGGCCCTTC 1

RESULT 1384
AAS29407/c
ID AAS29407 standard; DNA; 20 BP.
XX
AC AAS29407;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31585.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1358 CTCACACACAGCTGAAGAGG 1377
DB 20 CTCACACACAGCTGAAGAGG 1

RESULT 1385
AAS29410/c
ID AAS29410 standard; DNA; 20 BP.
XX
AC AAS29410;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31586.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1412 GAATGATTCAGAGATCAT 1431
DB 20 GAATGATTCAGAGATCAT 1

RESULT 1386

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AAS29413/c
ID AAS29413 standard; DNA; 20 BP.
XX
AC AAS29413;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31763.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1439 GGAAATGATGATAAAATTA 1458
DB 20 GGAAATGATGATAAAATTA 1
RESULT 1387
AAS29473/c
ID AAS29473 standard; DNA; 20 BP.
XX
AC AAS29473;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31465.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2004 TTTAAATAATTTCTACTCTG 2023
DB 20 TTTAAATAATTTCTACTCTG 1
RESULT 1388
AAS29488/c
ID AAS29488 standard; DNA; 20 BP.
XX
AC AAS29488;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31623.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2185 CCATTCTCCTGCTCAGCCT 2204
DB 20 CCATTCTCCTGCTCAGCCT 1
RESULT 1389
AAS29493/c
ID AAS29493 standard; DNA; 20 BP.
XX
AC AAS29493;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31625.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2213 GCTTGGCCTACAGTCATCTG 2232
DB 20 GCTTGGCCTACAGTCATCTG 1
RESULT 1390
AAS29256/c
ID AAS29256 standard; DNA; 20 BP.
XX
AC AAS29256;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 16520.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1785 TAGTTGACCTGTCTATAAGA 1804
DB 20 TAGTTGACCTGTCTATAAGA 1
RESULT 1391
AAS29295/c
ID AAS29295 standard; DNA; 20 BP.
XX
AC AAS29295;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31400.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 294 ATGCTGAGGAGCAGGCAAAAT 313
DB 20 ATGCTGAGGAGCAGGCAAAAT 1
RESULT 1392
AAS29322/c
ID AAS29322 standard; DNA; 20 BP.
XX
AC AAS29322;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31423.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 422 ATTAAGTCTGTGTGCAC 441
DB 20 ATTAAGTCTGTGTGCAC 1

RESULT 1393
AAS29323/c
ID AAS29323 standard; DNA; 20 BP.
XX
XX
AC AAS29323;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31561.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 450 ACTTATCTATGAAGAGGT 469
DB 20 ACTTATCTATGAAGAGGT 1

RESULT 1394
AAS29337/c
ID AAS29337 standard; DNA; 20 BP.
XX
XX
AC AAS29337;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31427.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 593 AGAGCACAGGAAATATATA 612
DB 20 AGAGCACAGGAAATATATA 1

RESULT 1395
AAS29368/c
ID AAS29368 standard; DNA; 20 BP.
XX
XX
AC AAS29368;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31437.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 949 GTGAATCTACAGGACGCCA 968
DB 20 GTGAATCTACAGGACGCCA 1
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RESULT 1396
AAS29378/c
ID AAS29378 standard; DNA; 20 BP.
XX
XX
AC AAS29378;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31440.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1051 TAGAATTTGAAGTTGAATCT 1070
DB 20 TAGAATTTGAAGTTGAATCT 1

RESULT 1397
AAS29380/c
ID AAS29380 standard; DNA; 20 BP.
XX
XX
AC AAS29380;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31578.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1068 TCTCTCGACTCAGAAGATTA 1087
DB 20 TCTCTCGACTCAGAAGATTA 1

RESULT 1398
AAS29409/c
ID AAS29409 standard; DNA; 20 BP.
XX
XX
AC AAS29409;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31449.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1401 AAAACTATAGTGAATGATTC 1420
DB 20 AAAACTATAGTGAATGATTC 1

RESULT 1399
AAS29427/c
ID AAS29427 standard; DNA; 20 BP.
XX
XX
AC AAS29427;
XX
DT 21-NOV-2001 (first entry)
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XX Human mdm2 antisense oligonucleotide 31454.
DE
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1566 ACCCAAGACAAAGAGAGAG 1585
DB 20 ACCCAAGACAAAGAGAGAG 1

RESULT 1400
AAS29428/c
ID AAS29428 standard; DNA; 20 BP.
XX
AC AAS29428;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31592.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1580 AGAGAGTGTGGAATCTAGTT 1599
DB 20 AGAGAGTGTGGAATCTAGTT 1

RESULT 1401
AAS29431/c
ID AAS29431 standard; DNA; 20 BP.
XX
AC AAS29431;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31593.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1624 GTGTGATTGTCAGGTCGA 1643
DB 20 GTGTGATTGTCAGGTCGA 1

RESULT 1402
AAS29438/c
ID AAS29438 standard; DNA; 20 BP.
XX
AC AAS29438;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31457.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;

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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1702 GTGCAAGAGCTAAAGAAA 1721
DB 20 GTGCAAGAGCTAAAGAAA 1

RESULT 1403
AAS29445/c
ID AAS29445 standard; DNA; 20 BP.
XX
AC AAS29445;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31601.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1787 GTTGACCTGCTATTAAGAGA 1806
DB 20 GTTGACCTGCTATTAAGAGA 1

RESULT 1404
AAS29452/c
ID AAS29452 standard; DNA; 20 BP.
XX
AC AAS29452;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31604.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1840 TTAGACAACCTGAAATTTAT 1859
DB 20 TTAGACAACCTGAAATTTAT 1

RESULT 1405
AAS29454/c
ID AAS29454 standard; DNA; 20 BP.
XX
AC AAS29454;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31606.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1855 TTTATTACATATATCAAG 1874
DB 20 TTTATTACATATATCAAG 1

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RESULT 1406
AAS29472/c
ID AAS29472 standard; DNA; 20 BP.
XX
XX
AC AAS29472;
XX
XX
DT 21-NOV-2001 (first entry)
XX
XX
DE Human mdm2 antisense oligonucleotide 31615.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1997 TCTAATTTTAAATAATTC 2016
DB 20 TCTAATTTTAAATAATTC 1

RESULT 1407
AAS29484/c
ID AAS29484 standard; DNA; 20 BP.
XX
XX
AC AAS29484;
XX
XX
DT 21-NOV-2001 (first entry)
XX
XX
DE Human mdm2 antisense oligonucleotide 31621.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2140 GGGTGATCTTGGCTCACTGC 2159
DB 20 GGGTGATCTTGGCTCACTGC 1

RESULT 1408
AAS29492/c
ID AAS29492 standard; DNA; 20 BP.
XX
XX
AC AAS29492;
XX
XX
DT 21-NOV-2001 (first entry)
XX
XX
DE Human mdm2 antisense oligonucleotide 31785.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2210 TTAGCTTGGCTACAGTCAT 2229
DB 20 TTAGCTTGGCTACAGTCAT 1

RESULT 1409
AAS29498/c
ID AAS29498 standard; DNA; 20 BP.
XX
XX
AC AAS29498;
XX
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```
DT 21-NOV-2001 (first entry)
XX
XX
DE Human mdm2 antisense oligonucleotide 31787.
XX
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2274 GGGTTTCACCGTGTAGCCA 2293
DB 20 GGGTTTCACCGTGTAGCCA 1

RESULT 1410
AAS29503/c
ID AAS29503 standard; DNA; 20 BP.
XX
XX
AC AAS29503;
XX
XX
DT 21-NOV-2001 (first entry)
XX
XX
DE Human mdm2 antisense oligonucleotide 31472.
XX
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2319 TGATCCGCCACCTCGGCCT 2338
DB 20 TGATCCGCCACCTCGGCCT 1

RESULT 1411
AAS29507/c
ID AAS29507 standard; DNA; 20 BP.
XX
XX
AC AAS29507;
XX
XX
DT 21-NOV-2001 (first entry)
XX
XX
DE Human mdm2 antisense oligonucleotide 31631.
XX
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
XX
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2351 GGATTACAGCATGAGCCAC 2370
DB 20 GGATTACAGCATGAGCCAC 1

RESULT 1412
AAS29273/c
ID AAS29273 standard; DNA; 20 BP.
XX
XX
AC AAS29273;
XX
XX
DT 21-NOV-2001 (first entry)
XX
XX
DE Human mdm2 antisense oligonucleotide 31552.
XX
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TTGGTCGCTTCTGGGGCTG 33
Db 20 TTGGTCGCTTCTGGGGCTG 1

RESULT 1413
AAS29290/c
ID AAS29290 standard; DNA; 20 BP.
XX
AC AAS29290;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31721.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 208 GGCCTCGTCTTCGCGAGTA 227
Db 20 GGCCTCGTCTTCGCGAGTA 1

RESULT 1414
AAS29302/c
ID AAS29302 standard; DNA; 20 BP.
XX
AC AAS29302;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31408.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 302 GAGCAGCAAAATGTGCAATA 321
Db 20 GAGCAGCAAAATGTGCAATA 1

RESULT 1415
AAS29312/c
ID AAS29312 standard; DNA; 20 BP.
XX
AC AAS29312;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31419.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 313 TGTGCAATACCAATGTCT 332
Db 20 TGTGCAATACCAATGTCT 1

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RESULT 1416
AAS29317/c
ID AAS29317 standard; DNA; 20 BP.
XX
AC AAS29317;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31559.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 361 CACAGATTCAGCTTCGGAA 380
Db 20 CACAGATTCAGCTTCGGAA 1

RESULT 1417
AAS29340/c
ID AAS29340 standard; DNA; 20 BP.
XX
AC AAS29340;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31734.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 619 TCTACAGGAACCTTGGTAGTA 638
Db 20 TCTACAGGAACCTTGGTAGTA 1

RESULT 1418
AAS29357/c
ID AAS29357 standard; DNA; 20 BP.
XX
AC AAS29357;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31571.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 824 TTCAGATGAATTATCTGGTG 843
Db 20 TTCAGATGAATTATCTGGTG 1

RESULT 1419
AAS29367/c
ID AAS29367 standard; DNA; 20 BP.
XX
AC AAS29367;

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XX 21-NOV-2001 (first entry)
DT Human mdm2 antisense oligonucleotide 31743.
DE
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 936 AGAAGCAGTAGCAGTGAATC 955
DB 20 AGAAGCAGTAGCAGTGAATC 1

RESULT 1420
AAS29391/c
ID AAS29391 standard; DNA; 20 BP.
XX
AC AAS29391;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31754.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1170 GATACAGATTCATTGGAAGA 1189
DB 20 GATACAGATTCATTGGAAGA 1

RESULT 1421
AAS29403/c
ID AAS29403 standard; DNA; 20 BP.
XX
AC AAS29403;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31447.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1311 AAAGGGAAGATAAAGGGGA 1330
DB 20 AAAGGGAAGATAAAGGGGA 1

RESULT 1422
AAS29489/c
ID AAS29489 standard; DNA; 20 BP.
XX
AC AAS29489;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31784.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2191 TCCTGCCTCAGCCTCCCAAT 2210
DB 20 TCCTGCCTCAGCCTCCCAAT 1

RESULT 1423
AAS29496/c
ID AAS29496 standard; DNA; 20 BP.
XX
AC AAS29496;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31627.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2253 TTTGTACTTTTGTAGTAGAGAC 2272
DB 20 TTTGTACTTTTGTAGTAGAGAC 1

RESULT 1424
AAS29246/c
ID AAS29246 standard; DNA; 20 BP.
XX
AC AAS29246;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 16510.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 GAGAGTGGATGATCCCGA 200
DB 20 GAGAGTGGATGATCCCGA 1

RESULT 1425
AAS29304/c
ID AAS29304 standard; DNA; 20 BP.
XX
AC AAS29304;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31411.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 305 CAGGCAAAATGTGCAATACCA 324
DB 305 CAGGCAAAATGTGCAATACCA 324
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Db      20 CAGCAAAATGTGCAATACCA 1

RESULT 1426
AAS29305/c
ID AAS29305 standard; DNA; 20 BP.
XX
AC AAS29305;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31412.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      306 AGGCAAAATGTGCAATACCA 325
      |||||
Db      20 AGGCAAAATGTGCAATACCA 1

RESULT 1427
AAS29314/c
ID AAS29314 standard; DNA; 20 BP.
XX
AC AAS29314;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31558.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      323 CAACATGCTGTACTACTG 342
      |||||
Db      20 CAACATGCTGTACTACTG 1

RESULT 1428
AAS29328/c
ID AAS29328 standard; DNA; 20 BP.
XX
AC AAS29328;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31728.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      515 TGAGAGCAACACATATTG 534
      |||||
Db      20 TGAGAGCAACACATATTG 1

RESULT 1429
AAS29332/c
ID AAS29332 standard; DNA; 20 BP.
XX

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AC AAS29332;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31730.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      549 GATCTTCTAGGAGATTGTT 568
      |||||
Db      20 GATCTTCTAGGAGATTGTT 1

RESULT 1430
AAS29342/c
ID AAS29342 standard; DNA; 20 BP.
XX
AC AAS29342;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31566.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      646 AGCAGGAATCATCGGACTCA 665
      |||||
Db      20 AGCAGGAATCATCGGACTCA 1

RESULT 1431
AAS29374/c
ID AAS29374 standard; DNA; 20 BP.
XX
AC AAS29374;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31439.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1017 TTGGATCAGGATTCAGTTTC 1036
      |||||
Db      20 TTGGATCAGGATTCAGTTTC 1

RESULT 1432
AAS29376/c
ID AAS29376 standard; DNA; 20 BP.
XX
AC AAS29376;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31577.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;

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KW atherosclerosis; tumour; cytostatic; anti psoriatic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1034 TTCAGATCAGTTTACTGTAG 1053
DB 20 TTCAGATCAGTTTACTGTAG 1

RESULT 1433
AAS29389/c
ID AAS29389 standard; DNA; 20 BP.
XX
AC AAS29389;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31443.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 GTGTATCAGCGAGGGAGAG 1168
DB 20 GTGTATCAGCGAGGGAGAG 1

RESULT 1434
AAS29396/c
ID AAS29396 standard; DNA; 20 BP.
XX
AC AAS29396;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31756.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1226 CACTTCATGCAATGAATGA 1245
DB 20 CACTTCATGCAATGAATGA 1

RESULT 1435
AAS29429/c
ID AAS29429 standard; DNA; 20 BP.
XX
AC AAS29429;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31769.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1605 CTTAATGCCATTGAACCTTG 1624
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DB 20 CTTAATGCCATTGAACCTTG 1

RESULT 1436
AAS29444/c
ID AAS29444 standard; DNA; 20 BP.
XX
AC AAS29444;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31600.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1757 TCAAATGATTGCTAACTT 1776
DB 20 TCAAATGATTGCTAACTT 1

RESULT 1437
AAS29468/c
ID AAS29468 standard; DNA; 20 BP.
XX
AC AAS29468;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31464.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1969 GAATATGCTAGCTCATCCTTT 1988
DB 20 GAATATGCTAGCTCATCCTTT 1

RESULT 1438
AAS29248/c
ID AAS29248 standard; DNA; 20 BP.
XX
AC AAS29248;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 16512.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 295 TGGTGAGGAGCAGGCAATG 314
DB 20 TGGTGAGGAGCAGGCAATG 1

RESULT 1439
AAS29283/c
ID AAS29283 standard; DNA; 20 BP.
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XX AAS29283;
AC
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31396.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 113 TGTCTTCGACGAGGAGCA 132
Db 20 TGTCTTCGACGAGGAGCA 1

RESULT 1440
AAS29309/c
ID AAS29309 standard; DNA; 20 BP.
XX
AC AAS29309;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31416.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 310 AAATGTGCAATACCAACATG 329
Db 20 AAATGTGCAATACCAACATG 1

RESULT 1441
AAS29330/c
ID AAS29330 standard; DNA; 20 BP.
XX
AC AAS29330;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31729.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 531 ATTGTATATTGTTCAATGA 550
Db 20 ATTGTATATTGTTCAATGA 1

RESULT 1442
AAS29371/c
ID AAS29371 standard; DNA; 20 BP.
XX
AC AAS29371;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31438.
XX
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```
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 983 TGATGCTGGTGAAGTGAAC 1002
Db 20 TGATGCTGGTGAAGTGAAC 1

RESULT 1443
AAS29386/c
ID AAS29386 standard; DNA; 20 BP.
XX
AC AAS29386;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31442.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1115 CTCAGATGAAGATGATGAGG 1134
Db 20 CTCAGATGAAGATGATGAGG 1

RESULT 1444
AAS29402/c
ID AAS29402 standard; DNA; 20 BP.
XX
AC AAS29402;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31759.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1301 TCCTGAAGATAAGGGAAG 1320
Db 20 TCCTGAAGATAAGGGAAG 1

RESULT 1445
AAS29415/c
ID AAS29415 standard; DNA; 20 BP.
XX
AC AAS29415;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31764.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1456 TTACACAAGCTTCACAATCA 1475
DB 20 TTACACAAGCTTCACAATCA 1

RESULT 1446
AAS29423/c
ID AAS29423 standard; DNA; 20 BP.
XX
XX
AC AAS29423;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31453.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1533 CAAGAAGATGTGAAGAGTT 1552
DB 20 CAAGAAGATGTGAAGAGTT 1

RESULT 1447
AAS29426/c
ID AAS29426 standard; DNA; 20 BP.
XX
XX
AC AAS29426;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31768.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1560 GAAGAAACCCCAAGACAAGA 1579
DB 20 GAAGAAACCCCAAGACAAGA 1

RESULT 1448
AAS29446/c
ID AAS29446 standard; DNA; 20 BP.
XX
XX
AC AAS29446;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31459.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1798 TATAAGAGAAATATATATTT 1817
DB 20 TATAAGAGAAATATATATTT 1

RESULT 1449
AAS29455/c
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ID AAS29455 standard; DNA; 20 BP.
XX
AC AAS29455;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31461.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1865 TATATCAAAAGTGAGAAAATG 1884
DB 20 TATATCAAAAGTGAGAAAATG 1

RESULT 1450
AAS29474/c
ID AAS29474 standard; DNA; 20 BP.
XX
XX
AC AAS29474;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31616.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2015 TCTACTCTGCTTTAAATGAG 2034
DB 20 TCTACTCTGCTTTAAATGAG 1

RESULT 1451
AAS29478/c
ID AAS29478 standard; DNA; 20 BP.
XX
XX
AC AAS29478;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31618.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2072 CATTAAATGTAACCTTATTA 2091
DB 20 CATTAAATGTAACCTTATTA 1

RESULT 1452
AAS29485/c
ID AAS29485 standard; DNA; 20 BP.
XX
XX
AC AAS29485;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31468.
```

XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2146 TCTTGGCTCACTGCAAGCTC 2165
|||||
Db 20 TCTTGGCTCACTGCAAGCTC 1

RESULT 1453

AAS29490/c
ID AAS29490 standard; DNA; 20 BP.

XX
AC AAS29490;

DT 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31469.

DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2198 TCAGCTCCCAATTAGCTTG 2217
|||||
Db 20 TCAGCTCCCAATTAGCTTG 1

RESULT 1454

AAS29497/c
ID AAS29497 standard; DNA; 20 BP.

XX
AC AAS29497;

DT 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31628.

DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2265 GTAGAGACAGGTTTACCG 2284
|||||
Db 20 GTAGAGACAGGTTTACCG 1

RESULT 1455

AAS29501/c
ID AAS29501 standard; DNA; 20 BP.

XX
AC AAS29501;

DT 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31629.

DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2298 GGTCTCGATCTCTGACCTC 2317
|||||
Db 20 GGTCTCGATCTCTGACCTC 1

RESULT 1456

AAS29297/c
ID AAS29297 standard; DNA; 20 BP.

XX
AC AAS29297;

DT 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31403.

DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 297 GTCAGGAGCAGGCAAAATGTG 316
|||||
Db 20 GTCAGGAGCAGGCAAAATGTG 1

RESULT 1457

AAS29311/c
ID AAS29311 standard; DNA; 20 BP.

XX
AC AAS29311;

DT 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31418.

DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 ATGTGCAATACCAACATGTC 331
|||||
Db 20 ATGTGCAATACCAACATGTC 1

RESULT 1458

AAS29341/c
ID AAS29341 standard; DNA; 20 BP.

XX
AC AAS29341;

DT 21-NOV-2001 (first entry)

XX Human mdm2 antisense oligonucleotide 31428.

DE Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 634 TAGTAGTCAATCAGCAGGAA 653
|||||
Db 20 TAGTAGTCAATCAGCAGGAA 1

RESULT 1459

```
AAS29356/c
ID AAS29356 standard; DNA; 20 BP.
XX
AC AAS29356;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31433.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 810 GAGACAGAGAAATTCAGA 829
Db 20 GAGACAGAGAAATTCAGA 1

RESULT 1460
AAS29373/c
ID AAS29373 standard; DNA; 20 BP.
XX
AC AAS29373;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31745.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1006 CAGGTGATTGGTGGATCAG 1025
Db 20 CAGGTGATTGGTGGATCAG 1

RESULT 1461
AAS29412/c
ID AAS29412 standard; DNA; 20 BP.
XX
AC AAS29412;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31450.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1434 GTTGAGGAAATGATGATAA 1453
Db 20 GTTGAGGAAATGATGATAA 1

RESULT 1462
AAS29417/c
ID AAS29417 standard; DNA; 20 BP.
XX
AC AAS29417;
XX
DT 21-NOV-2001 (first entry)
XX

DE Human mdm2 antisense oligonucleotide 31588.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AACTGAAGACTATTCTCAGC 1500
Db 20 AAGTGAAGACTATTCTCAGC 1

RESULT 1463
AAS29436/c
ID AAS29436 standard; DNA; 20 BP.
XX
AC AAS29436;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31596.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1684 TTATGGCTGCTTTACATGT 1703
Db 20 TTATGGCTGCTTTACATGT 1

RESULT 1464
AAS29449/c
ID AAS29449 standard; DNA; 20 BP.
XX
AC AAS29449;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31603.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1816 TTCTAACTATATAACCCCTAG 1835
Db 20 TTCTAACTATATAACCCCTAG 1

RESULT 1465
AAS29451/c
ID AAS29451 standard; DNA; 20 BP.
XX
AC AAS29451;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31460.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1832 CTAGGAATTTAGACAACCTG 1851
Db 20 CTAGGAATTTAGACAACCTG 1

RESULT 1466
AAS29479/c
ID AAS29479 standard; DNA; 20 BP.
XX
AC AAS29479;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31619.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2103 ACCGAGTCTGCTCTGTAC 2122
Db 20 ACCGAGTCTGCTCTGTAC 1

RESULT 1467
AAS29254/c
ID AAS29254 standard; DNA; 20 BP.
XX
AC AAS29254;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 16518.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1695 TTATCATGTGCAAGAGCT 1714
Db 20 TTATCATGTGCAAGAGCT 1

RESULT 1468
AAS29255/c
ID AAS29255 standard; DNA; 20 BP.
XX
AC AAS29255;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 16519.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1776 TATTTCCCTAGTTGACCTG 1795
Db 20 TATTTCCCTAGTTGACCTG 1

RESULT 1469
AAS29275/c
ID AAS29275 standard; DNA; 20 BP.
XX
AC AAS29275;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31394.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 GCCTGTGTGGCCTGTGTGT 48
Db 20 GCCTGTGTGGCCTGTGTGT 1

RESULT 1470
AAS29280/c
ID AAS29280 standard; DNA; 20 BP.
XX
AC AAS29280;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31716.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 CGAGCCCGAGGGCGGCCGC 89
Db 20 CGAGCCCGAGGGCGGCCGC 1

RESULT 1471
AAS29289/c
ID AAS29289 standard; DNA; 20 BP.
XX
AC AAS29289;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31556.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 202 GCCCAGGGCGTGTGCTTCC 221
Db 20 GCCCAGGGCGTGTGCTTCC 1

RESULT 1472
AAS29327/c
ID AAS29327 standard; DNA; 20 BP.
XX
AC AAS29327;
XX
DT 21-NOV-2001 (first entry)
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XX Human mdm2 antisense oligonucleotide 31562.
DE
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
  atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 503 ACGATTATATGATGAGAGC 522
DB 20 ACGATTATATGATGAGAGC 1

RESULT 1473
AAS29343/c
ID AAS29343 standard; DNA; 20 BP.
XX
AC AAS29343;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31735.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
  atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 656 ATCGGACTCAGGTACATCTG 675
DB 20 ATCGGACTCAGGTACATCTG 1

RESULT 1474
AAS29354/c
ID AAS29354 standard; DNA; 20 BP.
XX
AC AAS29354;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31570.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
  atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 787 CATCTAGAAGGAGAGCAATT 806
DB 20 CATCTAGAAGGAGAGCAATT 1

RESULT 1475
AAS29366/c
ID AAS29366 standard; DNA; 20 BP.
XX
AC AAS29366;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31574.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
  atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;

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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 927 TGTGTGAAAGAGCAGTAG 946
DB 20 TGTGTGAAAGAGCAGTAG 1

RESULT 1476
AAS29419/c
ID AAS29419 standard; DNA; 20 BP.
XX
AC AAS29419;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31452.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
  atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1499 GCCATCAACTTCTAGTAGCA 1518
DB 20 GCCATCAACTTCTAGTAGCA 1

RESULT 1477
AAS29441/c
ID AAS29441 standard; DNA; 20 BP.
XX
AC AAS29441;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31772.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
  atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1726 ATAGGCCCTGCCCAGTAGT 1745
DB 20 ATAGGCCCTGCCCAGTAGT 1

RESULT 1478
AAS29464/c
ID AAS29464 standard; DNA; 20 BP.
XX
AC AAS29464;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31463.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
  atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1933 GTAGTGAATAGTGAATACT 1952
DB 20 GTAGTGAATAGTGAATACT 1

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RESULT 1479
AAS29469/c
ID AAS29469 standard; DNA; 20 BP.
XX
XX
AC AAS29469;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31778.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1973 ATGTAGCTCATCTTTTACAC 1992
Db 20 ATGTAGCTCATCTTTTACAC 1

RESULT 1480
AAS29481/c
ID AAS29481 standard; DNA; 20 BP.
XX
XX
AC AAS29481;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31781.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2116 CTGTTACCCAGGCTGGAGTG 2135
Db 20 CTGTTACCCAGGCTGGAGTG 1

RESULT 1481
AAS29494/c
ID AAS29494 standard; DNA; 20 BP.
XX
XX
AC AAS29494;
XX
DT 21-NOV-2001 (first entry)
DE Human mdm2 antisense oligonucleotide 31786.
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2218 GCCTACAGTCATCGCCACC 2237
Db 20 GCCTACAGTCATCGCCACC 1

RESULT 1482
AAL40351
ID AAL40351 standard; DNA; 20 BP.
XX
XX
AC AAL40351;
XX

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DT 19-SEP-2002 (first entry)
XX
DE Human caspase 6 antisense inhibition related oligo SEQ ID No 70.
XX
XX
KW Muscular; cytostatic; nootropic; neuroprotective; ophthalmological;
KW antilipaeamic; osteopathic; caspase 6; Rieger's syndrome; bone metabolism;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2340 CCAAAGTGTGGGATTACAG 2359
Db 1 CCAAAGTGTGGGATTACAG 20

RESULT 1483
ABL44004
ID ABL44004 standard; DNA; 20 BP.
XX
XX
AC ABL44004;
XX
DT 11-APR-2002 (first entry)
DE Human chromosome 1p36-35 PCR primer SEQ ID NO:1048.
KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW PCR primer; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2337 CTCCCAAGTGTGGGATTA 2356
Db 1 CTCCCAAGTGTGGGATTA 20

RESULT 1484
ABL44438/c
ID ABL44438 standard; DNA; 20 BP.
XX
XX
AC ABL44438;
XX
DT 11-APR-2002 (first entry)
DE Human chromosome 1p36-35 PCR primer SEQ ID NO:1482.
KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW PCR primer; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2142 GTGATCTTGGCTCACTGCAA 2161
Db 20 GTGATCTTGGCTCACTGCAA 1

RESULT 1485
ABA92187
ID ABA92187 standard; DNA; 20 BP.
XX
XX
AC ABA92187;
XX
DT 06-JUN-2002 (first entry)
DE Polymorphism 506B13CA1 reverse PCR primer.
KW NALPN; nyctalopin; human; congenital stationary night blindness; CSNB;
KW glycosylphosphatidylinositol; GPI; proteoglycan; retina; polymorphism;

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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2338 TCCCAAGTCTGGGATTAC 2357
DB 1 TCCCAAGTCTGGGATTAC 20

RESULT 1486
ABA92208
ID ABA92208 standard; DNA; 20 BP.
XX
AC ABA92208;
XX
DT 06-JUN-2002 (first entry)
DE Reverse PCR primer for polymorphism 506B13CA1.
KW NYX; nyctalopin; human; congenital stationary night blindness; CSNB;
KW glycosylphosphatidylinositol; GPI; retina; SLRP;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2338 TCCCAAGTCTGGGATTAC 2357
DB 1 TCCCAAGTCTGGGATTAC 20

RESULT 1487
ABK86101/c
ID ABK86101 standard; DNA; 20 BP.
XX
AC ABK86101;
XX
DT 23-AUG-2002 (first entry)
DE Human MDM-2 oligonucleotide phosphorothioate 2'-O-MOE gapmer.
KW MDM-2; peptide linked oligomeric compound; ss; human;
KW phosphorothioate 2'-O-MOE gapmer oligonucleotide.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1695 TTTCATGTGCAAGAGCT 1714
DB 20 TTTCATGTGCAAGAGCT 1

RESULT 1488
ABL60510/c
ID ABL60510 standard; DNA; 20 BP.
XX
AC ABL60510;
XX
DT 12-AUG-2002 (first entry)
DE Human MDM2 mRNA fragment complementary oligo primer 2.
KW Pseudo-cyclic oligonucleotide; PCO; gene expression; protein kinase A;
KW nucleic acid detection; ribozyme inhibition; gene transcription; MDM2;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTGAGACAGGTGTCA 694
DB 20 GTGAGTGAGACAGGTGTCA 1
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RESULT 1489
ABK91100/c
ID ABK91100 standard; DNA; 20 BP.
XX
AC ABK91100;
XX
DT 05-DEC-2002 (first entry)
DE PCR primer Alu3, for human DNA derived from chromosome 21.
KW Human; fluorescent labelling technique; fluorescent intercalating dye;
KW nucleic acid detection; electrophoresis; diagnostic assay;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2341 CAAAGTCTGGGATTACAGG 2360
DB 20 CAAAGTCTGGGATTACAGG 1

RESULT 1490
ABZ79385
ID ABZ79385 standard; DNA; 20 BP.
XX
AC ABZ79385;
XX
DT 01-MAY-2003 (first entry)
DE Acetyl-Coenzyme A-carboxylase-alpha gene PCR primer, SEQ ID 72.
KW Human; enzyme; acetyl-Coenzyme A-carboxylase-alpha; ACC-alpha; cancer;
KW breast; ovary; PCR; primer; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2338 TCCCAAGTCTGGGATTAC 2357
DB 1 TCCCAAGTCTGGGATTAC 20

RESULT 1491
ACD27753/c
ID ACD27753 standard; DNA; 20 BP.
XX
AC ACD27753;
XX
DT 18-SEP-2003 (first entry)
DE Peptide linked oligomeric compound associated oligonucleotide #2.
KW Peptide linked oligomeric compound; diagnostic; therapeutic;
KW research reagent; protein production inhibitor;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1695 TTTCATGTGCAAGAGCT 1714
DB 20 TTTCATGTGCAAGAGCT 1

RESULT 1492
AAL60008/c
ID AAL60008 standard; DNA; 20 BP.
XX
AC AAL60008;
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XX 27-AUG-2003 (first entry)
DE Human GH-1 gene amplifying PCR primer, CRV156.lpl.
KW Human; growth hormone 1; GH-1; single nucleotide polymorphism; SNP;
KW gene therapy; PCR; primer; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2340 CCAAAGTGTGGGATTACAG 2359
DB 20 CCAAAGTGTGGGATTACAG 1
|||||

RESULT 1493
ADD21442/c
ID ADD21442 standard; DNA; 20 BP.
XX AC ADD21442;
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #5.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 GAGAGTGGATGATCCCGA 200
DB 20 GAGAGTGGATGATCCCGA 1
|||||

RESULT 1494
ADD21485/c
ID ADD21485 standard; DNA; 20 BP.
XX AC ADD21485;
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #48.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 202 GCCCAGGGCGTGGCTTCC 221
DB 20 GCCCAGGGCGTGGCTTCC 1
|||||

RESULT 1495
ADD21486/c
ID ADD21486 standard; DNA; 20 BP.
XX AC ADD21486;
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #49.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 208 GCGTCGTCTTCCGAGTA 227
DB 20 GCGTCGTCTTCCGAGTA 1
|||||

RESULT 1496
ADD21522/c
ID ADD21522 standard; DNA; 20 BP.
XX AC ADD21522;
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #85.-
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 496 TGACTAAACGATTATATGAT 515
DB 20 TGACTAAACGATTATATGAT 1
|||||

RESULT 1497
ADD21553/c
ID ADD21553 standard; DNA; 20 BP.
XX AC ADD21553;
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #116.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 824 TTCAGATGAATTATCTGGTG 843
DB 20 TTCAGATGAATTATCTGGTG 1
|||||

RESULT 1498
ADD21554/c
ID ADD21554 standard; DNA; 20 BP.
XX AC ADD21554;
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #117.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 833 ATTATCTGCTGAACGACAAA 852
DB 20 ATTATCTGCTGAACGACAAA 1
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Db      20 ATTATCTGGTGAACGACAAA 1

RESULT 1499
ADD21555/c
ID      ADD21555 standard; DNA; 20 BP.
XX
XX
AC      ADD21555;
XX
DT      15-JAN-2004 (first entry)
XX
XX      Human mdm2 antisense oligonucleotide #118.
XX      antisense oligonucleotide; human; mdm2; hyperproliferation;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      844 AACGACAAGAAAGCCAC 863
Db      20 AACGACAAGAAAGCCAC 1

RESULT 1500
ADD21567/c
ID      ADD21567 standard; DNA; 20 BP.
XX
XX
AC      ADD21567;
XX
DT      15-JAN-2004 (first entry)
XX
XX      Human mdm2 antisense oligonucleotide #130.
XX      antisense oligonucleotide; human; mdm2; hyperproliferation;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      983 TGATGCTGGTGAAGTGAAC 1002
Db      20 TGATGCTGGTGAAGTGAAC 1

RESULT 1501
ADD21568/c
ID      ADD21568 standard; DNA; 20 BP.
XX
XX
AC      ADD21568;
XX
DT      15-JAN-2004 (first entry)
XX
XX      Human mdm2 antisense oligonucleotide #131.
XX      antisense oligonucleotide; human; mdm2; hyperproliferation;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      996 AGTGAACATTTCAGGTGATTG 1015
Db      20 AGTGAACATTTCAGGTGATTG 1

RESULT 1502
ADD21579/c
ID      ADD21579 standard; DNA; 20 BP.
XX

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AC      ADD21579;
XX
DT      15-JAN-2004 (first entry)
XX
XX      Human mdm2 antisense oligonucleotide #142.
XX      antisense oligonucleotide; human; mdm2; hyperproliferation;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1092 CTTAGTGAAGAGCAAGA 1111
Db      20 CTTAGTGAAGAGCAAGA 1

RESULT 1503
ADD21596/c
ID      ADD21596 standard; DNA; 20 BP.
XX
XX
AC      ADD21596;
XX
DT      15-JAN-2004 (first entry)
XX
XX      Human mdm2 antisense oligonucleotide #159.
XX      antisense oligonucleotide; human; mdm2; hyperproliferation;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1283 CCTTCGTGAGATTGGCTTC 1302
Db      20 CCTTCGTGAGATTGGCTTC 1

RESULT 1504
ADD21616/c
ID      ADD21616 standard; DNA; 20 BP.
XX
XX
AC      ADD21616;
XX
DT      15-JAN-2004 (first entry)
XX
XX      Human mdm2 antisense oligonucleotide #179.
XX      antisense oligonucleotide; human; mdm2; hyperproliferation;
KW      hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1506 ACTTCTAGTAGCATTATTTA 1525
Db      20 ACTTCTAGTAGCATTATTTA 1

RESULT 1505
ADD21634/c
ID      ADD21634 standard; DNA; 20 BP.
XX
XX
AC      ADD21634;
XX
DT      15-JAN-2004 (first entry)
XX
XX      Human mdm2 antisense oligonucleotide #197.
XX      antisense oligonucleotide; human; mdm2; hyperproliferation;

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KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1702 GTGCAAGAGCTAAAGAA 1721
DB 20 GTGCAAGAGCTAAAGAA 1

RESULT 1506
ADD21641/c
ID ADD21641 standard; DNA; 20 BP.
XX
AC ADD21641;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #204.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1787 GTTGACCTGTATAGAGA 1806
DB 20 GTTGACCTGTATAGAGA 1

RESULT 1507
ADD21646/c
ID ADD21646 standard; DNA; 20 BP.
XX
AC ADD21646;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #209.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1823 TATATAACCTTAGGAATTTA 1842
DB 20 TATATAACCTTAGGAATTTA 1

RESULT 1508
ADD21650/c
ID ADD21650 standard; DNA; 20 BP.
XX
AC ADD21650;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #213.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1855 TTTATTACATATATCAAG 1874

KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1702 GTGCAAGAGCTAAAGAA 1721
DB 20 GTGCAAGAGCTAAAGAA 1

RESULT 1509
ADD21702/c
ID ADD21702 standard; DNA; 20 BP.
XX
AC ADD21702;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #265.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2341 CAAAGTCTGGGATTACAGG 2360
DB 20 CAAAGTCTGGGATTACAGG 1

RESULT 1510
ADD21712/c
ID ADD21712 standard; DNA; 20 BP.
XX
AC ADD21712;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #268.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 CACCTCACAGATTCAGCTT 375
DB 20 CACCTCACAGATTCAGCTT 1

RESULT 1511
ADD21719/c
ID ADD21719 standard; DNA; 20 BP.
XX
AC ADD21719;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #275.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 AGATTCAGCTTCGAACAA 383
DB 20 AGATTCAGCTTCGAACAA 1

RESULT 1512
ADD21734/c
ID ADD21734 standard; DNA; 20 BP.
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XX ADD21734;
AC
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #290.
XX
XX
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1230 TCATGCAATGAATGAATCC 1249
Db 20 TCATGCAATGAATGAATCC 1
RESULT 1513
ADD21748/c
ID ADD21748 standard; DNA; 20 BP.
XX
XX
AC ADD21748;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #304.
XX
XX
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1742 ATGTAGACACCAATTCAAA 1761
Db 20 ATGTAGACACCAATTCAAA 1
RESULT 1514
ADD21750/c
ID ADD21750 standard; DNA; 20 BP.
XX
XX
AC ADD21750;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #306.
XX
XX
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1762 TGATTGTGCTAACTATTTC 1781
Db 20 TGATTGTGCTAACTATTTC 1
RESULT 1515
ADD21438/c
ID ADD21438 standard; DNA; 20 BP.
XX
XX
AC ADD21438;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #1.
XX

KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCACCGCGGAGCTTGCGCTG 20
Db 20 GCACCGCGGAGCTTGCGCTG 1
RESULT 1516
ADD21451/c
ID ADD21451 standard; DNA; 20 BP.
XX
XX
AC ADD21451;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #14.
XX
XX
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1776 TATTTCCCTAGTTGACCTG 1795
Db 20 TATTTCCCTAGTTGACCTG 1
RESULT 1517
ADD21495/c
ID ADD21495 standard; DNA; 20 BP.
XX
XX
AC ADD21495;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #58.
XX
XX
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 299 GAGGAGCAGCGCAATGTGCA 318
Db 20 GAGGAGCAGCGCAATGTGCA 1
RESULT 1518
ADD21566/c
ID ADD21566 standard; DNA; 20 BP.
XX
XX
AC ADD21566;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #129.
XX
XX
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 971 GAATCCGATCTTGATCTG 990
Db 20 GAATCCGATCTTGATCTG 1

RESULT 1519
ADD21569/c
ID ADD21569 standard; DNA; 20 BP.
XX
AC
XX ADD21569;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #132.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1006 CAGGTGATTGTTGGATCAG 1025
Db 20 CAGGTGATTGTTGGATCAG 1

RESULT 1520
ADD21595/c
ID ADD21595 standard; DNA; 20 BP.
XX
AC ADD21595;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #158.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1275 TGTGGGCCCTTCGTGAGAA 1294
Db 20 TGTGGGCCCTTCGTGAGAA 1

RESULT 1521
ADD21627/c
ID ADD21627 standard; DNA; 20 BP.
XX
AC ADD21627;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #190.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1624 GTGTGATTGTCAAGGTGCA 1643
Db 20 GTGTGATTGTCAAGGTGCA 1

RESULT 1522
ADD21651/c
ID ADD21651 standard; DNA; 20 BP.
XX
AC ADD21651;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #214.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1865 TATATCAAAAGTGAGAAAATG 1884
Db 20 TATATCAAAAGTGAGAAAATG 1

RESULT 1523
ADD21653/c
ID ADD21653 standard; DNA; 20 BP.
XX
AC ADD21653;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #216.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1883 TGCCTCAATTACATAGATT 1902
Db 20 TGCCTCAATTACATAGATT 1

RESULT 1524
ADD21701/c
ID ADD21701 standard; DNA; 20 BP.
XX
AC ADD21701;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #264.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2334 GGCCTCCCAAAGTCTGGGA 2353
Db 20 GGCCTCCCAAAGTCTGGGA 1

RESULT 1525
ADD21726/c
ID ADD21726 standard; DNA; 20 BP.
XX
AC ADD21726;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #282.
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XX antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;  
KW  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 482 TGGCCAGTATATGACTA 501  
DB 20 TGGCCAGTATATGACTA 1  
RESULT 1526  
ADD21728/c  
ID ADD21728 standard; DNA; 20 BP.  
XX  
AC ADD21728;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human mdm2 antisense oligonucleotide #284.  
XX  
KW antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;  
KW  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 780 TCTACCTCATCTAGAGGAG 799  
DB 20 TCTACCTCATCTAGAGGAG 1  
RESULT 1527  
ADD21733/c  
ID ADD21733 standard; DNA; 20 BP.  
XX  
AC ADD21733;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human mdm2 antisense oligonucleotide #289.  
XX  
KW antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;  
KW  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1203 TCCTTAGCTGACTATTGGAA 1222  
DB 20 TCCTTAGCTGACTATTGGAA 1  
RESULT 1528  
ADD21752/c  
ID ADD21752 standard; DNA; 20 BP.  
XX  
AC ADD21752;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human mdm2 antisense oligonucleotide #308.  
XX  
KW antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;  
KW  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1782 CCTAGTTGACCTGTCTATA 1801  
DB 20 CCTAGTTGACCTGTCTATA 1  
RESULT 1529  
ADD21445/c  
ID ADD21445 standard; DNA; 20 BP.  
XX  
AC ADD21445;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human mdm2 antisense oligonucleotide #8.  
XX  
KW antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;  
KW  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 303 AGCAGGCAAAATGTGCAATAC 322  
DB 20 AGCAGGCAAAATGTGCAATAC 1  
RESULT 1530  
ADD21478/c  
ID ADD21478 standard; DNA; 20 BP.  
XX  
AC ADD21478;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human mdm2 antisense oligonucleotide #41.  
XX  
KW antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;  
KW  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 105 GATCCTGCTGCTTTGCGAGC 124  
DB 20 GATCCTGCTGCTTTGCGAGC 1  
RESULT 1531  
ADD21493/c  
ID ADD21493 standard; DNA; 20 BP.  
XX  
AC ADD21493;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human mdm2 antisense oligonucleotide #56.  
XX  
KW antisense oligonucleotide; human; mdm2; hyperproliferation;  
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;  
KW  
Query Match 0.8%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 297 GTGAGGAGCAGGCAATGTG 316  
DB 20 GTGAGGAGCAGGCAATGTG 1  
RESULT 1532
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ADD21505/c
ID  ADD21505 standard; DNA; 20 BP.
XX
AC  ADD21505;
XX
DT  15-JAN-2004 (first entry)
XX
DE  Human mdm2 antisense oligonucleotide #68.
KW  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  310 AAATGTCGAATACCAACATG 329
Db  ||||| ||||| ||||| ||||| |||||
    20 AAATGTCGAATACCAACATG 1

RESULT 1533
ADD21524/c
ID  ADD21524 standard; DNA; 20 BP.
XX
AC  ADD21524;
XX
DT  15-JAN-2004 (first entry)
XX
DE  Human mdm2 antisense oligonucleotide #87.
KW  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  515 TGAGAGCAACCAACATATTG 534
Db  ||||| ||||| ||||| ||||| |||||
    20 TGAGAGCAACCAACATATTG 1

RESULT 1534
ADD21533/c
ID  ADD21533 standard; DNA; 20 BP.
XX
AC  ADD21533;
XX
DT  15-JAN-2004 (first entry)
XX
DE  Human mdm2 antisense oligonucleotide #96.
KW  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  593 AGAGCAGAGAAATATATA 612
Db  ||||| ||||| ||||| ||||| |||||
    20 AGAGCAGAGAAATATATA 1

RESULT 1535
ADD21540/c
ID  ADD21540 standard; DNA; 20 BP.
XX
AC  ADD21540;
XX
DT  15-JAN-2004 (first entry)
XX
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DE  Human mdm2 antisense oligonucleotide #103.
XX
KW  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  669 ACATCTGTGAGTGAGAACAG 688
Db  ||||| ||||| ||||| ||||| |||||
    20 ACATCTGTGAGTGAGAACAG 1

RESULT 1536
ADD21550/c
ID  ADD21550 standard; DNA; 20 BP.
XX
AC  ADD21550;
XX
DT  15-JAN-2004 (first entry)
XX
DE  Human mdm2 antisense oligonucleotide #113.
KW  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  787 CATCTAGAGGAGGAGCAATT 806
Db  ||||| ||||| ||||| ||||| |||||
    20 CATCTAGAGGAGGAGCAATT 1

RESULT 1537
ADD21573/c
ID  ADD21573 standard; DNA; 20 BP.
XX
AC  ADD21573;
XX
DT  15-JAN-2004 (first entry)
XX
DE  Human mdm2 antisense oligonucleotide #136.
KW  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1046 TAGTGTAAGATTGGAAGTTG 1065
Db  ||||| ||||| ||||| ||||| |||||
    20 TAGTGTAAGATTGGAAGTTG 1

RESULT 1538
ADD21574/c
ID  ADD21574 standard; DNA; 20 BP.
XX
AC  ADD21574;
XX
DT  15-JAN-2004 (first entry)
XX
DE  Human mdm2 antisense oligonucleotide #137.
KW  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1051 TAGAATTTGACGTTGAATCT 1070
Db 20 TAGAATTTGAAGTTGAATCT 1

RESULT 1539
ADD21581/c
ID ADD21581 standard; DNA; 20 BP.
XX
AC ADD21581;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #144.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1105 GACAAGAACTCTCAGATCAA 1124
Db 20 GACAAGAACTCTCAGATCAA 1

RESULT 1540
ADD21594/c
ID ADD21594 standard; DNA; 20 BP.
XX
AC ADD21594;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #157.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1268 CAACAGATGTTGGCCCTTC 1287
Db 20 CAACAGATGTTGGCCCTTC 1

RESULT 1541
ADD21615/c
ID ADD21615 standard; DNA; 20 BP.
XX
AC ADD21615;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #178.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1499 GCCATCAACTTCTAGTAGCA 1518
Db 20 GCCATCAACTTCTAGTAGCA 1

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 1542
ADD21625/c
ID ADD21625 standard; DNA; 20 BP.
XX
AC ADD21625;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #188.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1605 CTTAATGCCATTGAACCTTG 1624
Db 20 CTTAATGCCATTGAACCTTG 1

RESULT 1543
ADD21628/c
ID ADD21628 standard; DNA; 20 BP.
XX
AC ADD21628;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #191.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1648 AAAATGTTGCATGTCCAT 1667
Db 20 AAAATGTTGCATGTCCAT 1

RESULT 1544
ADD21637/c
ID ADD21637 standard; DNA; 20 BP.
XX
AC ADD21637;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #200.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1726 ATAAGCCCTGCCCATGTGT 1745
Db 20 ATAAGCCCTGCCCATGTGT 1

RESULT 1545
ADD21668/c
ID ADD21668 standard; DNA; 20 BP.
XX
AC ADD21668;
XX
DT 15-JAN-2004 (first entry)
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XX Human mdm2 antisense oligonucleotide #231.
DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1997 TCCTAATTTTAAATAATTTTC 2016
DB 20 TCCTAATTTTAAATAATTTTC 1

RESULT 1546
ADD21685/c
ID ADD21685 standard; DNA; 20 BP.
XX
AC ADD21685;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #248.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2191 TCCTGCCTCAGCCTCCCAAT 2210
DB 20 TCCTGCCTCAGCCTCCCAAT 1

RESULT 1547
ADD21697/c
ID ADD21697 standard; DNA; 20 BP.
XX
AC ADD21697;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #260.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2298 GGTCTCGATCTCTGACCTC 2317
DB 20 GGTCTCGATCTCTGACCTC 1

RESULT 1548
ADD21721/c
ID ADD21721 standard; DNA; 20 BP.
XX
AC ADD21721;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #277.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;

XX Human mdm2 antisense oligonucleotide #231.
DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1997 TCCTAATTTTAAATAATTTTC 2016
DB 20 TCCTAATTTTAAATAATTTTC 1

RESULT 1546
ADD21685/c
ID ADD21685 standard; DNA; 20 BP.
XX
AC ADD21685;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #248.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2191 TCCTGCCTCAGCCTCCCAAT 2210
DB 20 TCCTGCCTCAGCCTCCCAAT 1

RESULT 1547
ADD21697/c
ID ADD21697 standard; DNA; 20 BP.
XX
AC ADD21697;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #260.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2298 GGTCTCGATCTCTGACCTC 2317
DB 20 GGTCTCGATCTCTGACCTC 1

RESULT 1548
ADD21721/c
ID ADD21721 standard; DNA; 20 BP.
XX
AC ADD21721;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #277.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;

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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 366 ATTCAGCTTCGGAACAAGA 385
DB 20 ATTCAGCTTCGGAACAAGA 1

RESULT 1549
ADD21741/c
ID ADD21741 standard; DNA; 20 BP.
XX
AC ADD21741;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #297.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1662 GTCCATGGCAAAACAGGACA 1681
DB 20 GTCCATGGCAAAACAGGACA 1

RESULT 1550
ADD21743/c
ID ADD21743 standard; DNA; 20 BP.
XX
AC ADD21743;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #299.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1682 TCTTATGGCTGCTTTACAT 1701
DB 20 TCTTATGGCTGCTTTACAT 1

RESULT 1551
ADD21450/c
ID ADD21450 standard; DNA; 20 BP.
XX
AC ADD21450;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #13.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1695 TTTACATGTGCAAGAAGCT 1714
DB 20 TTTACATGTGCAAGAAGCT 1

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RESULT 1552
ADD21460/c
ID ADD21460 standard; DNA; 20 BP.
XX
AC ADD21460;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #23.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 37 GGCCCTGTGTCTCGGAAGA 56
DB 20 GGCCCTGTGTCTCGGAAGA 1

RESULT 1553
ADD21476/c
ID ADD21476 standard; DNA; 20 BP.
XX
AC ADD21476;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #39.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 70 CGAGCCCGAGGGCGGCGC 89
DB 20 CGAGCCCGAGGGCGGCGC 1

RESULT 1554
ADD21477/c
ID ADD21477 standard; DNA; 20 BP.
XX
AC ADD21477;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #40.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 98 TGACCGAGATCTGTGTT 117
DB 20 TGACCGAGATCTGTGTT 1

RESULT 1555
ADD21521/c
ID ADD21521 standard; DNA; 20 BP.
XX
AC ADD21521;
XX
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DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #84.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 490 ATATTATGACTAAACGATTA 509
DB 20 ATATTATGACTAAACGATTA 1

RESULT 1556
ADD21570/c
ID ADD21570 standard; DNA; 20 BP.
XX
AC ADD21570;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #133.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1017 TTGGATCAGGATTCAGTTTC 1036
DB 20 TTGGATCAGGATTCAGTTTC 1

RESULT 1557
ADD21585/c
ID ADD21585 standard; DNA; 20 BP.
XX
AC ADD21585;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #148.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1149 GTGTATCAGCGGCGAGAG 1168
DB 20 GTGTATCAGCGGCGAGAG 1

RESULT 1558
ADD21593/c
ID ADD21593 standard; DNA; 20 BP.
XX
AC ADD21593;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #156.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1257 CCATCATTGCAACAGTG 1276
DB 20 CCATCATTGCAACAGTG 1

RESULT 1559
ADD21614/c
ID ADD21614 standard; DNA; 20 BP.
XX
AC ADD21614;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #177.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1489 ACTATTCTCAGCCATCAACT 1508
DB 20 ACTATTCTCAGCCATCAACT 1

RESULT 1560
ADD21618/c
ID ADD21618 standard; DNA; 20 BP.
XX
AC ADD21618;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #181.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1522 TTTATAGCAGCCAGAGAT 1541
DB 20 TTTATAGCAGCCAGAGAT 1

RESULT 1561
ADD21620/c
ID ADD21620 standard; DNA; 20 BP.
XX
AC ADD21620;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #183.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1541 TGTGAAGAGTTTGAAGGG 1560
DB 20 TGTGAAGAGTTTGAAGGG 1

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 1562
ADD21630/c
ID ADD21630 standard; DNA; 20 BP.
XX
AC ADD21630;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #193.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1667 TGGCAAAACAGGACATCTTA 1686
DB 20 TGGCAAAACAGGACATCTTA 1

RESULT 1563
ADD21635/c
ID ADD21635 standard; DNA; 20 BP.
XX
AC ADD21635;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #198.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1710 AAGCTAAAGAAAAGGAATAA 1729
DB 20 AAGCTAAAGAAAAGGAATAA 1

RESULT 1564
ADD21647/c
ID ADD21647 standard; DNA; 20 BP.
XX
AC ADD21647;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #210.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1832 CTAGGAATTTAGACAACCTG 1851
DB 20 CTAGGAATTTAGACAACCTG 1

RESULT 1565
ADD21652/c
ID ADD21652 standard; DNA; 20 BP.
XX
AC ADD21652;
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XX 15-JAN-2004 (first entry)
DT
XX Human mdm2 antisense oligonucleotide #215.
DE
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1872 AAGTGAGAAATGCTCAAT 1891
Db 20 AAGTGAGAAATGCTCAAT 1
XX
RESULT 1566
ADD21699/c
ID ADD21699 standard; DNA; 20 BP.
XX
AC ADD21699;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #262.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2319 TGATCCGCCACCTCGGCT 2338
Db 20 TGATCCGCCACCTCGGCT 1
XX
RESULT 1567
ADD21735/c
ID ADD21735 standard; DNA; 20 BP.
XX
AC ADD21735;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #291.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1341 AAAGCCAACTGGAATCTC 1360
Db 20 AAAGCCAACTGGAATCTC 1
XX
RESULT 1568
ADD21446/c
ID ADD21446 standard; DNA; 20 BP.
XX
AC ADD21446;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #9.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
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Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 331 CTGTACTACTGATGGTCT 350
Db 20 CTGTACTACTGATGGTCT 1
XX
RESULT 1569
ADD21481/c
ID ADD21481 standard; DNA; 20 BP.
XX
AC ADD21481;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #44.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 150 AGTGGTACGAGCGCCAGT 169
Db 20 AGTGGTACGAGCGCCAGT 1
XX
RESULT 1570
ADD21512/c
ID ADD21512 standard; DNA; 20 BP.
XX
AC ADD21512;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #75.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 351 GTAAACCCTCACAGATTCC 370
Db 20 GTAAACCCTCACAGATTCC 1
XX
RESULT 1571
ADD21516/c
ID ADD21516 standard; DNA; 20 BP.
XX
AC ADD21516;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #79.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 392 GGTAGACCAAGCCATTGC 411
Db 20 GGTAGACCAAGCCATTGC 411
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Db      20  GGTTAGACCAAGCCATTGC 1

RESULT 1572
ADD21527/c
ID  ADD21527 standard; DNA; 20 BP.
XX
XX
AC  ADD21527;
XX
XX
DT      15-JAN-2004 (first entry)
XX
XX
DE      Human mdm2 antisense oligonucleotide #90.
XX
XX
KW  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      538 ATTGTTCAAAATGATCTTCTA 557
      |||||
Db      20 ATTGTTCAAAATGATCTTCTA 1

RESULT 1573
ADD21528/c
ID  ADD21528 standard; DNA; 20 BP.
XX
XX
AC  ADD21528;
XX
XX
DT      15-JAN-2004 (first entry)
XX
XX
DE      Human mdm2 antisense oligonucleotide #91.
XX
XX
KW  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      549 GATCTTCTAGGAGATTGTT 568
      |||||
Db      20 GATCTTCTAGGAGATTGTT 1

RESULT 1574
ADD21529/c
ID  ADD21529 standard; DNA; 20 BP.
XX
XX
AC  ADD21529;
XX
XX
DT      15-JAN-2004 (first entry)
XX
XX
DE      Human mdm2 antisense oligonucleotide #92.
XX
XX
KW  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      559 GAGATTGTTGGCGTGCCA 578
      |||||
Db      20 GAGATTGTTGGCGTGCCA 1

RESULT 1575
ADD21534/c
ID  ADD21534 standard; DNA; 20 BP.
XX
XX
AC  ADD21534;
XX
XX
DT      15-JAN-2004 (first entry)
XX
XX
DE      Human mdm2 antisense oligonucleotide #97.
XX
XX
KW  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      600 AGGAAATATATACCATGAT 619
      |||||
Db      20 AGGAAATATATACCATGAT 1

RESULT 1576
ADD21546/c
ID  ADD21546 standard; DNA; 20 BP.
XX
XX
AC  ADD21546;
XX
XX
DT      15-JAN-2004 (first entry)
XX
XX
DE      Human mdm2 antisense oligonucleotide #109.
XX
XX
KW  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      740 GGAAGAGAAACCTTCATCTT 759
      |||||
Db      20 GGAAGAGAAACCTTCATCTT 1

RESULT 1577
ADD21556/c
ID  ADD21556 standard; DNA; 20 BP.
XX
XX
AC  ADD21556;
XX
XX
DT      15-JAN-2004 (first entry)
XX
XX
DE      Human mdm2 antisense oligonucleotide #119.
XX
XX
KW  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      857 ACGCCACAAATCTGATAGTA 876
      |||||
Db      20 ACGCCACAAATCTGATAGTA 1

RESULT 1578
ADD21606/c
ID  ADD21606 standard; DNA; 20 BP.
XX
XX
AC  ADD21606;
XX
XX
DT      15-JAN-2004 (first entry)
XX
XX
DE      Human mdm2 antisense oligonucleotide #169.
XX
XX
KW  antisense oligonucleotide; human; mdm2; hyperproliferation;
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KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
  Query Match      0.8%; Score 20; DB 1; Length 20;
  Best Local Similarity 100.0%; Pred. No. 1.8e+03;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1412 GAATGATTCACAGAGTGCAT 1431
Db 20 GAATGATTCACAGAGTGCAT 1

RESULT 1579
ADD21617/c
ID ADD21617 standard; DNA; 20 BP.
XX
AC ADD21617;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #180.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

  Query Match      0.8%; Score 20; DB 1; Length 20;
  Best Local Similarity 100.0%; Pred. No. 1.8e+03;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1517 CATTATTATAGCAGCCCAAG 1536
Db 20 CATTATTATAGCAGCCCAAG 1

RESULT 1580
ADD21669/c
ID ADD21669 standard; DNA; 20 BP.
XX
AC ADD21669;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #232.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

  Query Match      0.8%; Score 20; DB 1; Length 20;
  Best Local Similarity 100.0%; Pred. No. 1.8e+03;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2004 TTAAATAATTTCTACTCTG 2023
Db 20 TTAAATAATTTCTACTCTG 1

RESULT 1581
ADD21676/c
ID ADD21676 standard; DNA; 20 BP.
XX
AC ADD21676;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #239.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

  Query Match      0.8%; Score 20; DB 1; Length 20;
  Best Local Similarity 100.0%; Pred. No. 1.8e+03;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2111 TTGCTCTGTACCAGGCTG 2130
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Db 20 TTGCTCTGTACCAGGCTG 1

RESULT 1582
ADD21739/c
ID ADD21739 standard; DNA; 20 BP.
XX
AC ADD21739;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #295.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

  Query Match      0.8%; Score 20; DB 1; Length 20;
  Best Local Similarity 100.0%; Pred. No. 1.8e+03;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1642 GACCTAAAAATGTTGCATT 1661
Db 20 GACCTAAAAATGTTGCATT 1

RESULT 1583
ADD21441/c
ID ADD21441 standard; DNA; 20 BP.
XX
AC ADD21441;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #4.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

  Query Match      0.8%; Score 20; DB 1; Length 20;
  Best Local Similarity 100.0%; Pred. No. 1.8e+03;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 ATTAGTCGTACGAGGCC 166
Db 20 ATTAGTCGTACGAGGCC 1

RESULT 1584
ADD21473/c
ID ADD21473 standard; DNA; 20 BP.
XX
AC ADD21473;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #36.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

  Query Match      0.8%; Score 20; DB 1; Length 20;
  Best Local Similarity 100.0%; Pred. No. 1.8e+03;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 GTGTGTCGGAAGATGAGC 62
Db 20 GTGTGTCGGAAGATGAGC 1

RESULT 1585
ADD21474/c
ID ADD21474 standard; DNA; 20 BP.
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XX ADD21474;
XX 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #37.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
XX hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 GGAAGATGGAGCAAGAAGC 69
DB 20 GGAAGATGGAGCAAGAAGC 1

RESULT 1586
ADD21491/c
ID ADD21491 standard; DNA; 20 BP.
XX AC ADD21491;
XX 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #54.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
XX hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 294 ATGGTGAGGAGCAGGCAAAAT 313
DB 20 ATGGTGAGGAGCAGGCAAAAT 1

RESULT 1587
ADD21500/c
ID ADD21500 standard; DNA; 20 BP.
XX AC ADD21500;
XX 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #63.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
XX hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 305 CAGGCAAAATGCAATACCA 324
DB 20 CAGGCAAAATGCAATACCA 1

RESULT 1588
ADD21513/c
ID ADD21513 standard; DNA; 20 BP.
XX AC ADD21513;
XX 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #76.

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KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 361 CACAGATTCAGCTTCGGAA 380
DB 20 CACAGATTCAGCTTCGGAA 1

RESULT 1589
ADD21519/c
ID ADD21519 standard; DNA; 20 BP.
XX AC ADD21519;
XX 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #82.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
XX hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 450 ACTTATACTATGAAGAGGT 469
DB 20 ACTTATACTATGAAGAGGT 1

RESULT 1590
ADD21536/c
ID ADD21536 standard; DNA; 20 BP.
XX AC ADD21536;
XX 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #99.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
XX hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 619 TCTACAGGAACCTGGTAGTA 638
DB 20 TCTACAGGAACCTGGTAGTA 1

RESULT 1591
ADD21541/c
ID ADD21541 standard; DNA; 20 BP.
XX AC ADD21541;
XX 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #104.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
XX hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 682 AGAACAGGTGTACCTTGAA 701
Db |||||
20 AGAACAGGTGTACCTTGAA 1

RESULT 1592
ADD21547/c
ID ADD21547 standard; DNA; 20 BP.
XX
AC ADD21547;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #110.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 752 TTCATCTTCACATTGGTTT 771
Db |||||
20 TTCATCTTCACATTGGTTT 1

RESULT 1593
ADD21558/c
ID ADD21558 standard; DNA; 20 BP.
XX
AC ADD21558;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #121.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 880 CCTTTCCTTTGATGAAGC 899
Db |||||
20 CCTTTCCTTTGATGAAGC 1

RESULT 1594
ADD21563/c
ID ADD21563 standard; DNA; 20 BP.
XX
AC ADD21563;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #126.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 936 AGAAGCAGTACGATGC 955
Db |||||
20 AGAAGCAGTACGATGC 1

RESULT 1595
ADD21589/c
ID ADD21589 standard; DNA; 20 BP.
XX
AC ADD21589;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #152.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1196 TGAATTTCCCTTAGCTGACT 1215
Db |||||
20 TGAATTTCCCTTAGCTGACT 1

RESULT 1596
ADD21597/c
ID ADD21597 standard; DNA; 20 BP.
XX
AC ADD21597;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #160.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1292 GAATTGGCTTCCTGAAGATA 1311
Db |||||
20 GAATTGGCTTCCTGAAGATA 1

RESULT 1597
ADD21598/c
ID ADD21598 standard; DNA; 20 BP.
XX
AC ADD21598;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #161.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1301 TCCTGAAGATAAAGGGAAG 1320
Db |||||
20 TCCTGAAGATAAAGGGAAG 1

RESULT 1598
ADD21603/c
ID ADD21603 standard; DNA; 20 BP.
XX
AC ADD21603;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #166.
```


XX antisense oligonucleotide; human; mdm2; hyperproliferation;
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1358 CTCACACAAGCTGAAGAGG 1377
 Db 20 CTCACACAAGCTGAAGAGG 1

RESULT 1599

ADD21611/c
 ID ADD21611 standard; DNA; 20 BP.

XX
 AC ADD21611;

XX
 DT 15-JAN-2004 (first entry)

XX Human mdm2 antisense oligonucleotide #174.

XX antisense oligonucleotide; human; mdm2; hyperproliferation;
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1456 TTACACAAGCTTCACATCA 1475
 Db 20 TTACACAAGCTTCACATCA 1

RESULT 1600

ADD21631/c
 ID ADD21631 standard; DNA; 20 BP.

XX
 AC ADD21631;

XX
 DT 15-JAN-2004 (first entry)

XX Human mdm2 antisense oligonucleotide #194.

XX antisense oligonucleotide; human; mdm2; hyperproliferation;
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1675 CAGGACATCTTATGCGCTGC 1694
 Db 20 CAGGACATCTTATGCGCTGC 1

RESULT 1601

ADD21655/c
 ID ADD21655 standard; DNA; 20 BP.

XX
 AC ADD21655;

XX
 DT 15-JAN-2004 (first entry)

XX Human mdm2 antisense oligonucleotide #218.

XX antisense oligonucleotide; human; mdm2; hyperproliferation;
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1898 AGATTTCTTCTTTAGTAT 1917
 Db 20 AGATTTCTTCTTTAGTAT 1

RESULT 1602

ADD21656/c
 ID ADD21656 standard; DNA; 20 BP.

XX
 AC ADD21656;

XX
 DT 15-JAN-2004 (first entry)

XX Human mdm2 antisense oligonucleotide #219.

XX antisense oligonucleotide; human; mdm2; hyperproliferation;
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1905 TTCTTTTACTATAATTGAC 1924
 Db 20 TTCTTTTACTATAATTGAC 1

RESULT 1603

ADD21660/c
 ID ADD21660 standard; DNA; 20 BP.

XX
 AC ADD21660;

XX
 DT 15-JAN-2004 (first entry)

XX Human mdm2 antisense oligonucleotide #223.

XX antisense oligonucleotide; human; mdm2; hyperproliferation;
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1933 GTAGTGAATAGTGAATACT 1952
 Db 20 GTAGTGAATAGTGAATACT 1

RESULT 1604

ADD21664/c
 ID ADD21664 standard; DNA; 20 BP.

XX
 AC ADD21664;

XX
 DT 15-JAN-2004 (first entry)

XX Human mdm2 antisense oligonucleotide #227.

XX antisense oligonucleotide; human; mdm2; hyperproliferation;
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1969 GAATATGATGCTCATCCTTT 1988
 Db 20 GAATATGATGCTCATCCTTT 1

RESULT 1605

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ADD21667/c
ID ADD21667 standard; DNA; 20 BP.
XX
AC ADD21667;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #230.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1990 CACCAACTCCTAATTTTAA 209
DB 20 CACCAACTCCTAATTTTAA 1

RESULT 1606
ADD21672/c
ID ADD21672 standard; DNA; 20 BP.
XX
AC ADD21672;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #235.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2051 TTTTCTTAATATGTATATG 2070
DB 20 TTTTCTTAATATGTATATG 1

RESULT 1607
ADD21674/c
ID ADD21674 standard; DNA; 20 BP.
XX
AC ADD21674;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #237.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2072 CATTTAATGTAACTTATTA 2091
DB 20 CATTTAATGTAACTTATTA 1

RESULT 1608
ADD21677/c
ID ADD21677 standard; DNA; 20 BP.
XX
AC ADD21677;
XX
DT 15-JAN-2004 (first entry)
XX
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```
DE Human mdm2 antisense oligonucleotide #240.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2116 CTGTTACCCAGGCTGGAGTG 2135
DB 20 CTGTTACCCAGGCTGGAGTG 1

RESULT 1609
ADD21684/c
ID ADD21684 standard; DNA; 20 BP.
XX
AC ADD21684;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #247.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2185 CCATTCTCTGCTCAGCCT 2204
DB 20 CCATTCTCTGCTCAGCCT 1

RESULT 1610
ADD21715/c
ID ADD21715 standard; DNA; 20 BP.
XX
AC ADD21715;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #271.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 CTCACAGATTCCAGCTTCGG 378
DB 20 CTCACAGATTCCAGCTTCGG 1

RESULT 1611
ADD21720/c
ID ADD21720 standard; DNA; 20 BP.
XX
AC ADD21720;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #276.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 365 GATTCAGCTTCGGAACAAG 384
    |||||
Db 20 GATTCAGCTTCGGAACAAG 1

RESULT 1612
ADD21723/c
ID ADD21723 standard; DNA; 20 BP.
XX
AC ADD21723;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #279.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 368 TCCAGCTTCGGAACAAGAGA 387
    |||||
Db 20 TCCAGCTTCGGAACAAGAGA 1

RESULT 1613
ADD21747/c
ID ADD21747 standard; DNA; 20 BP.
XX
AC ADD21747;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #303.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1732 CCTGCCAGTATGTAGACAA 1751
    |||||
Db 20 CCTGCCAGTATGTAGACAA 1

RESULT 1614
ADD21447/c
ID ADD21447 standard; DNA; 20 BP.
XX
AC ADD21447;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #10.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 617 GATCTACAGGAACCTGGTAG 636
    |||||
Db 20 GATCTACAGGAACCTGGTAG 1

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RESULT 1615
ADD21453/c
ID ADD21453 standard; DNA; 20 BP.
XX
AC ADD21453;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #16.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1818 CTAACCTATATACCCCTAGGA 1837
    |||||
Db 20 CTAACCTATATACCCCTAGGA 1

RESULT 1616
ADD21472/c
ID ADD21472 standard; DNA; 20 BP.
XX
AC ADD21472;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #35.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 TGTGGCCCTGTGTGCGAA 53
    |||||
Db 20 TGTGGCCCTGTGTGCGAA 1

RESULT 1617
ADD21483/c
ID ADD21483 standard; DNA; 20 BP.
XX
AC ADD21483;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #46.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 165 CCAGTGCCCTGGCCCGGAGA 184
    |||||
Db 20 CCAGTGCCCTGGCCCGGAGA 1

RESULT 1618
ADD21484/c
ID ADD21484 standard; DNA; 20 BP.
XX
AC ADD21484;
XX
DT 15-JAN-2004 (first entry)

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XX Human mdm2 antisense oligonucleotide #47.
DE
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 174 TGGCCCGGAGAGTGAATGA 193
DB 20 TGGCCCGGAGAGTGAATGA 1
RESULT 1619
ADD21490/c
ID ADD21490 standard; DNA; 20 BP.
XX
AC ADD21490;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #53.
DE
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 293 GATGGTGAGGAGCAGGCAAA 312
DB 20 GATGGTGAGGAGCAGGCAAA 1
RESULT 1620
ADD21492/c
ID ADD21492 standard; DNA; 20 BP.
XX
AC ADD21492;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #55.
DE
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 296 GGTGAGGAGCAGGCAAAATGT 315
DB 20 GGTGAGGAGCAGGCAAAATGT 1
RESULT 1621
ADD21496/c
ID ADD21496 standard; DNA; 20 BP.
XX
AC ADD21496;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #59.
DE
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 300 AGGAGCAGCAAAATGTGCAA 319
DB 20 AGGAGCAGCAAAATGTGCAA 1
RESULT 1622
ADD21510/c
ID ADD21510 standard; DNA; 20 BP.
XX
AC ADD21510;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #73.
DE
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 323 CAACATGCTGTACTACTG 342
DB 20 CAACATGCTGTACTACTG 1
RESULT 1623
ADD21518/c
ID ADD21518 standard; DNA; 20 BP.
XX
AC ADD21518;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #81.
DE
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 422 ATTAAGTCTGTGTGTGCAC 441
DB 20 ATTAAGTCTGTGTGTGCAC 1
RESULT 1624
ADD21542/c
ID ADD21542 standard; DNA; 20 BP.
XX
AC ADD21542;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #105.
DE
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 691 GTCACTTGAAGGTGGAGT 710
DB 20 GTCACTTGAAGGTGGAGT 1
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RESULT 1625
ADD21551/c
ID ADD21551 standard; DNA; 20 BP.
XX
AC ADD21551;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #114.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 798 AGAGCAATTAGTGACAGACA 817
Db 20 AGAGCAATTAGTGACAGACA 1

RESULT 1626
ADD21575/c
ID ADD21575 standard; DNA; 20 BP.
XX
AC ADD21575;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #138.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1059 GAAGTTGAATCTCTCGACTC 1078
Db 20 GAAGTTGAATCTCTCGACTC 1

RESULT 1627
ADD21586/c
ID ADD21586 standard; DNA; 20 BP.
XX
AC ADD21586;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #149.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1161 GGGGAGAGTGATACAGATTC 1180
Db 20 GGGGAGAGTGATACAGATTC 1

RESULT 1628
ADD21604/c
ID ADD21604 standard; DNA; 20 BP.
XX
AC ADD21604;
XX

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DT 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #167.
DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1368 GCTGAAGAGGGCTTTGATGT 1387
Db 20 GCTGAAGAGGGCTTTGATGT 1

RESULT 1629
ADD21605/c
ID ADD21605 standard; DNA; 20 BP.
XX
AC ADD21605;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #168.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1401 AAAACTATAGTGAATGATTC 1420
Db 20 AAAACTATAGTGAATGATTC 1

RESULT 1630
ADD21638/c
ID ADD21638 standard; DNA; 20 BP.
XX
AC ADD21638;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #201.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 CCCAGTATGTAGACAACCAA 1755
Db 20 CCCAGTATGTAGACAACCAA 1

RESULT 1631
ADD21642/c
ID ADD21642 standard; DNA; 20 BP.
XX
AC ADD21642;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #205.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;

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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1798 TATAAGAGAATTATATATTT 1817
DB 20 TATAAGAGAATTATATATTT 1

RESULT 1632
ADD21681/c
ID ADD21681 standard; DNA; 20 BP.
XX
AC ADD21681;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #244.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2146 TCTTGGCTCACTGCAAGCTC 2165
DB 20 TCTTGGCTCACTGCAAGCTC 1

RESULT 1633
ADD21696/c
ID ADD21696 standard; DNA; 20 BP.
XX
AC ADD21696;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #259.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2290 GCCAGGATGGTCTCGATCTC 2309
DB 20 GCCAGGATGGTCTCGATCTC 1

RESULT 1634
ADD21703/c
ID ADD21703 standard; DNA; 20 BP.
XX
AC ADD21703;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #266.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2351 GGATTACAGGCATGAGCCAC 2370
DB 20 GGATTACAGGCATGAGCCAC 1
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RESULT 1635
ADD21732/c
ID ADD21732 standard; DNA; 20 BP.
XX
AC ADD21732;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #288.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1202 TTCCTTAGCTGACTATTGGA 1221
DB 20 TTCCTTAGCTGACTATTGGA 1

RESULT 1636
ADD21742/c
ID ADD21742 standard; DNA; 20 BP.
XX
AC ADD21742;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #298.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1672 AAACAGGACATCTTATGGCC 1691
DB 20 AAACAGGACATCTTATGGCC 1

RESULT 1637
ADD21753/c
ID ADD21753 standard; DNA; 20 BP.
XX
AC ADD21753;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #309.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1792 CCTGTCTATAAGAAATTAT 1811
DB 20 CCTGTCTATAAGAAATTAT 1

RESULT 1638
ADD21767/c
ID ADD21767 standard; DNA; 20 BP.
XX
AC ADD21767;
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XX 15-JAN-2004 (first entry)
XX Mouse mdm2 antisense oligonucleotide #8.
XX antisense oligonucleotide; mouse; mdm2; hyperproliferation;
XX hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 741 GAAGAGAAACCTTCATCTTC 760
DB 20 GAAGAGAAACCTTCATCTTC 1

RESULT 1639
ADD21443/C
ID ADD21443 standard; DNA; 20 BP.
XX
AC ADD21443;
XX
XX 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #6.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
XX hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 CTCCAAGCGCGAAACCCCG 292
DB 20 CTCCAAGCGCGAAACCCCG 1

RESULT 1640
ADD21531/C
ID ADD21531 standard; DNA; 20 BP.
XX
AC ADD21531;
XX
XX 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #94.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
XX hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 575 GCCAAGCTTCTCTGTGAAG 594
DB 20 GCCAAGCTTCTCTGTGAAG 1

RESULT 1641
ADD21532/C
ID ADD21532 standard; DNA; 20 BP.
XX
AC ADD21532;
XX
XX 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #95.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
XX hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
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Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 587 TGTGAAAGACACAGGAAAA 606
DB 20 TGTGAAAGACACAGGAAAA 1

RESULT 1642
ADD21571/C
ID ADD21571 standard; DNA; 20 BP.
XX
AC ADD21571;
XX
XX 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #134.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
XX hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1023 CAGGATTCAGTTTCAGATCA 1042
DB 20 CAGGATTCAGTTTCAGATCA 1

RESULT 1643
ADD21582/C
ID ADD21582 standard; DNA; 20 BP.
XX
AC ADD21582;
XX
XX 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #145.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
XX hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1115 CTCAGATGAAGATGATGAGG 1134
DB 20 CTCAGATGAAGATGATGAGG 1

RESULT 1644
ADD21583/C
ID ADD21583 standard; DNA; 20 BP.
XX
AC ADD21583;
XX
XX 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #146.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
XX hyperproliferative disorder; cancer; psoriasis; fibrosis;
XX
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1124 AGATGATGAGGTATATCAAG 1143
DB 20 AGATGATGAGGTATATCAAG 1
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Db 20 AGATGATGAGGTATATCAAG 1

RESULT 1645
ADD21592/c
ID ADD21592 standard; DNA; 20 BP.
XX
AC ADD21592;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #155.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1226 CACTTCATGCAATGAATGA 1245
|||||
Db 20 CACTTCATGCAATGAATGA 1

RESULT 1646
ADD21601/c
ID ADD21601 standard; DNA; 20 BP.
XX
AC ADD21601;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #164.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1333 TCTCTGAGAAAGCCAACTG 1352
|||||
Db 20 TCTCTGAGAAAGCCAACTG 1

RESULT 1647
ADD21624/c
ID ADD21624 standard; DNA; 20 BP.
XX
AC ADD21624;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #187.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1580 AGAGAGTGTGGAATCTAGTT 1599
|||||
Db 20 AGAGAGTGTGGAATCTAGTT 1

RESULT 1648
ADD21643/c
ID ADD21643 standard; DNA; 20 BP.
XX

AC ADD21643;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #206.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1804 AGAATTATATATTTCTAACT 1823
|||||
Db 20 AGAATTATATATTTCTAACT 1

RESULT 1649
ADD21654/c
ID ADD21654 standard; DNA; 20 BP.
XX
AC ADD21654;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #217.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1889 AATTACATAGATTCTTCT 1908
|||||
Db 20 AATTACATAGATTCTTCT 1

RESULT 1650
ADD21690/c
ID ADD21690 standard; DNA; 20 BP.
XX
AC ADD21690;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #253.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2218 GCCTACAGTCATCTGCCACC 2237
|||||
Db 20 GCCTACAGTCATCTGCCACC 1

RESULT 1651
ADD21469/c
ID ADD21469 standard; DNA; 20 BP.
XX
AC ADD21469;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #32.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;


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KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TTGGCTGCTTCTGGGGCTG 33
DB 20 TTGGCTGCTTCTGGGGCTG 1

RESULT 1652
ADD21475/c
ID ADD21475 standard; DNA; 20 BP.
XX
AC ADD21475;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #38.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 CAAGAAGCCGAGCCGAGGG 81
DB 20 CAAGAAGCCGAGCCGAGGG 1

RESULT 1653
ADD21487/c
ID ADD21487 standard; DNA; 20 BP.
XX
AC ADD21487;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #50.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 CTTCCGCGAGTAGTCAGTCCC 236
DB 20 CTTCCGCGAGTAGTCAGTCCC 1

RESULT 1654
ADD21499/c
ID ADD21499 standard; DNA; 20 BP.
XX
AC ADD21499;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #62.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 304 GCAGGCAAAATGTGCAATACC 323
DB 20 GCAGGCAAAATGTGCAATACC 1

RESULT 1655
ADD21504/c
ID ADD21504 standard; DNA; 20 BP.
XX
AC ADD21504;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #67.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 309 CAAATGTGCAATACCAACAT 328
DB 20 CAAATGTGCAATACCAACAT 1

RESULT 1656
ADD21515/c
ID ADD21515 standard; DNA; 20 BP.
XX
AC ADD21515;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #78.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 386 GACCCCTGGTTAGACCAAGC 405
DB 20 GACCCCTGGTTAGACCAAGC 1

RESULT 1657
ADD21535/c
ID ADD21535 standard; DNA; 20 BP.
XX
AC ADD21535;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #98.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 609 TATACCATGATCTACAGGAA 628
DB 20 TATACCATGATCTACAGGAA 1

RESULT 1658
ADD21544/c
ID ADD21544 standard; DNA; 20 BP.
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XX ADD21544;
AC
XX 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #107.
XX
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 718 AGGACCTTGTAAGAGCTT 737
Db 20 AGGACCTTGTAAGAGCTT 1

RESULT 1659
ADD21587/c
ID ADD21587 standard; DNA; 20 BP.
XX
XX ADD21587;
AC
XX 15-JAN-2004 (first entry)
DT
DE Human mdm2 antisense oligonucleotide #150.
XX
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1170 GATACAGATTTCATTGGAAGA 1189
Db 20 GATACAGATTTCATTGGAAGA 1

RESULT 1660
ADD21602/c
ID ADD21602 standard; DNA; 20 BP.
XX
XX ADD21602;
AC
XX 15-JAN-2004 (first entry)
DT
DE Human mdm2 antisense oligonucleotide #165.
XX
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1346 CAAACTGGAAACTCAACAC 1365
Db 20 CAAACTGGAAACTCAACAC 1

RESULT 1661
ADD21623/c
ID ADD21623 standard; DNA; 20 BP.
XX
XX ADD21623;
AC
XX 15-JAN-2004 (first entry)
DT
DE Human mdm2 antisense oligonucleotide #186.
XX

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KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1566 ACCCAGACAAAGAAGAGAG 1585
Db 20 ACCCAGACAAAGAAGAGAG 1

RESULT 1662
ADD21666/c
ID ADD21666 standard; DNA; 20 BP.
XX
XX ADD21666;
AC
XX 15-JAN-2004 (first entry)
DT
DE Human mdm2 antisense oligonucleotide #229.
XX
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1982 ATCCTTTACACCAACTCCTA 2001
Db 20 ATCCTTTACACCAACTCCTA 1

RESULT 1663
ADD21678/c
ID ADD21678 standard; DNA; 20 BP.
XX
XX ADD21678;
AC
XX 15-JAN-2004 (first entry)
DT
DE Human mdm2 antisense oligonucleotide #241.
XX
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2123 CCAGGCTGGAGTGCAGTGGG 2142
Db 20 CCAGGCTGGAGTGCAGTGGG 1

RESULT 1664
ADD21682/c
ID ADD21682 standard; DNA; 20 BP.
XX
XX ADD21682;
AC
XX 15-JAN-2004 (first entry)
DT
DE Human mdm2 antisense oligonucleotide #245.
XX
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2153 TCACTGCAAGCTCTGCCCTC 2172
 Db 20 TCACTGCAAGCTCTGCCCTC 1

RESULT 1665

ADD21700/c
 ID ADD21700 standard; DNA; 20 BP.

XX AC ADD21700;
 XX 15-JAN-2004 (first entry)
 DT Human mdm2 antisense oligonucleotide #263.
 DE antisense oligonucleotide; human; mdm2; hyperproliferation;
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2325 GCCCACCCTCGCCTCCCAAA 2344
 Db 20 GCCCACCCTCGCCTCCCAAA 1

RESULT 1666

ADD21717/c
 ID ADD21717 standard; DNA; 20 BP.

XX AC ADD21717;
 XX 15-JAN-2004 (first entry)
 DT Human mdm2 antisense oligonucleotide #273.
 DE antisense oligonucleotide; human; mdm2; hyperproliferation;
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 362 ACAGATCCAGCTTCGGGAAAC 381
 Db 20 ACAGATCCAGCTTCGGGAAAC 1

RESULT 1667

ADD21745/c
 ID ADD21745 standard; DNA; 20 BP.

XX AC ADD21745;
 XX 15-JAN-2004 (first entry)
 DT Human mdm2 antisense oligonucleotide #301.
 DE antisense oligonucleotide; human; mdm2; hyperproliferation;
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1712 GCTAAAGAAAAGGAAATAGC 1731
 Db 20 GCTAAAGAAAAGGAAATAGC 1

RESULT 1668

ADD21746/c

ID ADD21746 standard; DNA; 20 BP.
 XX AC ADD21746;
 XX 15-JAN-2004 (first entry)

XX Human mdm2 antisense oligonucleotide #302.
 DE antisense oligonucleotide; human; mdm2; hyperproliferation;
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1722 AGGAATAAGCCCTGCCCACT 1741
 Db 20 AGGAATAAGCCCTGCCCACT 1

RESULT 1669

ADD21790/c
 ID ADD21790 standard; DNA; 20 BP.

XX AC ADD21790;
 XX 15-JAN-2004 (first entry)
 DT Mouse mdm2 antisense oligonucleotide #31.
 DE antisense oligonucleotide; mouse; mdm2; hyperproliferation;
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1758 CAAATGATTGTGCTAACTTA 1777
 Db 20 CAAATGATTGTGCTAACTTA 1

RESULT 1670

ADD21448/c
 ID ADD21448 standard; DNA; 20 BP.

XX AC ADD21448;
 XX 15-JAN-2004 (first entry)
 DT Human mdm2 antisense oligonucleotide #11.
 DE antisense oligonucleotide; human; mdm2; hyperproliferation;
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1047 AGTGTAGAAATTTGAAGTTGA 1066
 Db 20 AGTGTAGAAATTTGAAGTTGA 1

RESULT 1671

ADD21501/c
 ID ADD21501 standard; DNA; 20 BP.

XX AC ADD21501;
 XX 15-JAN-2004 (first entry)
 DT Human mdm2 antisense oligonucleotide #64.

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XX antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 306 AGGCAATGTGCATACCAA 325
DB 20 AGGCAATGTGCATACCAA 1

RESULT 1672
ADD21507/c
ID ADD21507 standard; DNA; 20 BP.
XX
AC ADD21507;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #70.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 ATGTGCAATACCAACATGTC 331
DB 20 ATGTGCAATACCAACATGTC 1

RESULT 1673
ADD21523/c
ID ADD21523 standard; DNA; 20 BP.
XX
AC ADD21523;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #86.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 503 ACGATTATATGATGAGAAGC 522
DB 20 ACGATTATATGATGAGAAGC 1

RESULT 1674
ADD21548/c
ID ADD21548 standard; DNA; 20 BP.
XX
AC ADD21548;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #111.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 761 ACATTGGTTTCTAGACCAT 780
DB 20 ACATTGGTTTCTAGACCAT 1

RESULT 1675
ADD21552/c
ID ADD21552 standard; DNA; 20 BP.
XX
AC ADD21552;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #115.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 810 GAGACAGAGAAAATTCAGA 829
DB 20 GAGACAGAGAAAATTCAGA 1

RESULT 1676
ADD21608/c
ID ADD21608 standard; DNA; 20 BP.
XX
AC ADD21608;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #171.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1434 GTTGAGGAAAATGATGATAA 1453
DB 20 GTTGAGGAAAATGATGATAA 1

RESULT 1677
ADD21662/c
ID ADD21662 standard; DNA; 20 BP.
XX
AC ADD21662;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #225.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1948 ATACTTACTATATTTGACT 1967
DB 20 ATACTTACTATATTTGACT 1

RESULT 1678
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ADD21665/c
ID  ADD21665 standard; DNA; 20 BP.
XX
AC  ADD21665;
XX
XX  15-JAN-2004 (first entry)
DE
DE  Human mdm2 antisense oligonucleotide #228.
KW  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1773 ATGTAGCTCATCCTTTACAC 1992
Db  20 ATGTAGCTCATCCTTTACAC 1

RESULT 1679
ADD21671/c
ID  ADD21671 standard; DNA; 20 BP.
XX
AC  ADD21671;
XX
XX  15-JAN-2004 (first entry)
DE
DE  Human mdm2 antisense oligonucleotide #234.
KW  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2020 TCTGCTTAAATGAGAGTA 2039
Db  20 TCTGCTTAAATGAGAGTA 1

RESULT 1680
ADD21716/c
ID  ADD21716 standard; DNA; 20 BP.
XX
AC  ADD21716;
XX
XX  15-JAN-2004 (first entry)
DE
DE  Human mdm2 antisense oligonucleotide #272.
KW  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  360 TCACAGATTCAGCTTCGA 379
Db  20 TCACAGATTCAGCTTCGA 1

RESULT 1681
ADD21730/c
ID  ADD21730 standard; DNA; 20 BP.
XX
AC  ADD21730;
XX
XX  15-JAN-2004 (first entry)
DE
DE  Human mdm2 antisense oligonucleotide #286.
KW  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1200 ATTTCTTAGCTGACTATTG 1219
Db  20 ATTTCTTAGCTGACTATTG 1

RESULT 1682
ADD21749/c
ID  ADD21749 standard; DNA; 20 BP.
XX
AC  ADD21749;
XX
XX  15-JAN-2004 (first entry)
DE
DE  Human mdm2 antisense oligonucleotide #305.
KW  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1752 CCAATTCAAATGATTGTGCT 1771
Db  20 CCAATTCAAATGATTGTGCT 1

RESULT 1683
ADD21751/c
ID  ADD21751 standard; DNA; 20 BP.
XX
AC  ADD21751;
XX
XX  15-JAN-2004 (first entry)
DE
DE  Human mdm2 antisense oligonucleotide #307.
KW  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1772 AACCTATTTCCCTAGTTGA 1791
Db  20 AACCTATTTCCCTAGTTGA 1

RESULT 1684
ADD21482/c
ID  ADD21482 standard; DNA; 20 BP.
XX
AC  ADD21482;
XX
XX  15-JAN-2004 (first entry)
DE
DE  Human mdm2 antisense oligonucleotide #45.
KW  antisense oligonucleotide; human; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 CGAGCGCCAGTGCCTGGC 177
DB 20 CGAGCGCCAGTGCCTGGC 1

RESULT 1685
ADD21539/c
ID ADD21539 standard; DNA; 20 BP.
XX
AC ADD21539;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #102.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 656 ATCGGACTCAGTACATCTG 675
DB 20 ATCGGACTCAGTACATCTG 1

RESULT 1686
ADD21561/c
ID ADD21561 standard; DNA; 20 BP.
XX
AC ADD21561;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #124.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 915 ATAAGGAGATATGTTGTGA 934
DB 20 ATAAGGAGATATGTTGTGA 1

RESULT 1687
ADD21562/c
ID ADD21562 standard; DNA; 20 BP.
XX
AC ADD21562;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #125.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 927 TGTGTGAAGACAGTAG 946
DB 20 TGTGTGAAGACAGTAG 1

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RESULT 1688
ADD21565/c
ID ADD21565 standard; DNA; 20 BP.
XX
AC ADD21565;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #128.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 964 CGCATCGAATCCGATCTT 983
DB 20 CGCATCGAATCCGATCTT 1

RESULT 1689
ADD21572/c
ID ADD21572 standard; DNA; 20 BP.
XX
AC ADD21572;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #135.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1034 TTCAGATCAGTTTAGTGTAG 1053
DB 20 TTCAGATCAGTTTAGTGTAG 1

RESULT 1690
ADD21580/c
ID ADD21580 standard; DNA; 20 BP.
XX
AC ADD21580;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #143.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1100 AGAAGGACAAAGACTCTCAG 1119
DB 20 AGAAGGACAAAGACTCTCAG 1

RESULT 1691
ADD21584/c
ID ADD21584 standard; DNA; 20 BP.
XX
AC ADD21584;
XX
DT 15-JAN-2004 (first entry)

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XX Human mdm2 antisense oligonucleotide #147.
DE antisense oligonucleotide; human; mdm2; hyperproliferation;
XX hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1135 TATATCAAGTTACTGTGTAT 1154
Db 20 TATATCAAGTTACTGTGTAT 1

RESULT 1692
ADD21590/c
ID ADD21590 standard; DNA; 20 BP.
XX
AC ADD21590;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #153.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1207 TAGCTGACTATTGGAATGC 1226
Db 20 TAGCTGACTATTGGAATGC 1

RESULT 1693
ADD21591/c
ID ADD21591 standard; DNA; 20 BP.
XX
AC ADD21591;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #154.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1220 GAAATGCATTCATGCAATG 1239
Db 20 GAAATGCATTCATGCAATG 1

RESULT 1694
ADD21607/c
ID ADD21607 standard; DNA; 20 BP.
XX
AC ADD21607;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #170.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1816 TTCTAACTATATACCCCTAG 1835
Db 20 TTCTAACTATATACCCCTAG 1

Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1421 CAGAGAGTCATGCTTGAGG 1440
Db 20 CAGAGAGTCATGCTTGAGG 1

RESULT 1695
ADD21621/c
ID ADD21621 standard; DNA; 20 BP.
XX
AC ADD21621;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #184.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1550 GTTTGAAAGGGAAGAACCC 1569
Db 20 GTTTGAAAGGGAAGAACCC 1

RESULT 1696
ADD21633/c
ID ADD21633 standard; DNA; 20 BP.
XX
AC ADD21633;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #196.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1690 CCTGCTTTACATGTGCAAG 1709
Db 20 CCTGCTTTACATGTGCAAG 1

RESULT 1697
ADD21645/c
ID ADD21645 standard; DNA; 20 BP.
XX
AC ADD21645;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #208.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1816 TTCTAACTATATACCCCTAG 1835
Db 20 TTCTAACTATATACCCCTAG 1

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RESULT 1698
ADD21658/c
ID ADD21658 standard; DNA; 20 BP.
XX
XX
AC ADD21658;
XX
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #221.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1913 AGTATAATTGACCTACTTTG 1932
DB 20 AGTATAATTGACCTACTTTG 1
XX
RESULT 1699
ADD21661/c
ID ADD21661 standard; DNA; 20 BP.
XX
XX
AC ADD21661;
XX
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #224.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1940 AATAGTGAATCTACTACTATA 1959
DB 20 AATAGTGAATCTACTACTATA 1
XX
RESULT 1700
ADD21670/c
ID ADD21670 standard; DNA; 20 BP.
XX
XX
AC ADD21670;
XX
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #233.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2015 TCTACTCTGTCTTAATGAG 2034
DB 20 TCTACTCTGTCTTAATGAG 1
XX
RESULT 1701
ADD21673/c
ID ADD21673 standard; DNA; 20 BP.
XX
XX
AC ADD21673;
XX

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DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #236.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2059 AATATGTATATGACATTAA 2078
DB 20 AATATGTATATGACATTAA 1
XX
RESULT 1702
ADD21675/c
ID ADD21675 standard; DNA; 20 BP.
XX
XX
AC ADD21675;
XX
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #238.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2103 ACCGAGTCTTGCTCTGTATC 2122
DB 20 ACCGAGTCTTGCTCTGTATC 1
XX
RESULT 1703
ADD21683/c
ID ADD21683 standard; DNA; 20 BP.
XX
XX
AC ADD21683;
XX
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #246.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2176 GGGTTGCGACCATTCCTCTG 2195
DB 20 GGGTTGCGACCATTCCTCTG 1
XX
RESULT 1704
ADD21687/c
ID ADD21687 standard; DNA; 20 BP.
XX
XX
AC ADD21687;
XX
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #250.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

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Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2202 CCTCCCAATTAGCTTGGCCT 2221
Db 20 CCTCCCAATTAGCTTGGCCT 1

RESULT 1705:
ADD21693/c
ID ADD21693 standard; DNA; 20 BP.
XX
AC ADD21693;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #256.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2265 GTAGAGACAGGGTTTCACCG 2284
Db 20 GTAGAGACAGGGTTTCACCG 1

RESULT 1706
ADD21698/c
ID ADD21698 standard; DNA; 20 BP.
XX
AC ADD21698;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #261.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2307 CTCCTGACCTCGTGATCCGC 2326
Db 20 CTCCTGACCTCGTGATCCGC 1

RESULT 1707
ADD21713/c
ID ADD21713 standard; DNA; 20 BP.
XX
AC ADD21713;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #269.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 357 ACCTCAGATTCAGCTTC 376
Db 20 ACCTCAGATTCAGCTTC 1

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 367 TTCAGCTTCGGAACAAGAG 386
Db 20 TTCAGCTTCGGAACAAGAG 1

RESULT 1708
ADD21722/c
ID ADD21722 standard; DNA; 20 BP.
XX
AC ADD21722;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #278.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1381 TTCATGTTCTGATTGTAA 1400
Db 20 TTCATGTTCTGATTGTAA 1

RESULT 1710
ADD21470/c
ID ADD21470 standard; DNA; 20 BP.
XX
AC ADD21470;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #33.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1381 TTCATGTTCTGATTGTAA 1400
Db 20 TTCATGTTCTGATTGTAA 1

RESULT 1711
ADD21489/c
ID ADD21489 standard; DNA; 20 BP.
XX
AC ADD21489;

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XX 15-JAN-2004 (first entry)
 DT Human mdm2 antisense oligonucleotide #52.
 XX
 DE
 XX antisense oligonucleotide; human; mdm2; hyperproliferation;
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
 KW

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 289 CCCGATGCTGAGGACGAG 308
 Db 20 CCCGATGCTGAGGACGAG 1

RESULT 1712
 ADD21494/c
 ID ADD21494 standard; DNA; 20 BP.

XX
 AC ADD21494;

XX 15-JAN-2004 (first entry)

DT Human mdm2 antisense oligonucleotide #57.

DE
 XX antisense oligonucleotide; human; mdm2; hyperproliferation;
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
 KW

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 298 TGAGGAGCAGGCAATGTGC 317
 Db 20 TGAGGAGCAGGCAATGTGC 1

RESULT 1713
 ADD21517/c
 ID ADD21517 standard; DNA; 20 BP.

XX
 AC ADD21517;

XX 15-JAN-2004 (first entry)

DT Human mdm2 antisense oligonucleotide #80.

DE
 XX antisense oligonucleotide; human; mdm2; hyperproliferation;
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
 KW

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 AGCCATTGCTTTGAAGTTA 422
 Db 20 AGCCATTGCTTTGAAGTTA 1

RESULT 1714
 ADD21530/c
 ID ADD21530 standard; DNA; 20 BP.

XX
 AC ADD21530;

XX 15-JAN-2004 (first entry)

DT Human mdm2 antisense oligonucleotide #93.

DE
 XX antisense oligonucleotide; human; mdm2; hyperproliferation;
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
 KW

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 566 GTTTGGCGTGCCCAAGCTTCT 585
 Db 20 GTTTGGCGTGCCCAAGCTTCT 1

RESULT 1715
 ADD21545/c
 ID ADD21545 standard; DNA; 20 BP.

XX
 AC ADD21545;

XX 15-JAN-2004 (first entry)

DT Human mdm2 antisense oligonucleotide #108.

DE
 XX antisense oligonucleotide; human; mdm2; hyperproliferation;
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
 KW

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 727 TACAAGAGCTTCAGGAAGAG 746
 Db 20 TACAAGAGCTTCAGGAAGAG 1

RESULT 1716
 ADD21559/c
 ID ADD21559 standard; DNA; 20 BP.

XX
 AC ADD21559;

XX 15-JAN-2004 (first entry)

DT Human mdm2 antisense oligonucleotide #122.

DE
 XX antisense oligonucleotide; human; mdm2; hyperproliferation;
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
 KW

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 895 AAAGCCTGGCTCTGTGTGTA 914
 Db 20 AAAGCCTGGCTCTGTGTGTA 1

RESULT 1717
 ADD21564/c
 ID ADD21564 standard; DNA; 20 BP.

XX
 AC ADD21564;

XX 15-JAN-2004 (first entry)

DT Human mdm2 antisense oligonucleotide #127.

DE
 XX antisense oligonucleotide; human; mdm2; hyperproliferation;
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
 KW

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 949 GTGAATCTACAGGACGCCCA 968
 Db 20 GTGAATCTACAGGACGCCCA 1


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KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1757 TCAATGATTGGCTAACTT 1776
DB 20 TCAATGATTGGCTAACTT 1

RESULT 1725
ADD21649/c
ID ADD21649 standard; DNA; 20 BP.
XX
XX
AC ADD21649;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #212.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1850 TGAATTTTATTCACATATAT 1869
DB 20 TGAATTTTATTCACATATAT 1

RESULT 1726
ADD21688/c
ID ADD21688 standard; DNA; 20 BP.
XX
XX
AC ADD21688;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #251.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2210 TTAGCTTGGCTACAGTCAT 2229
DB 20 TTAGCTTGGCTACAGTCAT 1

RESULT 1727
ADD21740/c
ID ADD21740 standard; DNA; 20 BP.
XX
XX
AC ADD21740;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #296.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1652 TGGTTGCATTGTCCATGCA 1671
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DB 20 TGGTTGCATTGTCCATGCA 1

RESULT 1728
ADD21439/c
ID ADD21439 standard; DNA; 20 BP.
XX
XX
AC ADD21439;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #2.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 GGCCTGTGTGTCGGAAGA 56
DB 20 GGCCTGTGTGTCGGAAGA 1

RESULT 1729
ADD21440/c
ID ADD21440 standard; DNA; 20 BP.
XX
XX
AC ADD21440;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #3.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 CTCTGACCGAGATCCTGCTG 114
DB 20 CTCTGACCGAGATCCTGCTG 1

RESULT 1730
ADD21454/c
ID ADD21454 standard; DNA; 20 BP.
XX
XX
AC ADD21454;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #17.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1934 TAGTGAATAGTGAATACCTT 1953
DB 20 TAGTGAATAGTGAATACCTT 1

RESULT 1731
ADD21457/c
ID ADD21457 standard; DNA; 20 BP.
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XX AC ADD21457;
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #20.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
XX KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2256 GTACTTTTAGTAGACAGG 2275
Db 20 GTACTTTTAGTAGACAGG 1

RESULT 1732
ADD21497/c
ID ADD21497 standard; DNA; 20 BP.
XX AC ADD21497;
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #60.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
XX KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 301 GGAGCAGGCAATGTGCAAT 320
Db 20 GGAGCAGGCAATGTGCAAT 1

RESULT 1733
ADD21511/c
ID ADD21511 standard; DNA; 20 BP.
XX AC ADD21511;
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #74.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
XX KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 334 TACCTACTGATGGTGCTGTA 353
Db 20 TACCTACTGATGGTGCTGTA 1

RESULT 1734
ADD21549/c
ID ADD21549 standard; DNA; 20 BP.
XX AC ADD21549;
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #112.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
XX KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

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KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 774 AGACCATCTACCTCATCTAG 793
Db 20 AGACCATCTACCTCATCTAG 1

RESULT 1735
ADD21557/c
ID ADD21557 standard; DNA; 20 BP.
XX AC ADD21557;
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #120.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
XX KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 867 TCTGATAGTATTTCCCTTTC 886
Db 20 TCTGATAGTATTTCCCTTTC 1

RESULT 1736
ADD21576/c
ID ADD21576 standard; DNA; 20 BP.
XX AC ADD21576;
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #139.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
XX KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1068 TCTCTCGACTCAGAGATTA 1087
Db 20 TCTCTCGACTCAGAGATTA 1

RESULT 1737
ADD21577/c
ID ADD21577 standard; DNA; 20 BP.
XX AC ADD21577;
XX DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #140.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
XX KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1077 TCAGAAGATTATAGCCTTAG 1096
DB 20 TCAGAAGATTATAGCCTTAG 1

RESULT 1738
ADD21613/c
ID ADD21613 standard; DNA; 20 BP.
XX
AC ADD21613;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #176.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 AAGTGAAGACTATTCTCAGC 1500
DB 20 AAGTGAAGACTATTCTCAGC 1

RESULT 1739
ADD21632/c
ID ADD21632 standard; DNA; 20 BP.
XX
AC ADD21632;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #195.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1684 TTATGGCTGCTTTACATGT 1703
DB 20 TTATGGCTGCTTTACATGT 1

RESULT 1740
ADD21639/c
ID ADD21639 standard; DNA; 20 BP.
XX
AC ADD21639;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #202.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1745 TAGACAACCAATTCAAATGA 1764
DB 20 TAGACAACCAATTCAAATGA 1

RESULT 1741
ADD21648/c
ID ADD21648 standard; DNA; 20 BP.
XX
AC ADD21648;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #211.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1840 TTAGACAACCTGAAATTTAT 1859
DB 20 TTAGACAACCTGAAATTTAT 1

RESULT 1742
ADD21663/c
ID ADD21663 standard; DNA; 20 BP.
XX
AC ADD21663;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #226.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1956 TATAATTTGACTTGAATATG 1975
DB 20 TATAATTTGACTTGAATATG 1

RESULT 1743
ADD21680/c
ID ADD21680 standard; DNA; 20 BP.
XX
AC ADD21680;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #243.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2140 GGGTGATCTTGGCTCACTGC 2159
DB 20 GGGTGATCTTGGCTCACTGC 1

RESULT 1744
ADD21691/c
ID ADD21691 standard; DNA; 20 BP.
XX
AC ADD21691;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #254.
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XX antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2232 GCCACCAACCTGGCTAATT 2251
Db 20 GCCACCAACCTGGCTAATT 1

RESULT 1745
ADD21694/c
ID ADD21694 standard; DNA; 20 BP.
XX
AC ADD21694;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #257.
DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2274 GGGTTTCCCGTGTAGCCA 2293
Db 20 GGGTTTCCCGTGTAGCCA 1

RESULT 1746
ADD21695/c
ID ADD21695 standard; DNA; 20 BP.
XX
AC ADD21695;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #258.
DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2283 CGTGTAGCCAGGATGGTCT 2302
Db 20 CGTGTAGCCAGGATGGTCT 1

RESULT 1747
ADD21711/c
ID ADD21711 standard; DNA; 20 BP.
XX
AC ADD21711;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #267.
DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 315 TGCAATACCAACATGTCTGT 334
Db 20 TGCAATACCAACATGTCTGT 1

RESULT 1748
ADD21724/c
ID ADD21724 standard; DNA; 20 BP.
XX
AC ADD21724;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #280.
DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 369 CCAGCTTCGGAACAAGAGAC 388
Db 20 CCAGCTTCGGAACAAGAGAC 1

RESULT 1749
ADD21731/c
ID ADD21731 standard; DNA; 20 BP.
XX
AC ADD21731;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #287.
DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1201 TTTTCCTTAGCTGACTATTGG 1220
Db 20 TTTTCCTTAGCTGACTATTGG 1

RESULT 1750
ADD21736/c
ID ADD21736 standard; DNA; 20 BP.
XX
AC ADD21736;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #292.
DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1342 AAGCCAAACTGGAAACTCA 1361
Db 20 AAGCCAAACTGGAAACTCA 1

RESULT 1751

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ADD21737/c
ID ADD21737 standard; DNA; 20 BP.
XX
AC ADD21737;
XX
XX 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #293.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1622 TTGTGTGATTGTGCAAGTGC 1641
DB 20 TTGTGTGATTGTGCAAGTGC 1

RESULT 1752
ADD21444/c
ID ADD21444 standard; DNA; 20 BP.
XX
XX AC ADD21444;
XX
XX 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #7.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 295 TGGTGAGGAGCAGGCAATG 314
DB 20 TGGTGAGGAGCAGGCAATG 1

RESULT 1753
ADD21455/c
ID ADD21455 standard; DNA; 20 BP.
XX
XX AC ADD21455;
XX
XX 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #18.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2132 AGTGCAGTGGGTGATCTTGG 2151
DB 20 AGTGCAGTGGGTGATCTTGG 1

RESULT 1754
ADD21468/c
ID ADD21468 standard; DNA; 20 BP.
XX
XX AC ADD21468;
XX
XX 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #31.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCGCGCGAGCTTGCTGCTT 23
DB 20 CCGCGCGAGCTTGCTGCTT 1

RESULT 1755
ADD21503/c
ID ADD21503 standard; DNA; 20 BP.
XX
XX AC ADD21503;
XX
XX 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #66.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 308 GCAAAATGTGCAATACCAACA 327
DB 20 GCAAAATGTGCAATACCAACA 1

RESULT 1756
ADD21506/c
ID ADD21506 standard; DNA; 20 BP.
XX
XX AC ADD21506;
XX
XX 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #69.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 311 AATGTGCAATACCAACATGT 330
DB 20 AATGTGCAATACCAACATGT 1

RESULT 1757
ADD21514/c
ID ADD21514 standard; DNA; 20 BP.
XX
XX AC ADD21514;
XX
XX 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #77.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 372 GCTTCGGAACAAGAGACCTT 391
| | | | | | | | | | | | | | | | | |
Db 20 GCTTCGGAACAAGAGACCTT 1

RESULT 1758
ADD21520/c
ID ADD21520 standard; DNA; 20 BP.
XX
AC ADD21520;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #83.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 477 TATCTTGGCCAGTATATAT 496
| | | | | | | | | | | | | | | | | |
Db 20 TATCTTGGCCAGTATATAT 1

RESULT 1759
ADD21526/c
ID ADD21526 standard; DNA; 20 BP.
XX
AC ADD21526;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #89.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 531 ATTGTATATTCTCAATGA 550
| | | | | | | | | | | | | | | | | |
Db 20 ATTGTATATTCTCAATGA 1

RESULT 1760
ADD21588/c
ID ADD21588 standard; DNA; 20 BP.
XX
AC ADD21588;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #151.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1184 TGAAGAAGATCCTGAAATTT 1203
| | | | | | | | | | | | | | | | | |
Db 20 TGAAGAAGATCCTGAAATTT 1

RESULT 1761
ADD21610/c
ID ADD21610 standard; DNA; 20 BP.
XX
AC ADD21610;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #173.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1449 GATAAAATTACACAGCTTC 1468
| | | | | | | | | | | | | | | | | |
Db 20 GATAAAATTACACAGCTTC 1

RESULT 1762
ADD21659/c
ID ADD21659 standard; DNA; 20 BP.
XX
AC ADD21659;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #222.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1920 TTGACCTACTTTGGTAGTGG 1939
| | | | | | | | | | | | | | | | | |
Db 20 TTGACCTACTTTGGTAGTGG 1

RESULT 1763
ADD21679/c
ID ADD21679 standard; DNA; 20 BP.
XX
AC ADD21679;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #242.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2133 GTGCAGTGGGTGATCTTGGC 2152
| | | | | | | | | | | | | | | | | |
Db 20 GTGCAGTGGGTGATCTTGGC 1

RESULT 1764
ADD21452/c
ID ADD21452 standard; DNA; 20 BP.
XX
AC ADD21452;
XX
DT 15-JAN-2004 (first entry)
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XX Human mdm2 antisense oligonucleotide #15.
DE
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1785 TAGTTGACCTGTCTATAGA 1804
Db 20 TAGTTGACCTGTCTATAGA 1

RESULT 1765
ADD21471/c
ID ADD21471 standard; DNA; 20 BP.
XX
AC ADD21471;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #34.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GCCTGTGTGGCCCTGTGTGT 48
Db 20 GCCTGTGTGGCCCTGTGTGT 1

RESULT 1766
ADD21480/c
ID ADD21480 standard; DNA; 20 BP.
XX
AC ADD21480;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #43.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 GCAGCCAGGACCGTCCC 139
Db 20 GCAGCCAGGACCGTCCC 1

RESULT 1767
ADD21488/c
ID ADD21488 standard; DNA; 20 BP.
XX
AC ADD21488;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #51.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 AGGAAACTGGGAGTCTTGA 261
Db 20 AGGAAACTGGGAGTCTTGA 1

RESULT 1768
ADD21509/c
ID ADD21509 standard; DNA; 20 BP.
XX
AC ADD21509;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #72.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 314 GTGCAATACCAACATGTCTG 333
Db 20 GTGCAATACCAACATGTCTG 1

RESULT 1769
ADD21538/c
ID ADD21538 standard; DNA; 20 BP.
XX
AC ADD21538;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #101.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 646 AGCAGGAATCATCGGACTCA 665
Db 20 AGCAGGAATCATCGGACTCA 1

RESULT 1770
ADD21578/c
ID ADD21578 standard; DNA; 20 BP.
XX
AC ADD21578;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human mdm2 antisense oligonucleotide #141.
XX
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1084 ATTATAGCCTTAGTGAAGAA 1103
Db 20 ATTATAGCCTTAGTGAAGAA 1
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RESULT 1771
ADD21600/c
ID ADD21600 standard; DNA; 20 BP.
XX
AC ADD21600;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #163.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1325 AGGGAAATCTCTGAGAAAG 1344
Db 20 AGGGAAATCTCTGAGAAAG 1

RESULT 1772
ADD21644/c
ID ADD21644 standard; DNA; 20 BP.
XX
AC ADD21644;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #207.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1808 TTATATATTTCTACTATAT 1827
Db 20 TTATATATTTCTACTATAT 1

RESULT 1773
ADD21657/c
ID ADD21657 standard; DNA; 20 BP.
XX
AC ADD21657;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #220.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1908 TCCTTAGTATAATGACCTA 1927
Db 20 TCCTTAGTATAATGACCTA 1

RESULT 1774
ADD21689/c
ID ADD21689 standard; DNA; 20 BP.
XX
AC ADD21689;
XX

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DT 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #252.
XX antisense oligonucleotide; human; mdm2; hyperproliferation;
XX hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2213 GCTTGGCCTACATCATCTG 2232
Db 20 GCTTGGCCTACATCATCTG 1

RESULT 1775
ADD21692/c
ID ADD21692 standard; DNA; 20 BP.
XX
AC ADD21692;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #255.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2253 TTTGTACTTTTACTAGAC 2272
Db 20 TTTGTACTTTTACTAGAC 1

RESULT 1776
ADD21718/c
ID ADD21718 standard; DNA; 20 BP.
XX
AC ADD21718;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #274.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 363 CAGATTCCAGCTTCGGAACA 382
Db 20 CAGATTCCAGCTTCGGAACA 1

RESULT 1777
ADD21725/c
ID ADD21725 standard; DNA; 20 BP.
XX
AC ADD21725;
XX
DT 15-JAN-2004 (first entry)
DE Human mdm2 antisense oligonucleotide #281.
KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

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Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 481 TTGGCCAGTATTATGACT 500
DB 20 TTGGCCAGTATTATGACT 1

RESULT 1778

ADD21738/c
ID ADD21738 standard; DNA; 20 BP.

XX
AC ADD21738;

DT 15-JAN-2004 (first entry)

XX Human mdm2 antisense oligonucleotide #294.

DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1632 TGTCAGGTCGACCTAAAAA 1651
DB 20 TGTCAGGTCGACCTAAAAA 1

RESULT 1779

ADD21744/c
ID ADD21744 standard; DNA; 20 BP.

XX
AC ADD21744;

DT 15-JAN-2004 (first entry)

XX Human mdm2 antisense oligonucleotide #300.

DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1692 TGCTTTACATGTGCAAGAA 1711
DB 20 TGCTTTACATGTGCAAGAA 1

RESULT 1780

ADD21456/c
ID ADD21456 standard; DNA; 20 BP.

XX
AC ADD21456;

DT 15-JAN-2004 (first entry)

XX Human mdm2 antisense oligonucleotide #19.

DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2224 AGTCATCTGCCACCAACCT 2243
DB 20 AGTCATCTGCCACCAACCT 1

RESULT 1781

ADD21479/c
ID ADD21479 standard; DNA; 20 BP.

XX
AC ADD21479;

DT 15-JAN-2004 (first entry)

XX Human mdm2 antisense oligonucleotide #42.

DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 TGCTTTGCGAGCCGAGGCA 132
DB 20 TGCTTTGCGAGCCGAGGCA 1

RESULT 1782

ADD21498/c
ID ADD21498 standard; DNA; 20 BP.

XX
AC ADD21498;

DT 15-JAN-2004 (first entry)

XX Human mdm2 antisense oligonucleotide #61.

DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 GAGCAGGCAAAATGTGCAATA 321
DB 20 GAGCAGGCAAAATGTGCAATA 1

RESULT 1783

ADD21502/c
ID ADD21502 standard; DNA; 20 BP.

XX
AC ADD21502;

DT 15-JAN-2004 (first entry)

XX Human mdm2 antisense oligonucleotide #65.

DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 307 GGCAAAATGTGCAATACCAAC 326
DB 20 GGCAAAATGTGCAATACCAAC 1

RESULT 1784

ADD21508/c
ID ADD21508 standard; DNA; 20 BP.

XX
AC ADD21508;

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XX 15-JAN-2004 (first entry)
DT Human mdm2 antisense oligonucleotide #71.
DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 313 TGTGCAATACCAACATGTCT 332
DB 20 TGTGCAATACCAACATGTCT 1
RESULT 1785
ADD21525/c
ID ADD21525 standard; DNA; 20 BP.
XX
AC ADD21525;
XX
DT 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #88.
DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 525 CAACATATTGTATATTGTC 544
DB 20 CAACATATTGTATATTGTC 1
RESULT 1786
ADD21537/c
ID ADD21537 standard; DNA; 20 BP.
XX
AC ADD21537;
XX
DT 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #106.
DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 634 TAGTAGTCAATCAGCAGAA 653
DB 20 TAGTAGTCAATCAGCAGAA 1
RESULT 1787
ADD21543/c
ID ADD21543 standard; DNA; 20 BP.
XX
AC ADD21543;
XX
DT 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #106.
DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 704 TGGGAGTGATCAAAAGGACC 723
DB 20 TGGGAGTGATCAAAAGGACC 1
RESULT 1788
ADD21560/c
ID ADD21560 standard; DNA; 20 BP.
XX
AC ADD21560;
XX
DT 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #123.
DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 904 CTCTGTGTGTATTAAGGGAG 923
DB 20 CTCTGTGTGTATTAAGGGAG 1
RESULT 1789
ADD21599/c
ID ADD21599 standard; DNA; 20 BP.
XX
AC ADD21599;
XX
DT 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #162.
DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1311 AAAGGGAAGATAAAGGGGA 1330
DB 20 AAAGGGAAGATAAAGGGGA 1
RESULT 1790
ADD21612/c
ID ADD21612 standard; DNA; 20 BP.
XX
AC ADD21612;
XX
DT 15-JAN-2004 (first entry)
XX Human mdm2 antisense oligonucleotide #175.
DE antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
KW
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1466 TTCACAATCACAAGAAGTG 1485
DB 20 TTCACAATCACAAGAAGTG 1
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Db 20 TTCACATCACAGAAAGTG 1

RESULT 1791
ADD21686/c
ID ADD21686 standard; DNA; 20 BP.
XX AC
XX ADD21686;
XX
DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #249.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2198 TCAGCTCCCAATTAGCTTG 2217
Db 20 TCAGCTCCCAATTAGCTTG 1

RESULT 1792
ADD21714/c
ID ADD21714 standard; DNA; 20 BP.
XX AC
XX ADD21714;
XX
DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #270.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 CCTCACAGATCCAGCTTCG 377
Db 20 CCTCACAGATCCAGCTTCG 1

RESULT 1793
ADD21727/c
ID ADD21727 standard; DNA; 20 BP.
XX AC
XX ADD21727;
XX
DT 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #283.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 483 GGCCAGTATATTAGCTAA 502
Db 20 GGCCAGTATATTAGCTAA 1

RESULT 1794
ADD21729/c
ID ADD21729 standard; DNA; 20 BP.
XX AC
XX ADD21729;
XX
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AC ADD21729;
XX 15-JAN-2004 (first entry)
XX DE Human mdm2 antisense oligonucleotide #285.
XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 781 CTACCTCATCTAGACGAGA 800
Db 20 CTACCTCATCTAGACGAGA 1

RESULT 1795
ADE86781/c
ID ADE86781 standard; DNA; 20 BP.
XX AC
XX ADE86781;
XX
DT 29-JAN-2004 (first entry)
XX DE GATA primer #1.
XX KW ss; primer; molecular phenotyping; brain; lung; CD31+ cell;
KW lineage committed cell; survival; proliferation; differentiation;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2344 AGTGCTGGGATTACAGGCAT 2363
Db 20 AGTGCTGGGATTACAGGCAT 1

RESULT 1796
AAD64979
ID AAD64979 standard; DNA; 20 BP.
XX AC
XX AAD64979;
XX
DT 11-MAR-2004 (first entry)
XX DE Human mouse double minute (MDM2) sense oligonucleotide S7.
XX KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1018 TGGATCAGGATTCAGTTTCA 1037
Db 1 TGGATCAGGATTCAGTTTCA 20

RESULT 1797
AAD65012/c
ID AAD65012 standard; DNA; 20 BP.
XX AC
XX AAD65012;
XX
DT 11-MAR-2004 (first entry)
XX DE Human mouse double minute (MDM2) antisense oligonucleotide ASS-4.
XX KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
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KW therapeutic; antisense therapy; human; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 685 ACAGGTGTCACCTTGAAGGT 704
 DB 20 ACAGGTGTCACCTTGAAGGT 1

RESULT 1798
 AAD64999
 ID AAD64999 standard; DNA; 20 BP.
 XX
 AC
 AAD64999;
 XX
 DT 11-MAR-2004 (first entry)
 XX Human mouse double minute (MDM2) sense oligonucleotide S7-5.
 DE MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
 KW therapeutic; antisense therapy; human; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1038 GATCAGTTTGTAGTGAAGT 1057
 DB 1 GATCAGTTTGTAGTGAAGT 20

RESULT 1799
 AAD65006/C
 ID AAD65006 standard; DNA; 20 BP.
 XX
 AC
 AAD65006;
 XX
 DT 11-MAR-2004 (first entry)
 XX Human mouse double minute (MDM2) antisense oligonucleotide AS3.
 DE MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
 KW therapeutic; antisense therapy; human; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 780 TCTACCTCATCTAGAGGAG 799
 DB 20 TCTACCTCATCTAGAGGAG 1

RESULT 1800
 AAD64978
 ID AAD64978 standard; DNA; 20 BP.
 XX
 AC
 AAD64978;
 XX
 DT 11-MAR-2004 (first entry)
 XX Human mouse double minute (MDM2) sense oligonucleotide S5.
 DE MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
 KW therapeutic; antisense therapy; human; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 695 CCTTGAAGGTGGAGTGATC 714

DB 1 CCTTGAAGGTGGAGTGATC 20

RESULT 1801
 AAD64996
 ID AAD64996 standard; DNA; 20 BP.
 XX
 AC
 AAD64996;
 XX
 DT 11-MAR-2004 (first entry)
 XX Human mouse double minute (MDM2) sense oligonucleotide S7-2.
 DE MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
 KW therapeutic; antisense therapy; human; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1003 ATTACAGTGTGTTGGAT 1022
 DB 1 ATTACAGTGTGTTGGAT 20

RESULT 1802
 AAD65005/C
 ID AAD65005 standard; DNA; 20 BP.
 XX
 AC
 AAD65005;
 XX
 DT 11-MAR-2004 (first entry)
 XX Human mouse double minute (MDM2) antisense oligonucleotide AS1.
 DE MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
 KW therapeutic; antisense therapy; human; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 ACCTACAGATTCCAGCTTC 376
 DB 20 ACCTACAGATTCCAGCTTC 1

RESULT 1803
 AAD65009/C
 ID AAD65009 standard; DNA; 20 BP.
 XX
 AC
 AAD65009;
 XX
 DT 11-MAR-2004 (first entry)
 XX Human mouse double minute (MDM2) antisense oligonucleotide AS5-1.
 DE MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
 KW therapeutic; antisense therapy; human; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 669 ACATCTGTGAGTGAGAACAG 688
 DB 20 ACATCTGTGAGTGAGAACAG 1

RESULT 1804
 AAD64984
 ID AAD64984 standard; DNA; 20 BP.

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XX AAD64984;
AC
XX
DT 11-MAR-2004 (first entry)
DE Human mouse double minute (MDM2) sense oligonucleotide S3.
XX
XX MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 780 TCTACCTCATCTAGAGGAG 799
Db 1 TCTACCTCATCTAGAGGAG 20

RESULT 1805
AAD64988
ID AAD64988 standard; DNA; 20 BP.
XX
AC AAD64988;
XX
DT 11-MAR-2004 (first entry)
DE Human mouse double minute (MDM2) sense oligonucleotide S5-1.
XX
XX MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 669 ACATCTGTGAGTGAGACAG 688
Db 1 ACATCTGTGAGTGAGACAG 20

RESULT 1806
AAD65007/c
ID AAD65007 standard; DNA; 20 BP.
XX
AC AAD65007;
XX
DT 11-MAR-2004 (first entry)
DE Human mouse double minute (MDM2) antisense oligonucleotide AS6.
XX
XX MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1203 TCCTTAGCTGACTATTGGAA 1222
Db 20 TCCTTAGCTGACTATTGGAA 1

RESULT 1807
AAD65008/c
ID AAD65008 standard; DNA; 20 BP.
XX
AC AAD65008;
XX
DT 11-MAR-2004 (first entry)
DE Human mouse double minute (MDM2) antisense oligonucleotide AS8.
XX
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KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1230 TCATGCAATGAATGAATCC 1249
Db 20 TCATGCAATGAATGAATCC 1

RESULT 1808
AAD65015/c
ID AAD65015 standard; DNA; 20 BP.
XX
AC AAD65015;
XX
DT 11-MAR-2004 (first entry)
DE Human mouse double minute (MDM2) antisense oligonucleotide AS5-7.
XX
XX MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 717 AAGGACCTTGTACAAGAGCT 736
Db 20 AAGGACCTTGTACAAGAGCT 1

RESULT 1809
AAD65013/c
ID AAD65013 standard; DNA; 20 BP.
XX
AC AAD65013;
XX
DT 11-MAR-2004 (first entry)
DE Human mouse double minute (MDM2) antisense oligonucleotide AS5-5.
XX
XX MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 704 TGGGAGTGATCAAAAGGACC 723
Db 20 TGGGAGTGATCAAAAGGACC 1

RESULT 1810
AAD65014/c
ID AAD65014 standard; DNA; 20 BP.
XX
AC AAD65014;
XX
DT 11-MAR-2004 (first entry)
DE Human mouse double minute (MDM2) antisense oligonucleotide AS5-6.
XX
XX MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 709 GTGATCAAAAGGACCTTGTA 728
Db 20 GTGATCAAAAGGACCTTGTA 1

RESULT 1811
AAD5020/c
ID AAD5020 standard; DNA; 20 BP.
XX
AC
XX
AC AAD5020;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) antisense oligonucleotide AS7-5.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1038 GATCAGTTTACTGTGAGATT 1057
Db 20 GATCAGTTTACTGTGAGATT 1

RESULT 1812
AAD64990
ID AAD64990 standard; DNA; 20 BP.
XX
AC AAD64990;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) sense oligonucleotide S5-3.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 680 TGAGAACAGGTTGCACCTTG 699
Db 1 TGAGAACAGGTTGCACCTTG 20

RESULT 1813
AAD64977
ID AAD64977 standard; DNA; 20 BP.
XX
AC AAD64977;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) sense oligonucleotide S4.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 481 TTGCCAGTATATTATGACT 500
Db 1 TTGCCAGTATATTATGACT 20

RESULT 1814
AAD65021/c

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ID AAD65021 standard; RNA; 20 BP.
XX
AC AAD65021;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) antisense RNA oligonucleotide AS2-2H.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 675 GTGAGTGAGAACAGGTTGTC 694
Db 20 GTGAGTGAGAACAGGTTGTC 1

RESULT 1815
AAD64983
ID AAD64983 standard; DNA; 20 BP.
XX
AC AAD64983;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) sense oligonucleotide S2.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 369 CCAGCTTCGGAACAAGAGAC 388
Db 1 CCAGCTTCGGAACAAGAGAC 20

RESULT 1816
AAD64986
ID AAD64986 standard; DNA; 20 BP.
XX
AC AAD64986;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) sense oligonucleotide S8.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1230 TCATGCAATGAATGAATCC 1249
Db 1 TCATGCAATGAATGAATCC 20

RESULT 1817
AAD64992
ID AAD64992 standard; DNA; 20 BP.
XX
AC AAD64992;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) sense oligonucleotide S5-5.

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XX MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.
Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 704 TGGGATGATCAAAAGGACC 723
Db 1 TGGGATGATCAAAAGGACC 20

RESULT 1818
AAD64993
ID AAD64993 standard; DNA; 20 BP.
XX
AC AAD64993;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) sense oligonucleotide S5-6.
XX
DE MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 709 GTGATCAAAAGGACCTTGTA 728
Db 1 GTGATCAAAAGGACCTTGTA 20

RESULT 1819
AAD65004/c
ID AAD65004 standard; DNA; 20 BP.
XX
AC AAD65004;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) antisense oligonucleotide AS7.
XX
DE MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1018 TGGATCAGGATTCAGTTTCA 1037
Db 20 TGGATCAGGATTCAGTTTCA 1

RESULT 1820
AAD65017/c
ID AAD65017 standard; DNA; 20 BP.
XX
AC AAD65017;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) antisense oligonucleotide AS7-2.
XX
DE MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1003 ATTCAAGTGATTTGGTTCGAT 1022
Db 20 ATTCAAGTGATTTGGTTCGAT 1

RESULT 1821
AAD64991
ID AAD64991 standard; DNA; 20 BP.
XX
AC AAD64991;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) sense oligonucleotide S5-4.
XX
DE MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 685 ACAGGTGTCACTTGAAGGT 704
Db 1 ACAGGTGTCACTTGAAGGT 20

RESULT 1822
AAD65003/c
ID AAD65003 standard; DNA; 20 BP.
XX
AC AAD65003;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) antisense oligonucleotide AS5.
XX
DE MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 695 CCTTGAAGGTGGAGTGATC 714
Db 20 CCTTGAAGGTGGAGTGATC 1

RESULT 1823
AAD65019/c
ID AAD65019 standard; DNA; 20 BP.
XX
AC AAD65019;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human mouse double minute (MDM2) antisense oligonucleotide AS7-4.
XX
DE MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; antisense; ss.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1027 ATTCAAGTTTCAGATCAGTTT 1046
Db 20 ATTCAAGTTTCAGATCAGTTT 1

RESULT 1824
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AAD64985
ID AAD64985 standard; DNA; 20 BP.
XX
XX AAD64985;
AC
XX 11-MAR-2004 (first entry)
DT
XX Human mouse double minute (MDM2) sense oligonucleotide S6.
DE
XX MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1203 TCCTTAGCTGACTATTGGAA 1222
DB 1 TCCTTAGCTGACTATTGGAA 20

RESULT 1825
AAD65002/c
ID AAD65002 standard; DNA; 20 BP.
XX
XX AAD65002;
AC
XX 11-MAR-2004 (first entry)
DT
XX Human mouse double minute (MDM2) antisense oligonucleotide AS4.
DE
XX MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 481 TTGCCAGTATATTGACT 500
DB 20 TTGCCAGTATATTGACT 1

RESULT 1826
AAD65010/c
ID AAD65010 standard; DNA; 20 BP.
XX
XX AAD65010;
AC
XX 11-MAR-2004 (first entry)
DT
XX Human mouse double minute (MDM2) antisense oligonucleotide AS5-2.
DE
XX MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTCAGAACAGGTGTCA 694
DB 20 GTGAGTCAGAACAGGTGTCA 1

RESULT 1827
AAD65026/c
ID AAD65026 standard; RNA; 20 BP.
XX
XX AAD65026;
AC
XX 11-MAR-2004 (first entry)
DT
XX

DE Mouse double minute (MDM2) antisense RNA oligonucleotide AS.
XX
XX MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTCAGAACAGGTGTCA 694
DB 20 GTGAGTCAGAACAGGTGTCA 1

RESULT 1828
AAD64994
ID AAD64994 standard; DNA; 20 BP.
XX
XX AAD64994;
AC
XX 11-MAR-2004 (first entry)
DT
XX Human mouse double minute (MDM2) sense oligonucleotide S5-7.
DE
XX MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 717 AAGGACCTTGTACAGAGCT 736
DB 1 AAGGACCTTGTACAGAGCT 20

RESULT 1829
AAD65011/c
ID AAD65011 standard; DNA; 20 BP.
XX
XX AAD65011;
AC
XX 11-MAR-2004 (first entry)
DT
XX Human mouse double minute (MDM2) antisense oligonucleotide AS5-3.
DE
XX MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; antisense; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 680 TGAGAACAGGTGTACCTTG 699
DB 20 TGAGAACAGGTGTACCTTG 1

RESULT 1830
AAD64982
ID AAD64982 standard; DNA; 20 BP.
XX
XX AAD64982;
AC
XX 11-MAR-2004 (first entry)
DT
XX Human mouse double minute (MDM2) sense oligonucleotide S1.
DE
XX MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTCAGAACAGGTGTCA 694
DB 20 GTGAGTCAGAACAGGTGTCA 1

RESULT 1827
AAD65026/c
ID AAD65026 standard; RNA; 20 BP.
XX
XX AAD65026;
AC
XX 11-MAR-2004 (first entry)
DT
XX

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 357 ACCTCACAGATTCAGCTTC 376
Db 1 ACCTCACAGATTCAGCTTC 20

RESULT 1831
AAD64995
ID AAD64995 standard; DNA; 20 BP.
XX
AC AAD64995;
XX
DT 11-MAR-2004 (first entry)
DE Human mouse double minute (MDM2) sense oligonucleotide S7-1.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 998 TGAACATTCAGGTGATTGGT 1017
Db 1 TGAACATTCAGGTGATTGGT 20

RESULT 1832
AAD64998
ID AAD64998 standard; DNA; 20 BP.
XX
AC AAD64998;
XX
DT 11-MAR-2004 (first entry)
DE Human mouse double minute (MDM2) sense oligonucleotide S7-4.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1027 ATTCAGTTTCAGATCAGTTT 1046
Db 1 ATTCAGTTTCAGATCAGTTT 20

RESULT 1833
AAD65016/c
ID AAD65016 standard; DNA; 20 BP.
XX
AC AAD65016;
XX
DT 11-MAR-2004 (first entry)
DE Human mouse double minute (MDM2) antisense oligonucleotide AS7-1.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 998 TGAACATTCAGGTGATTGGT 1017
Db 20 TGAACATTCAGGTGATTGGT 1
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RESULT 1834
AAD64989
ID AAD64989 standard; DNA; 20 BP.
XX
AC AAD64989;
XX
DT 11-MAR-2004 (first entry)
DE Human mouse double minute (MDM2) sense oligonucleotide S5-2.
XX
KW MDM2; mouse double minute; tumour; cancer; colorectal cancer; cytostatic;
KW therapeutic; antisense therapy; human; ss.

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 675 GTGAGTGAGAACAGGTGTCA 694
Db 1 GTGAGTGAGAACAGGTGTCA 20

RESULT 1835
AAD50276/c
ID AAD50276 standard; DNA; 20 BP.
XX
AC AAD50276;
XX
DT 24-MAR-2003 (first entry)
DE Oligonucleotide #3, used in the invention.
XX
KW Therapy; research reagent; diagnostic; phosphorothioate backbone; ss.
XX

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1695 TTTCATGTGCAAGAAGCT 1714
Db 20 TTTCATGTGCAAGAAGCT 1

RESULT 1836
ABZ99055
ID ABZ99055 standard; DNA; 20 BP.
XX
AC ABZ99055;
XX
DT 17-OCT-2003 (first entry)
DE Human PDE4C oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2122 CCCAGGCTGGAGTGCAGTGG 2141
Db 1 CCCAGGCTGGAGTGCAGTGG 20

RESULT 1837
ABZ97964
ID ABZ97964 standard; DNA; 20 BP.
XX
AC ABZ97964;
XX
DT 17-OCT-2003 (first entry)
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XX DE Human RANTES oligonucleotide sequence.
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2187 ATTCTCTGCTGCTCAGCCTCC 2206
Db 1 ATTCTCTGCTGCTCAGCCTCC 20

RESULT 1838
ADM65742
ID ADM65742 standard; DNA; 20 BP.
XX AC ADM65742;
XX DT 03-JUN-2004 (first entry)
XX DE Human Y chromosome non-recombining region polymorphic fragment #301.
XX KW ethnic origin determination; polymorphic site determination;
KW Y chromosome; paternity testing; forensic; diagnosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2341 CAAAGTCTGGGATTACAGG 2360
Db 1 CAAAGTCTGGGATTACAGG 20

RESULT 1839
ADM65739
ID ADM65739 standard; DNA; 20 BP.
XX AC ADM65739;
XX DT 03-JUN-2004 (first entry)
XX DE Human Y chromosome non-recombining region polymorphic fragment #300.
XX KW ethnic origin determination; polymorphic site determination;
KW Y chromosome; paternity testing; forensic; diagnosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2341 CAAAGTCTGGGATTACAGG 2360
Db 1 CAAAGTCTGGGATTACAGG 20

RESULT 1840
ADM65575/c
ID ADM65575 standard; DNA; 20 BP.
XX AC ADM65575;
XX DT 03-JUN-2004 (first entry)
XX DE NRY polymorphism detection primer #489.
XX KW ethnic origin determination; polymorphic site determination;
KW Y chromosome; paternity testing; forensic; diagnosis;
Query Match 0.8%; Score 20; DB 1; Length 20;

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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2342 AAAGTCTGGGATTACAGGC 2361
Db 20 AAAGTCTGGGATTACAGGC 1

RESULT 1841
ADM65745
ID ADM65745 standard; DNA; 20 BP.
XX AC ADM65745;
XX DT 03-JUN-2004 (first entry)
XX DE Human Y chromosome non-recombining region polymorphic fragment #302.
XX KW ethnic origin determination; polymorphic site determination;
KW Y chromosome; paternity testing; forensic; diagnosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2341 CAAAGTCTGGGATTACAGG 2360
Db 1 CAAAGTCTGGGATTACAGG 20

RESULT 1842
ADM65578/c
ID ADM65578 standard; DNA; 20 BP.
XX AC ADM65578;
XX DT 03-JUN-2004 (first entry)
XX DE NRY polymorphism detection primer #491.
XX KW ethnic origin determination; polymorphic site determination;
KW Y chromosome; paternity testing; forensic; diagnosis;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2342 AAAGTCTGGGATTACAGGC 2361
Db 20 AAAGTCTGGGATTACAGGC 1

RESULT 1843
ABD30995
ID ABD30995 standard; DNA; 20 BP.
XX AC ABD30995;
XX DT 29-JUL-2004 (first entry)
XX DE Human RANTES-derived oligonucleotide SEQ ID 13206.
XX KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2187 ATTCTCTGCTCAGCCTCC 2206
Db 1 ATTCTCTGCTCAGCCTCC 20

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RESULT 1844
ABD32086
ID ABD32086 standard; DNA; 20 BP.
XX
AC ABD32086;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human PDE4C-derived oligonucleotide SEQ ID 14297.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2122 CCCAGGCTGGAGTGCAGTGG 2141
Db 1 CCCAGGCTGGAGTGCAGTGG 20

RESULT 1845
ADI80086/c
ID ADI80086 standard; DNA; 20 BP.
XX
AC ADI80086;
XX
DT 22-APR-2004 (first entry)
XX
DE Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 87.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; nontropic; neuroprotective; immunosuppressive;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2333 CGGCTCCCAAGTCTGGG 2352
Db 20 CGGCTCCCAAGTCTGGG 1

RESULT 1846
ADI80221
ID ADI80221 standard; DNA; 20 BP.
XX
AC ADI80221;
XX
DT 22-APR-2004 (first entry)
XX
DE Human transforming growth factor-beta 2 target DNA region, SEQ ID No 222.
XX
KW antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
KW cytostatic; nontropic; neuroprotective; immunosuppressive;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2333 CGGCTCCCAAGTCTGGG 2352
Db 1 CGGCTCCCAAGTCTGGG 20

RESULT 1847
ADI30045/c
ID ADI30045 standard; DNA; 20 BP.
XX
AC ADI30045;
XX

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DT 22-APR-2004 (first entry)
XX
DE Human dual specific phosphatase 4 DNA, antisense oligonucleotide #65.
XX
KW Antisense therapy; human; dual specific phosphatase 4;
KW hyperproliferative disorder; developmental disorder; apoptosis;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2280 CACCCTGTTAGCCAGGATGG 2299
Db 20 CACCCTGTTAGCCAGGATGG 1

RESULT 1848
ADJ59829
ID ADJ59829 standard; DNA; 20 BP.
XX
AC ADJ59829;
XX
DT 06-MAY-2004 (first entry)
XX
DE Oligonucleotide associated to RANTES #78.
XX
KW interleukin; IL-4 receptor; IL-5 receptor; lung disease;
KW airway inflammation; allergy; asthma; impeded respiration;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2187 ATTCTCTGCTCAGCTCC 2206
Db 1 ATTCTCTGCTCAGCTCC 20

RESULT 1849
ADJ60940
ID ADJ60940 standard; DNA; 20 BP.
XX
AC ADJ60940;
XX
DT 06-MAY-2004 (first entry)
XX
DE Oligonucleotide associated to PDE4C #6.
XX
KW interleukin; IL-4 receptor; IL-5 receptor; lung disease;
KW airway inflammation; allergy; asthma; impeded respiration;

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2122 CCCAGGCTGGAGTGCAGTGG 2141
Db 1 CCCAGGCTGGAGTGCAGTGG 20

RESULT 1850
ADL23339
ID ADL23339 standard; DNA; 20 BP.
XX
AC ADL23339;
XX
DT 20-MAY-2004 (first entry)
XX
DE Primer #1 for amplification of D6S105.
XX
KW ss; primer; diagnosis; cervical intraepithelial neoplasia; CIN;
KW allelic deletion; PHIT; fragile histidine triad gene; PR;

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XX 01-JUL-2004 (first entry)
DT Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:1145.
DE
XX
XX Chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2331 CTCGGCCTCCCAAGTGCTG 2350
DB 20 CTCGGCCTCCCAAGTGCTG 1

RESULT 1858
ADO46429
ID ADO46429 standard; DNA; 20 BP.
XX
XX ADO46429;
AC
XX
DT 15-JUL-2004 (first entry)
DE Human oligonucleotide #1795.
XX
KW Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
KW CCR1; CCR3; Botaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2122 CCCAGGCTGGAGTGCACTGG 2141
DB 1 CCCAGGCTGGAGTGCACTGG 20

RESULT 1859
ADO45319
ID ADO45319 standard; DNA; 20 BP.
XX
XX ADO45319;
AC
XX
DT 15-JUL-2004 (first entry)
DE Human oligonucleotide #685.
XX
KW Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
KW CCR1; CCR3; Botaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2187 ATTCCTCGCTCAGCTCC 2206
DB 1 ATTCCTCGCTCAGCTCC 20

RESULT 1860
ADP12093/C
ID ADP12093 standard; DNA; 20 BP.
XX
XX ADP12093;
AC
XX
DT 12-AUG-2004 (first entry)
DE Set 2 right PCR primer for marker probe #199.
XX
KW transplant rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss; primer.

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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1598 TTGCCCCCTTAATGCCATTG 1617
DB 20 TTGCCCCCTTAATGCCATTG 1

RESULT 1861
ADP10937
ID ADP10937 standard; DNA; 20 BP.
XX
XX ADP10937;
AC
XX
DT 12-AUG-2004 (first entry)
DE Set 1 left PCR primer for marker probe #282.
XX
KW transplant rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss; primer.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1660 TTGTCCATGCGCAAAACAGGA 1679
DB 1 TTGTCCATGCGCAAAACAGGA 20

RESULT 1862
ADP11268/C
ID ADP11268 standard; DNA; 20 BP.
XX
XX ADP11268;
AC
XX
DT 12-AUG-2004 (first entry)
DE Set 1 right PCR primer for marker probe #282.
XX
KW transplant rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss; primer.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1721 AAGGAATAAGCCCTGCCCAG 1740
DB 20 AAGGAATAAGCCCTGCCCAG 1

RESULT 1863
ADN30395/C
ID ADN30395 standard; DNA; 20 BP.
XX
XX ADN30395;
AC
XX
DT 12-AUG-2004 (first entry)
DE Human Notch2 DNA antisense oligonucleotide #67.
XX
KW Human; Notch2; ss; antisense oligonucleotide; phosphorothioate linkage;
KW 2'-O-methoxyethyl sugar moiety; 5-methylcytosine; autoimmune disorder;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2294 GGATGCTCGATCTCTGA 2313
DB 1 GGATGCTCGATCTCTGA 20

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Db      20 GGATGCTCGATCTCTCTGA 1

RESULT 1864
ADQ75057/c
ID   ADQ75057 standard; DNA; 20 BP.
XX
AC   ADQ75057;
XX
XX
DT   23-SEP-2004 (first entry)
XX
DE   Ligand conjugated oligomeric compound associated oligo seqid 7.
XX
DE   virucide; oligonucleotide binder; protein binder; serum binder;
KW   vascular protein binder; cellular protein binder; oligomeric compound;

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1695 TTTACATGTGCAAGAAGCT 1714
      |||||
Db      20 TTTACATGTGCAAGAAGCT 1

RESULT 1865
AAF84350/c
ID   AAF84350 standard; DNA; 22 BP.
XX
AC   AAF84350;
XX
XX
DT   20-JUN-2001 (first entry)
XX
DE   Human CYP2C18i PCR primer #6.
XX
KW   Gene polymorphism; drug-metabolising enzyme; PCR primer; CYP2C18i; ss.

Query Match      0.8%; Score 20; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2346 TGCTGGGATTACAGGCATGA 2365
      |||||
Db      20 TGCTGGGATTACAGGCATGA 1

RESULT 1866
AAS11629
ID   AAS11629 standard; DNA; 22 BP.
XX
AC   AAS11629;
XX
XX
DT   24-OCT-2001 (first entry)
XX
DE   Human CYP2B6 allele sequencing primer seqCYP2B6-7P for exon 7.
XX
KW   CYP2B6; cytostatic; gene therapy; genotyping; cancer; metabolism; ss;
KW   human; cancer susceptibility; environmental carcinogen;

Query Match      0.8%; Score 20; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2352 GATTACAGGCATGAGCCACC 2371
      |||||
Db      1 GATTACAGGCATGAGCCACC 20

RESULT 1867
ADB04761
ID   ADB04761 standard; DNA; 25 BP.
XX

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AC   ADB04761;
XX
DT   20-NOV-2003 (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 5747.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;

Query Match      0.8%; Score 20; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2274 GGGTTTCACCGTGTAGCCA 2293
      |||||
Db      6 GGGTTTCACCGTGTAGCCA 25

RESULT 1868
ABL60500/c
ID   ABL60500 standard; DNA; 26 BP.
XX
AC   ABL60500;
XX
XX
DT   12-AUG-2002 (first entry)
XX
DE   Human MDM2 mRNA fragment complementary oligo 12.
XX
KW   Pseudo-cyclic oligonucleotide; PCO; gene expression; protein kinase A;
KW   nucleic acid detection; ribozyme inhibition; gene transcription; MDM2;

Query Match      0.8%; Score 20; DB 1; Length 26;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      674 TGTGAGTGAGAACAGGTGTCA 694
      |||||
Db      21 TGTGAGTGAGAACAGGTGTCA 1

RESULT 1869
AAH37414
ID   AAH37414 standard; DNA; 23 BP.
XX
AC   AAH37414;
XX
XX
DT   14-AUG-2001 (first entry)
XX
DE   SNP specific lower PCR primer SEQ ID 210.
XX
KW   Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW   SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match      0.8%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 1.9e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2345 GTCTGGGATTACAGGCATGAGC 2367
      |||||
Db      1 GTGATGGGATTATAGGCATGAGC 23

RESULT 1870
ABZ83516
ID   ABZ83516 standard; DNA; 23 BP.
XX
AC   ABZ83516;
XX
XX
DT   14-MAY-2003 (first entry)
XX
DE   Toxicologically relevant human PCR primer #675.
XX
KW   Toxicologically relevant gene; toxicological response; PCR primer; ss.

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XX
Query Match 0.8%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 1.9e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2292 CAGGATGGTCTCGATCTCTCGAC 2314
DB 1 CAGGATGGTCTCGATCTCTCGAC 23
RESULT 1871
AAI71673/c
ID AAI71673 standard; DNA; 24 BP.
XX AAI71673;
XX
XX
DT 15-JAN-2002 (first entry)
DE Human myosin heavy chain 12-14 coding sequence PCR primer #1.
XX
KW Human; myosin heavy chain 12-14; Prader Willi syndrome; PCR primer;
KW Klinefelter syndrome; inflammation; kinetic illness; gene therapy; ss.
Query Match 0.8%; Score 19.8; DB 1; Length 24;
Best Local Similarity 91.3%; Pred. No. 1.9e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2147 CTGGCTCACTGCAAGCTCTGCC 2169
DB 24 CTGGCTCACTGCAAGCTCTGCC 2
RESULT 1872
AAS00333
ID AAS00333 standard; DNA; 24 BP.
XX AAS00333;
XX
XX
DT 17-MAY-2001 (first entry)
DE PCR primer #2, used to amplify human RAD51 gene at position -2339.
XX
XX
KW Human; RAD51; breast cancer; BRCA1; BRCA2; PCR primer; ss.
XX
Query Match 0.8%; Score 19.8; DB 1; Length 24;
Best Local Similarity 91.3%; Pred. No. 1.9e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2193 CTGCTCAGCTCTCCCAATTAGCT 2215
DB 1 CTGCTCAGCTCTCCCAAGTAACT 23
RESULT 1873
AAD42696
ID AAD42696 standard; DNA; 24 BP.
XX AAD42696;
XX
XX
DT 15-NOV-2002 (first entry)
DE Primer #2 used to construct Hdm2 mutant plasmid.
XX
KW Human; detection; cancer; ARF-p19 protein; cell cycle regulator; tumour;
KW cell cycle arrest; cell growth; hyperproliferative signal; therapeutic;
Query Match 0.8%; Score 19.8; DB 1; Length 24;
Best Local Similarity 91.3%; Pred. No. 1.9e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 307 GGCAAAATGCAATACCAACATG 329

DB 2 GCCATATGTCATACACATG 24
RESULT 1874
ABL50916
ID ABL50916 standard; DNA; 24 BP.
XX ABL50916;
XX
XX
DT 24-JUN-2002 (first entry)
DE Human dihydropyrrrole-5-carboxylate reductase 15 PCR primer 1.
XX
XX
KW Human; dihydropyrrrole-5-carboxylate reductase 15; cancer; enzyme;
KW human immunodeficiency virus infection; HIV infection; PCR primer; ss.
Query Match 0.8%; Score 19.8; DB 1; Length 24;
Best Local Similarity 91.3%; Pred. No. 1.9e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2263 TAGTAGACAGAGGGTTTCACCGT 2285
DB 2 TAGTAGACAGAGGATTTTCAACAT 24
RESULT 1875
ABV74727
ID ABV74727 standard; DNA; 24 BP.
XX ABV74727;
XX
XX
DT 03-FEB-2003 (first entry)
DE Human clathrin light chain 13.64 PCR primer #2.
XX
XX
KW Human; clathrin light chain 13.64; tumour; haemopathy; HIV infection;
KW immunological disease; inflammation; cytostatic; anti-HIV; PCR; primer;
Query Match 0.8%; Score 19.8; DB 1; Length 24;
Best Local Similarity 91.3%; Pred. No. 1.9e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2092 TTTTCTTGGACCGAGTCTTGC 2114
DB 1 TTTTCTTGGACCGAGTCTTGC 23
RESULT 1876
ADB04581
ID ADB04581 standard; DNA; 25 BP.
XX ADB04581;
XX
XX
DT 20-NOV-2003 (first entry)
DE Human MDZ7 scanning oligonucleotide SEQ ID 5567.
XX
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
Query Match 0.8%; Score 19.8; DB 1; Length 25;
Best Local Similarity 91.3%; Pred. No. 1.9e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2089 TTATTTTGGACCGAGTCT 2111
DB 1 TTTTCTTGGACCGAGTCT 23
RESULT 1877
ADB04735
ID ADB04735 standard; DNA; 25 BP.

XX ADB04735;
AC
XX
DT 20-NOV-2003 (first entry)
DE Human MD27 scanning oligonucleotide SEQ ID 5721.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
Query Match 0.8%; Score 19.8; DB 1; Length 25;
Best Local Similarity 91.3%; Pred. No. 1.9e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2246 CTAATTTTGTACTTTTAGTAG 2268
DB 3 CTAATATTTTGTATTTTAGTAG 25
RESULT 1878
ADB04662
ID ADB04662 standard; DNA; 25 BP.
XX
AC ADB04662;
XX
DT 20-NOV-2003 (first entry)
DE Human MD27 scanning oligonucleotide SEQ ID 5648.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
Query Match 0.8%; Score 19.8; DB 1; Length 25;
Best Local Similarity 91.3%; Pred. No. 1.9e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2173 CCCGGGTTCCACATTCCTCTG 2195
DB 3 CCTGGGTTCCACATTCCTCTG 25
RESULT 1879
ADB04580
ID ADB04580 standard; DNA; 25 BP.
XX
AC ADB04580;
XX
DT 20-NOV-2003 (first entry)
DE Human MD27 scanning oligonucleotide SEQ ID 5566.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
Query Match 0.8%; Score 19.8; DB 1; Length 25;
Best Local Similarity 91.3%; Pred. No. 1.9e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2089 TTATTTTGTGACCGAGTCT 2111
DB 2 TTTTGTGACCGAGTCT 24
RESULT 1880
AB222656/C
ID AB222656 standard; DNA; 26 BP.
XX
AC AB222656;
XX
DT 31-MAR-2003 (first entry)
DE Human PEPT1 PCR primer PEPT1#1 R.
XX

KW Human; PEPT1; PEPT2; intestinal peptide transporter; transport;
KW transporter; PCR primer; ss.
Query Match 0.8%; Score 19.8; DB 1; Length 26;
Best Local Similarity 91.3%; Pred. No. 1.9e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2350 GGGATTACAGGCATGAGCCACCG 2372
DB 26 GGGATTACAGGCCTTGAGCTACCG 4
RESULT 1881
AAA39394/C
ID AAA39394 standard; DNA; 26 BP.
XX
AC AAA39394;
XX
DT 04-OCT-2000 (first entry)
DE Alu repeat 3' end consensus oligonucleotide SEQ ID NO:7.
XX
KW Alu 3' end primer; human genome; allele; phenotype; screening;
KW polymorphic; characterisation; ss.
Query Match 0.8%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 1.9e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2099 TGAGACCGAGTCTGCTGTATACC 2124
DB 26 TGAGACCGAGTCTGCTGTATGCC 1
RESULT 1882
AAA62473/C
ID AAA62473 standard; DNA; 26 BP.
XX
AC AAA62473;
XX
DT 21-NOV-2000 (first entry)
DE Human SECX 2826468 probe.
XX
KW Human; secreted protein; SECX; cancer; cytostatic; vaccine; probe;
KW expression analysis; ss.
Query Match 0.8%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 1.9e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2269 AGACAGGGTTTACCGTGTAGCCAG 2294
DB 26 ACATGGGGTCTCACCGTGTAGCCAG 1
RESULT 1883
AAR64089/C
ID AAR64089 standard; DNA; 26 BP.
XX
AC AAR64089;
XX
DT 06-APR-2001 (first entry)
DE Primer #33.
XX
KW Human; lipoprotein lipase; LPL; stenosis; ss.
Query Match 0.8%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 1.9e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ID	ADN62195 standard; DNA; 26 BP.	XX	ADN62195;	XX	01-JUL-2004 (first entry)	XX	Human NOV20a RTQ-PCR probe.	DE	Human; ss; PCR; NOVX; diabetes; obesity; infectious disease; anorexia; cancer-associated cachexia; cancer; neurodegenerative disorder;	KW	Query Match 0.8%; Score 19.6; DB 1; Length 26; Best Local Similarity 84.6%; Pred. No. 1.9e+03; Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	QY	2228 ATCTGCCACACACCTGGCTAATTTT 2253	DB	1 ATGCACCACTCTCTGGCTAATTTT 26	RESULT 1888	AAV40598	ID	AAV40598 standard; DNA; 21 BP.	XX	AAV40598;	XX	21-DEC-1998 (first entry)	XX	Human TSC gene exon 16 reverse primer hTSCex16.	DE	Thiazide-sensitive Na-Cl cotransporter; TSC; hTSC gene; human; ion transport; Gitelman's syndrome; Bartter's syndrome;	KW	Query Match 0.8%; Score 19.4; DB 1; Length 21; Best Local Similarity 95.2%; Pred. No. 1.9e+03; Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	QY	2346 TGCTGGGATTACAGGCATGAG 2366	DB	1 TGCTGGGTTTACAGGCATGAG 21	RESULT 1889	AAH86419	ID	AAH86419 standard; DNA; 21 BP.	XX	AAH86419;	XX	29-SEP-1999 (first entry)	XX	PCR primer PDZK5.6P used to amplify DNA encoding MMSC1 protein.	DE	Human; MMSC1 protein; MMAC1 interacting protein; tumour suppression; MMAC1 pathway; immunogen; cancer; cell neoplastic growth; PCR primer; ss.	KW	Query Match 0.8%; Score 19.4; DB 1; Length 21; Best Local Similarity 95.2%; Pred. No. 1.9e+03; Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	QY	2110 CTGTGCTCTGTACCCAGGCTG 2130	DB	1 CTGTGCTCTGTACCCAGGCTG 21	RESULT 1890	AAH38522	ID	AAH38522 standard; DNA; 21 BP.	XX	AAH38522;	XX	14-AUG-2001 (first entry)	XX	SNP specific lower PCR primer SEQ ID 1318.	DE
QY	2102 GACCGAGTCTTGCTCTGTACCCAGG 2127	DB	26 GACACAGTCTCGCTCAGTTACCCAGG 1	RESULT 1884	AAH22716/c	ID	AAH22716 standard; DNA; 26 BP.	XX	AAH22716;	XX	07-SEP-2001 (first entry)	XX	Human secreted protein (SECX) specific oligo.	DE	Secreted protein; SECX; cancer; human; cytostatic; gene therapy;	KW	PCR primer; probe; ss.	Query Match 0.8%; Score 19.6; DB 1; Length 26; Best Local Similarity 84.6%; Pred. No. 1.9e+03; Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	QY	2269 AGACAGGGTTTACCGTGTAGCCAG 2294	DB	26 ACATGGGGTCTCACCGTGTAGCCAG 1	RESULT 1885	ABK61474/c	ID	ABK61474 standard; DNA; 26 BP.	XX	ABK61474;	XX	18-JUN-2002 (first entry)	XX	Human NOV3 Exon linking PCR primer #2.	DE	Human; ss; NOVX; gene therapy; cardiomyopathy; atherosclerosis; cell signal processing disorder; metabolic pathway modulation disorder;	KW	Query Match 0.8%; Score 19.6; DB 1; Length 26; Best Local Similarity 84.6%; Pred. No. 1.9e+03; Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	QY	2190 CTCTGCTCAGCTTCCCAATTAGCT 2215	DB	26 CTCTGCTCAGCTTCCCAATTAGCT 1	RESULT 1886	ABX97292	ID	ABX97292 standard; DNA; 26 BP.	XX	ABX97292;	XX	20-MAY-2003 (first entry)	XX	Human NOV-associated probe from primer-probe set Ag3293.	DE	NOVX; cytostatic; cardiant; antiarteriosclerotic; antiasthmatic; cancer; hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine;	KW	Query Match 0.8%; Score 19.6; DB 1; Length 26; Best Local Similarity 84.6%; Pred. No. 1.9e+03; Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	QY	2228 ATCTGCCACACCTGGCTAATTTT 2253	DB	1 ATGCACCACTCTCTGGCTAATTTT 26	RESULT 1887	ADN62195		

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XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match      0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2341 CAAAGTCTGGGATTACAGGC 2361
DB 1 CAAAGTCTGGGATTACAGGC 21

RESULT 1891
AAH40070
ID AAH40070 standard; DNA; 21 BP.
XX
AC AAH40070;
XX
DT 14-AUG-2001 (first entry)
DE SNP specific lower PCR primer SEQ ID 2866.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match      0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2283 CGTGTAGCCAGGATGCTCTC 2303
DB 1 CATGTTAGCCAGGATGCTCTC 21

RESULT 1892
AAH24567/c
ID AAH24567 standard; DNA; 21 BP.
XX
AC AAH24567;
XX
DT 07-AUG-2001 (first entry)
DE Human Alu sequence-specific primer Alu-Sense.
KW Human; Alu; metastatic potential determination; cancer;
KW chorioallantoic membrane; CAM; avian embryo; intravasation;

Query Match      0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2343 AAGTGTGGGATTACAGGCAT 2363
DB 21 AAGTGTGGGATTACAGGCGT 1

RESULT 1893
ABQ74069
ID ABQ74069 standard; DNA; 21 BP.
XX
AC ABQ74069;
XX
DT 11-OCT-2002 (first entry)
DE Microsatellite typing and sequencing D6S105 5' primer.
KW Homozygous stem cell; major histocompatibility complex; MHC; HLA;
KW human leukocyte antigen; immunotype; genotype; microsatellite; probe;

Query Match      0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 2350 GGGATTACAGGCATGAGCCAC 2370
DB 1 GGGATTACAGGCAGGAGCCAC 21

RESULT 1894
ABS98158
ID ABS98158 standard; DNA; 21 BP.
XX
AC ABS98158;
XX
DT 23-DEC-2002 (first entry)
DE Human multidrug resistance gene polymorphic sequence #60.
XX
KW Human; ds; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1;
KW cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTF;

Query Match      0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2278 TTCACCGTGTACCCAGGATG 2298
DB 1 TTCACCGTGTACCCAGGATG 21

RESULT 1895
ABS97183
ID ABS97183 standard; DNA; 21 BP.
XX
AC ABS97183;
XX
DT 23-DEC-2002 (first entry)
DE Human CYP450A2 promoter polymorphism #1.
XX
KW Human; ds; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1;
KW cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTF;

Query Match      0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 TGATCGCCACCTCGGCTC 2339
DB 1 TGATCGCCACCTCGGCTC 21

RESULT 1896
ABS98107/c
ID ABS98107 standard; DNA; 21 BP.
XX
AC ABS98107;
XX
DT 23-DEC-2002 (first entry)
DE Human multidrug resistance gene polymorphic sequence #9.
XX
KW Human; ds; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1;
KW cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTF;

Query Match      0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2174 CCGGGTTCCGACCATCTCTCT 2194
DB 21 CCGGGTTCCGACCATCTCTCT 1

RESULT 1897

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ABS98163
ID ABS98163 standard; DNA; 21 BP.
XX
AC ABS98163;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human multidrug resistance gene polymorphic sequence #65.
XX
KW Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

Query Match 0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2351 GGATTACAGGCGTGAGCCACC 2371
DB 1 GGATTACAGGCGTGAGCCACC 21

RESULT 1898
ABS98105/c
ID ABS98105 standard; DNA; 21 BP.
XX
AC ABS98105;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human multidrug resistance gene polymorphic sequence #7.
XX
KW Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

Query Match 0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2314 CCTCGTGATCCGCCACCTCG 2334
DB 21 CCTCGTGATCCGCCCGCTCG 1

RESULT 1899
ADE14130/c
ID ADE14130 standard; DNA; 21 BP.
XX
AC ADE14130;
XX
DT 29-JAN-2004 (first entry)
XX
DE Optineurin promoter motif, repeat element or regulatory region #239.
XX
KW Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
SNP; glaucoma; progressive ocular hypertensive disorder;

Query Match 0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2332 TCGGCTCCCAAGTGTGGG 2352
DB 21 TCGGCTCCCAAGTGTGGG 1

RESULT 1900
ADH59601/c
ID ADH59601 standard; DNA; 21 BP.
XX
AC ADH59601;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human Y chromosome non-recombining region polymorphic fragment #247.
XX
KW ethnic origin determination; polymorphic site determination;
Y chromosome; paternity testing; forensic; diagnosis;

Query Match 0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DE Non-nucleotide probe of the invention #5.
XX
KW non-nucleotide probe; Bacterial Artificial Chromosome clone; BAC; ss;
KW probe.

Query Match 0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGACAGGGTTTC 2280
DB 21 TTTTAGTAGACAGGGTTTC 1

RESULT 1901
ADH59613
ID ADH59613 standard; DNA; 21 BP.
XX
AC ADH59613;
XX
DT 25-MAR-2004 (first entry)
XX
DE Non-nucleotide probe of the invention #17.
XX
KW non-nucleotide probe; Bacterial Artificial Chromosome clone; BAC; ss;
KW probe.

Query Match 0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGACAGGGTTTC 2280
DB 1 TTTTAGTAGACAGGGTTTC 21

RESULT 1902
AD23739
ID AD23739 standard; DNA; 21 BP.
XX
AC AD23739;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human LPDLR PCR primer #19.
XX
KW lipase; LPDL; LPDLR; lipase deficiency; atherosclerosis;
fatty liver disease; dyslipidaemia; hypercholesterolaemia;

Query Match 0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2352 GATTACAGCATGACCCG 2372
DB 1 GATTACAGCATGACCCG 21

RESULT 1903
ADM65580
ID ADM65580 standard; DNA; 21 BP.
XX
AC ADM65580;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human Y chromosome non-recombining region polymorphic fragment #247.
XX
KW ethnic origin determination; polymorphic site determination;
Y chromosome; paternity testing; forensic; diagnosis;

Query Match 0.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2277 TTTCCCGTGTAGCCAGGAT 2297
 ||||| ||||| ||||| |||||
 Db 1 TTTCCCTTGTAGCCAGGAT 21

RESULT 1904
 ADO55495
 ID ADO55495 standard; DNA; 21 BP.
 XX
 AC ADO55495;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE HIV gene expression analysis primer SB704 following siRNA inhibition.
 XX
 KW ss; primer; anti-HIV; virucide; gene therapy; small interfering RNA;
 KW siRNA; HIV; genome; diagnosis.

Query Match 0.8%; Score 19.4; DB 1; Length 21;
 Best Local Similarity 95.2%; Pred. No. 1.9e+03;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2346 TGCTGGGATTACAGGATGAG 2366
 ||||| ||||| ||||| |||||
 Db 1 TGCTGGGATTACAGGCGTGAG 21

RESULT 1905
 AAX09910/c
 ID AAX09910 standard; DNA; 22 BP.
 XX
 AC AAX09910;
 XX
 DT 24-MAR-1999 (first entry)
 XX
 DE Human biallelic polymorphic marker downstream primer #216.
 XX
 KW Polymorphism; biallelic; human; forensic; paternity testing; disease;
 KW detection; phenotypic typing; characteristic; infection; hereditary;

Query Match 0.8%; Score 19.4; DB 1; Length 22;
 Best Local Similarity 95.2%; Pred. No. 1.9e+03;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2234 CACCACACCTGGCTAAATTTT 2254
 ||||| ||||| ||||| |||||
 Db 21 CACCACACCTGGTTAAATTTT 1

RESULT 1906
 AAF29797/c
 ID AAF29797 standard; DNA; 22 BP.
 XX
 AC AAF29797;
 XX
 DT 09-APR-2001 (first entry)
 XX
 DE Preseniline-1 gene promoter PCR primer Prom22R.
 XX
 KW Human; PSEN1; Alzheimer's disease; polymorphism; diagnosis;
 KW preseniline-1; chromosome 14; PCR primer; ss.

Query Match 0.8%; Score 19.4; DB 1; Length 22;
 Best Local Similarity 95.2%; Pred. No. 1.9e+03;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2260 TTTTAGTAGACAGCGGTTTC 2280
 ||||| ||||| ||||| |||||
 Db 21 TTTTAGTAGACAGCGGTTTC 1

RESULT 1907
 ADC24360
 ID ADC24360 standard; DNA; 22 BP.
 XX
 AC ADC24360;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE PCR primer for amplifying the BRCA1 gene #SEQ ID 50.
 XX
 KW DNA amplification; copy number; polymerase chain reaction; PCR; primer;
 KW ss.

Query Match 0.8%; Score 19.4; DB 1; Length 22;
 Best Local Similarity 95.2%; Pred. No. 1.9e+03;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2340 CCAAAGTGTGGGATTACAGG 2360
 ||||| ||||| ||||| |||||
 Db 1 CCAAAGTGTAGGATTACAGG 21

RESULT 1908
 ADH13395/c
 ID ADH13395 standard; DNA; 23 BP.
 XX
 AC ADH13395;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Human malignant neoplasia-related PCR primer SeqID244.
 XX
 KW malignant neoplasia; cytostatic; breast cancer; ovarian cancer;
 KW gastric cancer; colon cancer; oesophageal cancer; mesenchymal cancer;

Query Match 0.8%; Score 19.4; DB 1; Length 23;
 Best Local Similarity 95.2%; Pred. No. 1.9e+03;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2145 ATCTTGGCTCACTGCAAGCTC 2165
 ||||| ||||| ||||| |||||
 Db 23 ATCTTGGCTCACTGCAACCTC 3

RESULT 1909
 ABS56410
 ID ABS56410 standard; DNA; 24 BP.
 XX
 AC ABS56410;
 XX
 DT 23-JAN-2003 (first entry)
 XX
 DE Human DNA mismatch repair gene 10.45 specific RT-PCR primer, #2.
 XX
 KW Human; RT-PCR; ss; DNA mismatch repair gene 10.45; tumour; haemopathy;
 KW human immunodeficiency virus; HIV; immunological disease; inflammation;

Query Match 0.8%; Score 19.4; DB 1; Length 24;
 Best Local Similarity 95.2%; Pred. No. 2e+03;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2103 ACCGAGTCTTGTCTGTACC 2123
 ||||| ||||| ||||| |||||
 Db 1 ACCGAGTCTTGTCTGTACC 21

RESULT 1910
 ABK14172
 ID ABK14172 standard; DNA; 24 BP.
 XX
 AC ABK14172;
 XX
 DT 21-MAY-2002 (first entry)

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XX Insulin like growth factor binding protein 11.88 cDNA RT-PCR primer #2.
DE
XX
KW Insulin like growth factor binding protein 11.88; primer; ss; cytostatic;
KW embryo development dysmorphia; malignant tumour; gene therapy; cancer;

Query Match      0.8%; Score 19.4; DB 1; Length 24;
Best Local Similarity 95.2%; Pred. No. 2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2106 GAGTCTTGCTCTGTATCCAC 2126
DB 4 GAGTCTTGCTCTGTATCCAC 24

RESULT 1911
ABV76761/c
ID ABV76761 standard; DNA; 24 BP.
XX
AC ABV76761;
XX
DT 07-MAR-2003 (first entry)
XX
DE Ras GTP enzyme-activating protein 20.68 RT-PCR primer, SEQ ID NO:3.
XX
DE Ras GTP enzyme-activating protein 20.68; cancer suppressor protein-20.68;
KW recombinant production; gene therapy; cancer; tumour; HIV infection;
KW

Query Match      0.8%; Score 19.4; DB 1; Length 24;
Best Local Similarity 95.2%; Pred. No. 2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2187 ATTCTCTGCTCAGCTCC 2207
DB 21 ATTCTCTGCTCAGCTCC 1

RESULT 1912
ABL42193
ID ABL42193 standard; DNA; 24 BP.
XX
AC ABL42193;
XX
DT 12-JUN-2002 (first entry)
XX
DE PCR primer #2 for human cartilage connective protein 10.67 cDNA.
DE
XX Human; cartilage connective protein 10.67; disease; PCR primer; ss.
XX

Query Match      0.8%; Score 19.4; DB 1; Length 24;
Best Local Similarity 95.2%; Pred. No. 2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2106 GAGTCTTGCTCTGTATCCAC 2126
DB 4 GAGTCTTGCTCTGTATCCAC 24

RESULT 1913
ABS55854
ID ABS55854 standard; DNA; 24 BP.
XX
AC ABS55854;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human SOX3 protein 13.31 cDNA RT-PCR primer #1.
DE
XX Human; SOX3 protein 13.31; primer; ss; malignant tumour; haemopathy;
KW HIV infection; human immunodeficiency virus; immunological disease;
KW

Query Match      0.8%; Score 19.4; DB 1; Length 24;

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Best Local Similarity 95.2%; Pred. No. 2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2351 GGATTACAGCATGAGCCAC 2371
DB 1 GGATTACAGCATGAGCCAC 21

RESULT 1914
ABZ24886
ID ABZ24886 standard; DNA; 24 BP.
XX
AC ABZ24886;
XX
DT 25-MAR-2003 (first entry)
XX
DE High-mobility component protein 12.87 PCR primer #2.
XX
DE High-mobility component protein 12.87; cancer; HIV infection; cytostatic;
KW anti-HIV; PCR; primer; ss.
KW

Query Match      0.8%; Score 19.4; DB 1; Length 24;
Best Local Similarity 95.2%; Pred. No. 2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2106 GAGTCTTGCTCTGTATCCAC 2126
DB 4 GAGTCTTGCTCTGTATCCAC 24

RESULT 1915
AAT63214
ID AAT63214 standard; DNA; 20 BP.
XX
AC AAT63214;
XX
DT 17-JUN-1997 (first entry)
XX
DE Primer Alu 5' used in Inter-Alu PCR for PAC isolation.
DE
XX S182 gene; familial Alzheimer's disease; diagnosis; transgenic animal;
KW polymerase chain reaction; PCR; primer; artificial chromosome; PAC; ss.
KW

Query Match      0.8%; Score 19.2; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.9e+03;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2351 GGATTACAGCATGAGCCAC 2370
DB 1 GGATTACAGCATGAGCCAC 20

RESULT 1916
ADL72189/c
ID ADL72189 standard; DNA; 23 BP.
XX
AC ADL72189;
XX
DT 20-MAY-2004 (first entry)
XX
DE Alu-specific primer AD-1.
DE
XX Nucleic acid amplification; Alu; fluorescence in-situ hybridization;
KW FISH; primer; PCR; ss.
KW

Query Match      0.8%; Score 19.2; DB 1; Length 23;
Best Local Similarity 81.8%; Pred. No. 2e+03;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2098 TTGAGACCGAGTCTTCTCTGT 2119
DB 22 TTGAGACCGAGTCTTCTCTGT 1

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RESULT 1917
AAV52725/c
ID AAV52725 standard; DNA; 24 BP.
XX
XX
AC AAV52725;
XX
DT 21-DEC-1998 (first entry)
XX
XX Hepatocyte nuclear factor 1 alpha gene STS UC-39 forward primer.
DE
DE Hepatocyte nuclear factor 1 alpha; HNF-1 alpha; MODY3; human;
XX
KW Hepatocyte nuclear factor; maturity onset diabetes of the young; diabetes;
KW transcription factor;
Query Match 0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2099 TGAGACGAGTCTTGCTCTGTTAC 2122
DB 24 TGAGATGGAGTCTTGCTCTGTTGC 1

RESULT 1918
AAV27978
ID AAX27978 standard; cDNA; 24 BP.
XX
XX
AC AAX27978;
XX
DT 08-JUN-1999. (first entry)
XX
XX PCR primer for B18hum coding sequence.
DE
DE B18hum; bronchoalveolar protein; peroxisome-associated polypeptide;
KW lung injury; oxidative stress-related disorder; inflammatory disease;
KW
Query Match 0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2267 AGAGACAGGGTTTCACCGTCTTAG 2290
DB 1 AGAGACAGGGTTTCACCATCTTGG 24

RESULT 1919
AAV27181
ID AAA27181 standard; DNA; 24 BP.
XX
XX
AC AAA27181;
XX
DT 11-SEP-2000 (first entry)
XX
DE Reverse primer P2 for target sequence human P2 gene.
KW
KW P2; CX5C chemokine; Chromosome 5q31; gene therapy; asthma; PCR primer;
KW allergic rhinitis; urticaria; anaphylactic shock; hives; hay fever; human;
Query Match 0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2115 TCTGTTACCCAGGCTGGAGTGCAG 2138
DB 1 TATGTCACCCAGGCTGGGGTGCAG 24

RESULT 1920
AAV92846
ID AAF92846 standard; DNA; 24 BP.
XX
XX
AC AAF92846;
XX
XX

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DT 17-MAY-2001 (first entry)
XX
DE Human ABC1 transcription factor binding site #9.
XX
XX High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.
XX
Query Match 0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2293 AGGATGGTCTCGATCTCTGACCT 2316
DB 1 AGGTGGTTTTCGAACCTCTGACCT 24

RESULT 1921
AAH40034/c
ID AAH40034 standard; DNA; 24 BP.
XX
XX
AC AAH40034;
XX
DT 14-AUG-2001 (first entry)
XX
XX SNP specific lower PCR primer SEQ ID 2830.
DE
DE Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW
Query Match 0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2334 GGCTCCCAAGCTCTGGGATTAC 2357
DB 24 GGACTCTCTAAAGTCTGGAATTAC 1

RESULT 1922
AAI66532
ID AAI66532 standard; DNA; 24 BP.
XX
XX
AC AAI66532;
XX
DT 11-DEC-2001 (first entry)
XX
DE Human pterin-molybdenum oxidoreductase 10 cDNA PCR primer #2.
KW
KW Human; pterin-molybdenum oxidoreductase 10; cancer; haemopathy;
KW immunological disease; HIV infection; inflammation; gene therapy;
KW
Query Match 0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2117 TGTATCCAGGCTGGAGTGCAGTG 2140
DB 1 TGTATCCAGGCTGGAGTGCAGTG 24

RESULT 1923
ABA82841/c
ID ABA82841 standard; DNA; 24 BP.
XX
XX
AC ABA82841;
XX
XX
DT 07-FEB-2002 (first entry)
XX
XX Human protective DNA sequence CNI-00746 fragment #6.
DE
DE Human; protective sequence; cell death; cancer; autoimmune disease;
KW neurological disorder; stroke; cytostatic; neuroprotective; gene therapy;
KW

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Query Match      0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2262 TTAGTAGACAGCGGTTTCACCGT 2285
DB 24 TTAGTAGACAGCGGTTTCACCAT 1

RESULT 1924
ABL41332
ID ABL41332 standard; DNA; 24 BP.
XX
AC ABL41332;
XX
DT 22-MAY-2002 (first entry)
DE Human mitochondrial ATPase coupling factor F69.35 PCR primer 2.
DE Human; mitochondrial ATPase coupling factor F69.35; sugar; fat; protein;
KW metabolic disturbance; PCR; primer; ss.

Query Match      0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2102 GACCGAGTCTTGCTCTGTATCCCA 2125
DB 1 GACAGAGTCTTGTCTGTGTGCCCA 24

RESULT 1925
ABS56119
ID ABS56119 standard; DNA; 24 BP.
XX
AC ABS56119;
XX
DT 22-JAN-2003 (first entry)
DE RT-PCR primer #2 for cDNA encoding human zinc finger protein 11.55.
DE Human; zinc finger protein 11.55; malignant tumour; haemopathy;
KW human immunodeficiency virus infection; HIV infection;

Query Match      0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2100 GAGACCGAGTCTTGCTCTGTATCC 2123
DB 1 GAGACGGAGTCTTGCTCGTCACCC 24

RESULT 1926
ABS56756
ID ABS56756 standard; DNA; 24 BP.
XX
AC ABS56756;
XX
DT 30-JAN-2003 (first entry)
DE DNA topoisomerase II-beta (TOP2B), 9.02 RT-PCR primer #2.
DE DNA topoisomerase II-beta 9.02; TOP2B 9.02; cancer; HIV infection; PCR;
KW primer; amplification; ss.

Query Match      0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2103 ACCGAGTCTTGCTCTGTATCCCA 2126
DB 1 ACAGAGTCTTGCTCTGTGCCCA 24
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RESULT 1927
ABK52730
ID ABK52730 standard; DNA; 24 BP.
XX
AC ABK52730;
XX
DT 27-AUG-2002 (first entry)
DE Human Mch2 protein 11.55. RT-PCR primer #2.
DE Human; Mch2 protein 11.55; cancer; human immunodeficiency virus; HIV;
KW reverse transcriptase PCR; RT-PCR; primer; ss.

Query Match      0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2100 GAGACCGAGTCTTGCTCTGTATCC 2123
DB 1 GAGACGGAGTCTCGCTCTGTGCC 24

RESULT 1928
ABQ77952
ID ABQ77952 standard; DNA; 24 BP.
XX
AC ABQ77952;
XX
DT 30-JAN-2003 (first entry)
DE Mitochondrial translation initiation factor 10.01 RT-PCR primer 2.
DE Human; mitochondrial translation initiation factor 10.01;
KW recombinant production; gene therapy; sugar metabolism disorder;

Query Match      0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2104 CCGAGTCTTGCTCTGTATCCAGG 2127
DB 1 CCGAGTCTCGCTCTGTACCCAGG 24

RESULT 1929
ABL41338
ID ABL41338 standard; DNA; 24 BP.
XX
AC ABL41338;
XX
DT 22-MAY-2002 (first entry)
DE Human TFIID subunit p30beta protein 12.54 PCR primer SEQ ID NO 3.
DE Human; TFIID subunit p30beta protein 12.54; tumour; inflammation;
KW protein metabolism dysfunction; immunological disease; haemopathy; HIV;

Query Match      0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2108 GTCTCTCTGTGTATCCAGGCTGG 2131
DB 1 GTCTCTCTGTGTGCCAGGCTGG 24

RESULT 1930
ABK89466
ID ABK89466 standard; DNA; 24 BP.
XX
AC ABK89466;
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XX 05-NOV-2002 (first entry)
XX Human large protein 17.6 specific RT-PCR primer, #1.
XX Human; RT-PCR; ss; large protein 17.6; embryonic development deformity;
XX protein metabolism disturbance; tumour; antagonist;
Query Match 0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 3; Gaps 0;
QY 2104 CCGAGTCTTGCTCTGTACCCAG 2127
DB 1 CAGGGTCTTGCTCTGTACCCAG 24

RESULT 1931
ABA94088
ID ABA94088 standard; DNA; 24 BP.
XX
AC ABA94088;
XX
DT 08-MAY-2002 (first entry)
XX Human tumour suppressor factor 11.77 PCR primer 2 SEQ ID NO:4.
XX Human; tumour suppressor factor 11.77; cytostatic; haemostatic; virucide;
XX immunomodulatory; antiinflammatory; gene therapy; malignant tumour;
Query Match 0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 3; Gaps 0;
QY 2103 ACCGAGTCTTGCTCTGTACCCAG 2126
DB 1 ACGGAGTCTTGCTCTGTGCCCCAG 24

RESULT 1932
ABS56496
ID ABS56496 standard; DNA; 24 BP.
XX
AC ABS56496;
XX
DT 22-JAN-2003 (first entry)
XX Human cell signal/architecture protein 10.56 RT-PCR primer #2.
XX Human; ss; cell signal/architecture protein 10.56; PCR; primer;
XX nervous disorder; RT-PCR; reverse transcriptase PCR.
Query Match 0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 3; Gaps 0;
QY 2102 GACCGAGTCTTGCTCTGTACCCA 2125
DB 1 GATGGAGTCTTGCTCTGTGCCCCA 24

RESULT 1933
ABA01638
ID ABA01638 standard; DNA; 24 BP.
XX
AC ABA01638;
XX
DT 05-FEB-2002 (first entry)
XX Human tyrosinase 12 PCR primer 2 SEQ ID NO:4.
XX Human; tyrosinase 12; cytostatic; virucidal; immunomodulatory;
XX antiinflammatory; haemostatic; diagnosis; malignancy; haemopathy;

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Query Match 0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 3; Gaps 0;
QY 2103 ACCGAGTCTTGCTCTGTACCCAG 2126
DB 1 ACAGGGTCTTGCTCTGTACCCAG 24

RESULT 1934
ABK90209
ID ABK90209 standard; DNA; 24 BP.
XX
AC ABK90209;
XX
DT 21-OCT-2002 (first entry)
XX Human transcription binding factor (CBF-C) RT-PCR primer #1.
XX Human; ss; primer; CBF-C; 13.42; transcription binding factor;
XX gamma subunit; protein metabolism disorder; reverse transcriptase PCR.
Query Match 0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 3; Gaps 0;
QY 2108 GTCTTGTCTTGCTCTGTACCCAGCTGG 2131
DB 1 GTCTCGTCTTGCTCGCCAGGCTGG 24

RESULT 1935
ABV74685
ID ABV74685 standard; DNA; 24 BP.
XX
AC ABV74685;
XX
DT 03-FEB-2003 (first entry)
XX Human SOX3 protein 10.67 PCR primer #2.
XX Human; SOX3 protein 10.67; haemophilia A; PCR; primer;
XX pseudohypertrophic muscular dystrophy; bo-Fu-Lai syndrome; ss.
Query Match 0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 3; Gaps 0;
QY 2103 ACCGAGTCTTGCTCTGTACCCAG 2126
DB 1 ACAGTGTCTTGCTCTGTACCCAG 24

RESULT 1936
AAS19678/c
ID AAS19678 standard; DNA; 24 BP.
XX
AC AAS19678;
XX
DT 09-APR-2002 (first entry)
XX RT-PCR primer #2 for cDNA encoding human tyrosinase 12.
XX Human; tyrosinase 12; malignant tumour; haemopathy; HIV infection;
XX human immunodeficiency virus; cytostatic; immunological disease;
Query Match 0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 3; Gaps 0;
QY 2125 AGGCTGGAGTGCAGTGGTGATCT 2148
DB 1 AGGCTGGAGTGCAGTGGTGATCT 2148

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Db      24 AGGCTGGAGTGCATGCTGTGATCT 1

RESULT 1937
ABK12883
ID      ABK12883 standard; DNA; 24 BP.
XX
XX
AC      ABK12883;
XX
DT      18-JUN-2002 (first entry)
XX
DE      Ras GTP activator protein 12, RT-PCR primer 2.
XX
KW      Ras GTP activator protein 12; malignant tumour; haemopathy; HIV;
KW      human immunodeficiency virus infection; immunological disease;

Query Match      0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2102 GACCGAGTCTTGCTCTGTACCCA 2125
      ||| ||||| ||||| |||||
Db      1 GACGGGTCTTACTCTGTACCCA 24

RESULT 1938
ABA05003
ID      ABA05003 standard; DNA; 24 BP.
XX
XX
AC      ABA05003;
XX
DT      20-FEB-2002 (first entry)
XX
DE      Human tyrosine kinase 14 coding sequence PCR primer #2.
XX
KW      Human; tyrosine kinase 14; cancer; haemopathy; HIV infection;
KW      immunological disease; inflammation; developmental disorder; cytostatic;

Query Match      0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2102 GACCGAGTCTTGCTCTGTACCCA 2125
      ||| ||||| ||||| |||||
Db      1 GATGGAGTCTTGCTCTGTACCCA 24

RESULT 1939
ABA95476
ID      ABA95476 standard; DNA; 24 BP.
XX
XX
AC      ABA95476;
XX
DT      04-APR-2002 (first entry)
XX
DE      Human dihydroorotase 11 PCR primer #1.
XX
KW      Human; dihydroorotase 11; cytostatic; haemostatic; virucide; PCR primer;
KW      immunomodulatory; antiinflammatory; gene therapy; enzyme; tumour;

Query Match      0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2100 GAGACCGAGTCTTGCTCTGTACCC 2123
      ||||| ||||| ||||| |||||
Db      1 GAGACAGAGTCTCGCTCTGTACCC 24

RESULT 1940
ADC48698
ID      ADC48698 standard; DNA; 24 BP.
XX

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AC      ADC48698;
XX
DT      18-DEC-2003 (first entry)
XX
DE      Human epilepsy associated protein-11.77, RT-PCR primer #2.
XX
KW      Human; epilepsy associated protein-11.77; cancer; haematopathy;
KW      HIV infection; immune disease; reverse transcriptase-PCR; RT-PCR; primer;

Query Match      0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2102 GACCGAGTCTTGCTCTGTACCCA 2125
      ||| ||||| ||||| |||||
Db      1 GACGGAGCCTTGCTCTGTACCCA 24

RESULT 1941
ABZ57061
ID      ABZ57061 standard; DNA; 24 BP.
XX
XX
AC      ABZ57061;
XX
DT      24-MAR-2003 (first entry)
XX
DE      Excitatory amino acid transport protein 13.53 RT-PCR primer, SEQ ID NO:4.
XX
KW      Human; excitatory amino acid transport protein 13.53;
KW      recombinant production; gene therapy; glutamic acid transport disorder;

Query Match      0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2322 TCCGCCACCTCGGCTCCCAAG 2345
      ||| ||||| ||||| |||||
Db      1 TCCTCCACCTTGCTTCCCAAG 24

RESULT 1942
ADG83872
ID      ADG83872 standard; DNA; 24 BP.
XX
XX
AC      ADG83872;
XX
DT      11-MAR-2004 (first entry)
XX
DE      Human SLC6A14 forward PCR primer SEQ ID NO:13.
XX
KW      differentiation; ulcerative colitis; Crohn's disease;
KW      target genetic marker gene; human; PCR primer; ss.

Query Match      0.8%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2345 GTCTGGATTACAGGCATGAGCC 2368
      ||||| ||||| ||||| |||||
Db      1 GTCTGAGATTACAGGTGTGAGCC 24

RESULT 1943
ADB04577
ID      ADB04577 standard; DNA; 25 BP.
XX
XX
AC      ADB04577;
XX
DT      20-NOV-2003 (first entry)
XX
DE      Human MD27 scanning oligonucleotide SEQ ID 5563.
XX
KW      Cytostatic; immunostimulant; gene therapy; vaccine; human;

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KW  zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
Query Match      0.8%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2086 TTATTATTTTGTGAGACCGAGT 2109
DB  2 TTTTGTGAGACGAGT 25

RESULT 1944
ADB04583
ID  ADB04583 standard; DNA; 25 BP.
XX
AC  ADB04583;
XX
DT  20-NOV-2003 (first entry)
XX
DE  Human MD27 scanning oligonucleotide SEQ ID 5569.
XX
KW  Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW  zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;

Query Match      0.8%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2092 TTTTGTGAGACCGAGTCTGTCT 2115
DB  2 TTTTGTGAGACGAGTCTGTCT 25

RESULT 1945
ADB04677
ID  ADB04677 standard; DNA; 25 BP.
XX
AC  ADB04677;
XX
DT  20-NOV-2003 (first entry)
XX
DE  Human MD27 scanning oligonucleotide SEQ ID 5663.
XX
KW  Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW  zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;

Query Match      0.8%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2186 CATTCCTGCTCAGCTCCCA 2209
DB  1 CATTCCTGCTCAGTCTCCGA 24

RESULT 1946
ADB04586
ID  ADB04586 standard; DNA; 25 BP.
XX
AC  ADB04586;
XX
DT  20-NOV-2003 (first entry)
XX
DE  Human MD27 scanning oligonucleotide SEQ ID 5572.
XX
KW  Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW  zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;

Query Match      0.8%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2094 TTTTGTGAGACCGAGTCTGTCT 2117

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DB  1 TTTTGTGAGACGAGTCTGTCT 24

RESULT 1947
ADB04747
ID  ADB04747 standard; DNA; 25 BP.
XX
AC  ADB04747;
XX
DT  20-NOV-2003 (first entry)
XX
DE  Human MD27 scanning oligonucleotide SEQ ID 5733.
XX
KW  Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW  zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;

Query Match      0.8%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 2e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2256 GTACTTTTAGTAGAGACGGGTTT 2279
DB  1 GTATTTTAGTAGAGACGGGGTTT 24

RESULT 1948
AAT94763
ID  AAT94763 standard; DNA; 19 BP.
XX
AC  AAT94763;
XX
DT  25-MAR-2003 (revised)
DT  18-FEB-1998 (first entry)
XX
DE  Human progesterone receptor gene primer.
XX
KW  Human; progesterone receptor; breast cancer; ovarian cancer; mutant;

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2342 AAAGTCTGGGATTACAGG 2360
DB  1 AAAGTCTGGGATTACAGG 19

RESULT 1949
AAT84754
ID  AAT84754 standard; DNA; 19 BP.
XX
AC  AAT84754;
XX
DT  04-NOV-1997 (first entry)
XX
DE  FISH primer for human progesterone receptor intron G.
XX
KW  Breast; ovarian; cancer; diagnosis; risk; predisposition; human;
KW  detection; point mutation; progesterone; receptor; FISH; primer;

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2342 AAAGTCTGGGATTACAGG 2360
DB  1 AAAGTCTGGGATTACAGG 19

RESULT 1950
AAH38677
ID  AAH38677 standard; DNA; 19 BP.

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XX AAH38677;
AC
XX 14-AUG-2001 (first entry)
DT
XX SNP specific upper PCR primer SEQ ID 1473.
DE
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agamaglobulinaemia; diabetes insipidus; cancer;

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2346 TGCTGGGATTACAGCATG 2364
DB 1 TGCTGGGATTACAGCATG 19

RESULT 1951
AAH38221
ID AAH38221 standard; DNA; 19 BP.
XX
XX AAH38221;
AC
XX 14-AUG-2001 (first entry)
DT
XX SNP specific upper PCR primer SEQ ID 1017.
DE
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agamaglobulinaemia; diabetes insipidus; cancer;

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2346 TGCTGGGATTACAGCATG 2364
DB 1 TGCTGGGATTACAGCATG 19

RESULT 1952
ABL44474/c
ID ABL44474 standard; DNA; 19 BP.
XX
XX ABL44474;
AC
XX 11-APR-2002 (first entry)
DT
XX Human chromosome 1p36-35 PCR primer SEQ ID NO:1518.
DE
XX Human chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW PCR primer; ss.

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2337 CTCCCAAGTGTGGGATT 2355
DB 19 CTCCCAAGTGTGGGATT 1

RESULT 1953
ADK41249/c
ID ADK41249 standard; DNA; 19 BP.
XX
XX ADK41249;
AC
XX 06-MAY-2004 (first entry)
DT
XX Human chromosome 19 DNA primer/probe SEQ ID No 7.
DE
XX

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KW sequence polymorphism analysis; human; chromosome 19q; cancer; RAI; ss;
KW single nucleotide polymorphism; SNP; probe; primer.

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2275 GGTTTCACCGTGTAGCCA 2293
DB 19 GGTTTCACCGTGTAGCCA 1

RESULT 1954
ADK41375/c
ID ADK41375 standard; DNA; 19 BP.
XX
XX ADK41375;
AC
XX 06-MAY-2004 (first entry)
DT
XX Human chromosome 19 RAI il forward primer.
DE
XX sequence polymorphism analysis; human; chromosome 19q; cancer; RAI; ss;
KW single nucleotide polymorphism; SNP; primer.

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2275 GGTTTCACCGTGTAGCCA 2293
DB 19 GGTTTCACCGTGTAGCCA 1

RESULT 1955
ADO23055
ID ADO23055 standard; cDNA; 19 BP.
XX
XX ADO23055;
AC
XX 01-JUL-2004 (first entry)
DT
XX Human p53-binding protein, mdm2, SDO target region #6.
DE
XX Human; ss; SDO; short double stranded oligonucleotide; cleavage site;
KW viral infection; malignant tumour; genetic disease; metabolic disease;

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1555 AAAGGGAAGAAACCAAGA 1573
DB 1 AAAGGGAAGAAACCAAGA 19

RESULT 1956
ADO23052
ID ADO23052 standard; cDNA; 19 BP.
XX
XX ADO23052;
AC
XX 01-JUL-2004 (first entry)
DT
XX Human p53-binding protein, mdm2, SDO target region #3.
DE
XX Human; ss; SDO; short double stranded oligonucleotide; cleavage site;
KW viral infection; malignant tumour; genetic disease; metabolic disease;

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1695 TTTACATGTGCAAGAAGC 1713
Db 1 TTTACATGTGCAAGAAGC 19

RESULT 1957
ADO23051
ID ADO23051 standard; cDNA; 19 BP.
XX
AC
XX ADO23051;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human p53-binding protein, mdm2, SDO target region #2.
XX
KW Human; ss; SDO; short double stranded oligonucleotide; cleavage site;
KW viral infection; malignant tumour; genetic disease; metabolic disease;

Query Match 0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1765 TTGTGCTAACTATTTCCT 1783
Db 1 TTGTGCTAACTATTTCCT 19

RESULT 1958
ADO23053
ID ADO23053 standard; cDNA; 19 BP.
XX
AC
XX ADO23053;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human p53-binding protein, mdm2, SDO target region #4.
XX
KW Human; ss; SDO; short double stranded oligonucleotide; cleavage site;
KW viral infection; malignant tumour; genetic disease; metabolic disease;

Query Match 0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 CCAACATGCTGTACCTAC 340
Db 1 CCAACATGCTGTACCTAC 19

RESULT 1959
ADO22917
ID ADO22917 standard; cDNA; 19 BP.
XX
AC
XX ADO22917;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human p53-binding protein, mdm2, SDO target region #1.
XX
KW Human; ss; SDO; short double stranded oligonucleotide; cleavage site;
KW viral infection; malignant tumour; genetic disease; metabolic disease;

Query Match 0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 369 CCAGCTTCGGAACAAGAGA 387
Db 1 CCAGCTTCGGAACAAGAGA 19

RESULT 1960
ADO23054
ID ADO23054 standard; cDNA; 19 BP.
XX
AC
XX ADO23054;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human p53-binding protein, mdm2, SDO target region #5.
XX
KW Human; ss; SDO; short double stranded oligonucleotide; cleavage site;
KW viral infection; malignant tumour; genetic disease; metabolic disease;

Query Match 0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1635 CAAGGTCGACCTAAAAATG 1653
Db 1 CAAGGTCGACCTAAAAATG 19

RESULT 1961
ADO80008
ID ADO80008 standard; DNA; 19 BP.
XX
AC
XX ADO80008;
XX
DT 26-AUG-2004 (first entry)
XX
DE CENPC1 extend primer #59.
XX
KW Cytostatic; Gene therapy; breast cancer; human; DLG1; KIAA0783; DPF3;
KW CENPC1; SNP; single nucleotide polymorphism; centromere protein C1;

Query Match 0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2342 AAAGTCTGGGATTACAGG 2360
Db 1 AAAGTCTGGGATTACAGG 19

RESULT 1962
ADO61537
ID ADO61537 standard; RNA; 19 BP.
XX
AC
XX ADO61537;
XX
DT 09-SEP-2004 (first entry)
XX
DE Anti-MDM2 siRNA related DNA sequence SEQ ID NO:1239.
XX
KW ss; siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;
KW RNA interference.

Query Match 0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1128 GATGAGGTATATCAAGTTA 1146
Db 1 GATGAGGTATATCAAGTTA 19

RESULT 1963
ADO61535
ID ADO61535 standard; RNA; 19 BP.
XX
AC
XX ADO61535;
XX
DT 09-SEP-2004 (first entry)
XX
DE Anti-MDM2 siRNA related DNA sequence SEQ ID NO:1237.
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XX
KW ss; siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;
KW RNA interference.

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 920 GGAGATATGTTGTGAAGA 938
Db 1 GGAGATATGTTGTGAAGA 19

RESULT 1964
ADQ61536
ID ADQ61536 standard; RNA; 19 BP.
XX
AC ADQ61536;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human MDM2 mRNA fragment complementary oligo primer 6.
XX
DE Pseudo-cyclic oligonucleotide; PCO; gene expression; protein kinase A;
KW nucleic acid detection; ribozyme inhibition; gene transcription; MDM2;

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 860 CCACAATCTGATAGTATT 878
Db 1 CCACAATCTGATAGTATT 19

RESULT 1965
ADQ61538
ID ADQ61538 standard; RNA; 19 BP.
XX
AC ADQ61538;
XX
DT 09-SEP-2004 (first entry)
XX
DE Anti-MDM2 siRNA related DNA sequence SEQ ID NO:1240.
KW ss; siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;
KW RNA interference.

Query Match      0.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1559 GGAGAAACCCCAAGACAAA 1577
Db 1 GGAGAAACCCCAAGACAAA 19

RESULT 1966
ABS59253/c
ID ABS59253 standard; DNA; 20 BP.
XX
AC ABS59253;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human CAS gene antisense oligonucleotide, ISIS 138206.
XX
DE Human; ss; antisense; cellular apoptosis susceptibility gene;
KW antinflammatory; antitumour; cytostatic; CAS; CSE1; CSP;

Query Match      0.8%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 676 TGAGTGAGAACAGGTGTCAC 695
Db 20 TGNGTGAGAACAGGTGTCAC 1

RESULT 1970
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QY 2335 GCCTCCCAAGTCTCTGGGA 2353
Db 19 GCCTCCCAAGTCTCTGGGA 1

RESULT 1967
ABL60514/c
ID ABL60514 standard; DNA; 20 BP.
XX
AC ABL60514;
XX
DT 12-AUG-2002 (first entry)
XX
DE Human MDM2 mRNA fragment complementary oligo primer 6.
XX
DE Pseudo-cyclic oligonucleotide; PCO; gene expression; protein kinase A;
KW nucleic acid detection; ribozyme inhibition; gene transcription; MDM2;

Query Match      0.8%; Score 19; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 672 TCTGTGAGTGAGAACAGGTG 691
Db 20 TCTGTGAGTGAGAACAGGTG 1

RESULT 1968
ABL60513/c
ID ABL60513 standard; DNA; 20 BP.
XX
AC ABL60513;
XX
DT 12-AUG-2002 (first entry)
XX
DE Human MDM2 mRNA fragment complementary oligo primer 5.
KW Pseudo-cyclic oligonucleotide; PCO; gene expression; protein kinase A;
KW nucleic acid detection; ribozyme inhibition; gene transcription; MDM2;

Query Match      0.8%; Score 19; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 674 TGTGAGTGAGAACAGGTGTC 693
Db 20 TGTGAGTGAGAACAGGTGTC 1

RESULT 1969
ABL60512/c
ID ABL60512 standard; DNA; 20 BP.
XX
AC ABL60512;
XX
DT 12-AUG-2002 (first entry)
XX
DE Human MDM2 mRNA fragment complementary oligo primer 4.
XX
DE Pseudo-cyclic oligonucleotide; PCO; gene expression; protein kinase A;
KW nucleic acid detection; ribozyme inhibition; gene transcription; MDM2;

Query Match      0.8%; Score 19; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 676 TGAGTGAGAACAGGTGTCAC 695
Db 20 TGNGTGAGAACAGGTGTCAC 1

RESULT 1970
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ABL60511/c
ID  ABL60511 standard; DNA; 20 BP.
XX
AC  ABL60511;
XX
DT  12-AUG-2002 (first entry)
XX
DE  Human MDM2 mRNA fragment complementary oligo primer 3.
XX
KW  Pseudo-cyclic oligonucleotide; PCO; gene expression; protein kinase A;
KW  nucleic acid detection; ribozyme inhibition; gene transcription; MDM2;

Query Match      0.8%; Score 19; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  677 GAGTGAGACAGGTCAC 696
DB  20 GNGTGAGACAGGTCAC 1

RESULT 1971
ADD2177/c
ID  ADD2177 standard; DNA; 20 BP.
XX
AC  ADD2177;
XX
DT  15-JAN-2004 (first entry)
XX
DE  Mouse mdm2 antisense oligonucleotide #18.
XX
KW  antisense oligonucleotide; mouse; mdm2; hyperproliferation;
KW  hyperproliferative disorder; cancer; psoriasis; fibrosis;

Query Match      0.8%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1018 TGGATCAGGATTCAGTTTC 1036
DB  20 TGGATCAGGATTCAGTTTC 2

RESULT 1972
ADF47745/c
ID  ADF47745 standard; DNA; 20 BP.
XX
AC  ADF47745;
XX
DT  26-FEB-2004 (first entry)
XX
DE  Human 5-HT7 receptor gene promoter related PCR primer.
XX
KW  human; 5-HT7 receptor promoter; barbiturate-inducible element;
KW  serotonin mediated response; gastrointestinal; neuroleptic;

Query Match      0.8%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2352 GATTACAGGCATGACCCAC 2370
DB  19 GATTACAGGCATGACCCAC 1

RESULT 1973
ADM14508/c
ID  ADM14508 standard; DNA; 20 BP.
XX
AC  ADM14508;
XX
DT  01-JUL-2004 (first entry)
XX

DE  Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:695.
XX
KW  chimeric; antisense oligonucleotide; phosphorothioate; human;
KW  microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;

Query Match      0.8%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2336 CCTCCCAAGTCTGGGAT 2354
DB  20 CCTCCCAAGTCTGGGAT 2

RESULT 1974
ADM15268/c
ID  ADM15268 standard; DNA; 20 BP.
XX
AC  ADM15268;
XX
DT  01-JUL-2004 (first entry)
XX
DE  Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:1455.
XX
KW  chimeric; antisense oligonucleotide; phosphorothioate; human;
KW  microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;

Query Match      0.8%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2330 CCTCGGCTCCCAAGTGC 2348
DB  19 CCTCGGCTCCCAAGTGC 1

RESULT 1975
AAH38422/c
ID  AAH38422 standard; DNA; 22 BP.
XX
AC  AAH38422;
XX
DT  14-AUG-2001 (first entry)
XX
DE  SNP specific lower PCR primer SEQ ID 1218.
XX
KW  Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW  SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

Query Match      0.8%; Score 19; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY  2234 CACCACCTGGCTAATTTT 2254
DB  22 CACCACCTGGCTAGTTTTT 2

RESULT 1976
ADO47348
ID  ADO47348 standard; DNA; 23 BP.
XX
AC  ADO47348;
XX
DT  15-JUL-2004 (first entry)
XX
DE  Human SORBS1 gene sequencing primer #54.
XX
KW  Single nucleotide polymorphism; SNP; human;
KW  sorbin and SH3-domain-containing-1 gene; SORBS1; sequence determination;

Query Match      0.8%; Score 19; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2e+03;

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2353 ATTACAGGCATGAGCCACC 2371
 Db 1 ATTACAGGCATGAGCCACC 19

RESULT 1977
 AAI66603/c
 ID AAI66603 standard; DNA; 24 BP.
 XX
 AC AAI66603;
 DT 07-JAN-2002 (first entry)
 DE Human ubiquitin-like protein 13 cDNA specific RT-PCR primer 2.
 XX
 KW Ubiquitin-like protein 13; cytostatic; virucidal; immunomodulatory;
 KW antinflammatory; cancer; hemopathy; HIV infection; RT-PCR; primer; ss.

Query Match 0.8%; Score 19; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2100 GAGACCGAGTCTTGCTCG 2118
 Db 23 GAGACCGAGTCTTGCTCG 5

RESULT 1978
 AAF24672/c
 ID - AAF24672 standard; DNA; 25 BP.
 XX
 AC AAF24672;
 DT 20-APR-2001 (first entry)
 DE PCR primer for exon 15 of the human HMG-CoA reductase gene.
 XX
 KW 3-hydroxy-3-methylglutaryl-coenzyme A reductase gene; dyslipidemia;
 KW HMG-CoA reductase gene; genetic marker; cardiovascular disease;

Query Match 0.8%; Score 19; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2143 TGATCTTGGCTCACTGCAA 2161
 Db 22 TGATCTTGGCTCACTGCAA 4

RESULT 1979
 ADB04760
 ID ADB04760 standard; DNA; 25 BP.
 XX
 AC ADB04760;
 DT 20-NOV-2003 (first entry)
 DE Human MD27 scanning oligonucleotide SEQ ID 5746.
 XX
 KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

Query Match 0.8%; Score 19; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTACCGTGTAGCC 2292
 Db 7 GGGTTTACCGTGTAGCC 25

RESULT 1980
 AAQ82257/c
 ID AAQ82257 standard; DNA; 22 BP.
 XX
 AC AAQ82257;
 DT 25-MAR-2003 (revised)
 DT 07-SEP-1995 (first entry)
 XX
 DE Chromosome 11 (locus D11S115) STS primer CSRL-4b6-tA.
 XX
 KW sequence sampled mapping; genomic analysis; complex genome mapping;

Query Match 0.8%; Score 18.8; DB 1; Length 22;
 Best Local Similarity 90.9%; Pred. No. 2e+03;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2094 TTTTGTGAGACCGAGTCTTGCT 2115
 Db 22 TTTTGTGAGACCGAGTCTTGCT 1

RESULT 1981
 AAT71928/c
 ID AAT71928 standard; DNA; 22 BP.
 XX
 AC AAT71928;
 DT 18-AUG-1997 (first entry)
 DE Primer detects marker 4072-2 in HH region of chromosome 6p2.1.
 XX
 KW Primer; polymerase chain reaction; amplify; hereditary haemochromatosis;
 KW HH; mutation; HH-associated allele; base-pair polymorphism; HHP-1;

Query Match 0.8%; Score 18.8; DB 1; Length 22;
 Best Local Similarity 90.9%; Pred. No. 2e+03;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2113 GCTCTGTATCCAGGCTGGAGT 2134
 Db 22 GCTCTGTATCCAGGCTGGAGT 1

RESULT 1982
 AAT71925/c
 ID AAT71925 standard; DNA; 22 BP.
 XX
 AC AAT71925;
 DT 18-AUG-1997 (first entry)
 DE Primer detects marker 3216-1 in HH region of chromosome 6p2.1.
 XX
 KW Primer; polymerase chain reaction; amplify; hereditary haemochromatosis;
 KW HH; mutation; HH-associated allele; base-pair polymorphism; HHP-1;

Query Match 0.8%; Score 18.8; DB 1; Length 22;
 Best Local Similarity 90.9%; Pred. No. 2e+03;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2113 GCTCTGTATCCAGGCTGGAGT 2134
 Db 22 GCTCTGTATCCAGGCTGGAGT 1

RESULT 1983
 AAT72000/c
 ID AAT72000 standard; DNA; 22 BP.
 XX
 AC AAT72000;
 DT 18-AUG-1997 (first entry)

XX Primer detects marker 4072-2 in HH region of chromosome 6p2.1.
 XX
 KW Primer; polymerase chain reaction; amplify; hereditary haemochromatosis;
 KW HH; mutation; HH-associated allele; base-pair polymorphism; HHP-1;
 KW
 Query Match 0.8%; Score 18.8; DB 1; Length 22;
 Best Local Similarity 90.9%; Pred. No. 2e+03;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2113 GCTCTGTTACCCAGGCTGGAGT 2134
 DB 22 GCTCTATTGCCAGGCTGGAGT 1

RESULT 1984
 AAT71997/c
 ID AAT71997 standard; DNA; 22 BP.
 XX
 AC AAT71997;
 XX
 DT 18-AUG-1997 (first entry)
 XX
 DE Primer detects marker 3216-1 in HH region of chromosome 6p2.1.
 XX
 KW Primer; polymerase chain reaction; amplify; hereditary haemochromatosis;
 KW HH; mutation; HH-associated allele; base-pair polymorphism; HHP-1;
 KW
 Query Match 0.8%; Score 18.8; DB 1; Length 22;
 Best Local Similarity 90.9%; Pred. No. 2e+03;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2113 GCTCTGTTACCCAGGCTGGAGT 2134
 DB 22 GCTCTATTGCCAGGCTGGAGT 1

RESULT 1985
 AAZ32938
 ID AAZ32938 standard; DNA; 22 BP.
 XX
 AC AAZ32938;
 XX
 DT 09-FEB-2000 (first entry)
 XX
 DE Sequence tagged site (STS) 66111.T7 probe forward PCR primer.
 XX
 KW MKK4; mitogen activated protein kinase; MAPK; MAPK pathway; mutation;
 KW somatic; signal transduction; apoptosis; stress; cytokine; induction;
 KW
 Query Match 0.8%; Score 18.8; DB 1; Length 22;
 Best Local Similarity 90.9%; Pred. No. 2e+03;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2261 TTTAGTAGACAGGTTTCAC 2282
 DB 1 TTTAGTAGACAGGTTTCAC 22

RESULT 1986
 AAH38401/c
 ID AAH38401 standard; DNA; 22 BP.
 XX
 AC AAH38401;
 XX
 DT 14-AUG-2001 (first entry)
 XX
 DE SNP specific upper PCR primer SEQ ID 1197.
 XX
 KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
 KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
 KW
 Query Match 0.8%; Score 18.8; DB 1; Length 22;

Best Local Similarity 90.9%; Pred. No. 2e+03;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2301 CTCGATCTCTGACCTCGTGAT 2322
 DB 22 CTCAAACTCTGACCTCGTGAT 1

RESULT 1987
 AAF62067
 ID AAF62067 standard; DNA; 22 BP.
 XX
 AC AAF62067;
 XX
 DT 04-MAY-2001 (first entry)
 XX
 DE Reverse PCR primer IL10SR for IL-10 promoter amplification.
 XX
 KW Human; immunoreponse; interleukin 10; IL-10; genotype; cancer;
 KW systemic lupus erythematosus; systemic vasculitis; Fely's syndrome;
 KW
 Query Match 0.8%; Score 18.8; DB 1; Length 22;
 Best Local Similarity 90.9%; Pred. No. 2e+03;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2097 TTTGAGACCGAGTCTTGCTCTG 2118
 DB 1 TTTGAGACAGAGTCTGCTCTG 22

RESULT 1988
 AAL46346
 ID AAL46346 standard; DNA; 22 BP.
 XX
 AC AAL46346;
 XX
 DT 19-JUL-2002 (first entry)
 XX
 DE Human M30 protein coding sequence PCR primer hm30_nn_a5.
 XX
 KW Neurodegenerative disease; M30; M31; M32; M33; stroke;
 KW fragile X syndrome; Huntington's disease; Parkinson's disease;
 KW
 Query Match 0.8%; Score 18.8; DB 1; Length 22;
 Best Local Similarity 90.9%; Pred. No. 2e+03;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2101 AGACCGAGTCTTGCTCTGTAC 2122
 DB 1 AGACAGAGTCTTGCTCTGTTC 22

RESULT 1989
 ACA88980/c
 ID ACA88980 standard; DNA; 22 BP.
 XX
 AC ACA88980;
 XX
 DT 08-JUL-2003 (first entry)
 XX
 DE Selection and amplification of genetic markers PCR related primer #91.
 XX
 KW Genetic marker selection; multiplex PCR amplification;
 KW prenatal diagnostic testing; foetal sex determination;
 KW
 Query Match 0.8%; Score 18.8; DB 1; Length 22;
 Best Local Similarity 90.9%; Pred. No. 2e+03;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2096 TTTTGAGACCGAGTCTTGCTCT 2117
 DB 22 TGTTGAGACAGAGTCTTGCTCT 1

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RESULT 1990
AAH77082
ID AAH77082 standard; DNA; 24 BP.
XX
XX
AC AAH77082;
XX
XX
DT 15-DEC-2001 (first entry)
DE
DE Human vesicular transport-associated protein 9 RT-PCR primer, SEQ ID:4.
XX
XX
KW Human; vesicular transport-associated protein 9; recombinant production;
KW malignant tumour; cancer; blood disease; HIV infection;

Query Match 0.8%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred. No. 2.1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2106 GAGTCTTGCTCTGTACCCAGG 2127
Db 3 GAGTCTTGCTCTGTACCCAGG 24

RESULT 1991
AAH91382/c
ID AAH91382 standard; DNA; 24 BP.
XX
XX
AC AAH91382;
XX
XX
DT 09-OCT-2001 (first entry)
DE
DE Human inflammatory bowel disease associated polymorphic site #457.
XX
XX
KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;

Query Match 0.8%; Score 18.8; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 2.1e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2274 GGGTTTACCGTGTAGCCAGG 2296
Db 23 GGGTTTACCGTGTAGCCAGG 1

RESULT 1992
ABK49351
ID ABK49351 standard; DNA; 24 BP.
XX
XX
AC ABK49351;
XX
XX
DT 15-JUL-2002 (first entry)
DE
DE RNA polymerase II associated protein 9.57 cDNA RT-PCR primer #2.
XX
XX
KW RNA polymerase II associated protein 9.57; ss; haemopathy; cancer;
KW human immunodeficiency virus; HIV; reverse transcriptase; RT-PCR; primer.

Query Match 0.8%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred. No. 2.1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2107 AGTCTTGCTCTGTACCCAGG 2128
Db 3 AGTCTTGCTCTGTACCCAGG 24

RESULT 1993
ABA04737
ID ABA04737 standard; DNA; 24 BP.
XX
XX
AC ABA04737;
XX
XX

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DT 22-FEB-2002 (first entry)
XX
XX Human alkylation DNA protein cysteine methyltransferase 11 PCR primer #2.
DE
XX
KW Human; alkylation DNA protein cysteine methyltransferase 11; cytostatic;
KW haemostatic; virucide; immunomodulatory; antiinflammatory; gene therapy;

Query Match 0.8%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred. No. 2.1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2250 TTTTGTACTTTTAGTAGAGA 2271
Db 3 TTTTGTACTTTTAGTAGAGA 24

RESULT 1994
ABZ21179
ID ABZ21179 standard; DNA; 24 BP.
XX
XX
AC ABZ21179;
XX
XX
DT 25-MAR-2003 (first entry)
DE
DE Human transformer-2-beta protein 21.89 PCR primer #2.
XX
XX
KW Human; transformer-2-beta protein 21.89; tumour; haemopathy; PCR;
KW HIV infection; immunological disease; inflammation; cytostatic; anti-HIV;

Query Match 0.8%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred. No. 2.1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2107 AGTCTTGCTCTGTACCCAGG 2128
Db 3 AGTCTTGCTCTGTACCCAGG 24

RESULT 1995
ABZ79587
ID ABZ79587 standard; DNA; 24 BP.
XX
XX
AC ABZ79587;
XX
XX
DT 27-JUN-2003 (first entry)
DE
DE Hydrogenase 9.46 related PCR primer #SEQ ID 4.
XX
XX
KW Hydrogenase; 9.46; enzyme; hypertension; peptic ulcer; bronchial asthma;
KW nephrotic syndrome; Parkinson's disease; PCR; primer; ss.

Query Match 0.8%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred. No. 2.1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2267 AGACACAGGGTTTCCCGTGT 2288
Db 1 AGACACAGGGTTTCCCATGTT 22

RESULT 1996
AAL55813/c
ID AAL55813 standard; DNA; 24 BP.
XX
XX
AC AAL55813;
XX
XX
DT 25-SEP-2003 (first entry)
DE
DE RT-PCR primer 1 to isolate cDNA encoding human fasciclin protein 9_46.
XX
XX
KW Human; fasciclin and elongation protein; 9.46; nervous system; agonist;
KW developmental malformation; primer; RT-PCR; PCR; ss.

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Query Match 0.8%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred. No. 2.1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2351 GGATTACAGGCATGAGCCACCG 2372
||||| ||||||| ||||||| |||||||
Db 24 GGATAACAGGCATGAGCCACTG 3

RESULT 1997
ADC56863/c
ID ADC56863 standard; DNA; 24 BP.
XX
AC ADC56863;
XX
DT 18-DEC-2003 (first entry)
XX
DE RT-PCR primer Seq ID3 related to human protein 8-91.
XX
KW human; protein 8-91; diabetes; cancer; PCR; primer; RT-PCR;
KW reverse transcription PCR; ss.

Query Match 0.8%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred. No. 2.1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2351 GGATTACAGGCATGAGCCACCG 2372
||||| ||||||| ||||||| |||||||
Db 24 GGATTACAGGCATGAGCCACTG 3

RESULT 1998
AAC96023
ID AAC96023 standard; DNA; 25 BP.
XX
AC AAC96023;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA HLA-C gene PCR primer #35.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;

Query Match 0.8%; Score 18.8; DB 1; Length 25;
Best Local Similarity 90.9%; Pred. No. 2.1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2046 TTTTCTTCTTAATATGTAT 2067
||||| ||||||| ||||||| |||||||
Db 1 TTTTCTTCTTGAATATGTAT 22

RESULT 1999
AAI65600
ID AAI65600 standard; DNA; 25 BP.
XX
AC AAI65600;
XX
DT 03-JAN-2002 (first entry)
XX
DE Primer for microsatellite marker DI6S299, used to localise IBD1.
XX
KW Human; inflammatory bowel disease 1 protein; IBD1; IBDiprox;
KW intestinal inflammatory disease; apoptosis; NF-kappa B; cancer;

Query Match 0.8%; Score 18.8; DB 1; Length 25;
Best Local Similarity 90.9%; Pred. No. 2.1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2341 CAAAGTGTGGATTACAGCA 2362
||||| ||||||| ||||||| |||||||
Db 2 CCAACTGTGGATTACAGCA 23

RESULT 2000
ADB04582
ID ADB04582 standard; DNA; 25 BP.
XX
AC ADB04582;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5568.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
Query Match 0.8%; Score 18.8; DB 1; Length 25;
Best Local Similarity 90.9%; Pred. No. 2.1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2090 TATTTTTTTTGAGACCGAGTCT 2111
||||| ||||||| ||||||| |||||||
Db 1 TTTTCTTCTTGAATATGTAT 22

Search completed: January 25, 2005, 16:22:12
Job time : 113 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 25, 2005, 16:02:10 ; Search time 44 Seconds
(without alignments)

3.729 Million cell updates/sec

Title: US-09-966-724B-2-COPY

Perfect score: 2372

Sequence: 1 GCACCGCGGAGCTTGCTG.....ATTACAGCATGAGCCACCG 2372

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 1271 seqs, 34589 residues

Total number of hits satisfying chosen parameters: 2542

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1104 summaries

Database : rge.db.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86.4	3.6	100	1	AX901508
2	86.4	3.6	100	1	AX902820
3	86.4	3.6	100	1	BD037041
4	86.4	3.6	100	1	BD038353
5	85	3.6	94	1	AR421510
6	85	3.6	94	1	AX982204
7	85	3.6	94	1	BD17063
8	81.2	3.4	94	1	AX912163
9	81.2	3.4	94	1	BD047696
10	80.6	3.4	92	1	AX197468
11	80.6	3.4	94	1	AX197476
12	80.6	3.4	94	1	AX197483
13	80.6	3.4	95	1	AX916923
14	80.6	3.4	95	1	BD052456
15	80.2	3.4	89	1	AY003889
16	80.2	3.4	89	1	AY003892
17	80	3.4	100	1	AX899255
18	80	3.4	100	1	BD034788
19	79	3.3	94	1	AX197487
20	78.4	3.3	90	1	AX911782
21	78.4	3.3	90	1	BD047315
22	78	3.3	86	1	AX903206
23	78	3.3	86	1	BD038739
24	74.2	3.1	92	1	AX197472
25	73	3.1	73	1	BD074010
26	72.8	3.1	76	1	AX901901
27	72.8	3.1	76	1	BD037434
28	71.4	3.0	84	1	AX900729
29	71.4	3.0	84	1	BD036262
30	71	3.0	79	1	AX912245
31	71	3.0	79	1	BD047778
32	70.8	3.0	84	1	AX97063
33	70.2	3.0	92	1	AX899552

34	70.2	3.0	92	1	BD035085
35	66.6	2.8	85	1	AX421270
36	66.6	2.8	85	1	AX981964
37	66.6	2.8	85	1	BD116823
38	65.4	2.8	84	1	AR051521
39	65.4	2.8	84	1	AR072661
40	65.4	2.8	84	1	AR073206
41	62.2	2.6	81	1	AX900153
42	62.2	2.6	81	1	BD035686
43	60	2.5	60	1	CQ542955
44	60	2.5	68	1	AX523103
45	58.4	2.5	68	1	AX523168
46	56.8	2.4	68	1	AX522779
47	56.2	2.4	69	1	AX260697
48	54.4	2.3	65	1	AX901137
49	54.4	2.3	65	1	BD036670
50	52	2.2	60	1	AX523219
51	52	2.2	68	1	AR416502
52	52	2.2	68	1	AX977196
53	52	2.2	68	1	BD112055
54	51.6	2.2	66	1	AF087511
55	51	2.2	68	1	AX899244
56	51	2.2	68	1	BD034777
57	50.2	2.1	64	1	AX903935
58	50.2	2.1	64	1	BD039468
59	50	2.1	63	1	AX322319
60	49.4	2.1	51	1	CQ006684
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62	48	2.0	64	1	HUMUT5223A
63	47.8	2.0	51	1	AX161490
64	47.8	2.0	51	1	AX163313
65	47.8	2.0	51	1	AX163451
66	47.8	2.0	51	1	AX199317
67	47.2	2.0	52	1	AX522922
68	46.8	2.0	51	1	AR444761
69	46.8	2.0	59	1	AX396956
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77	46.2	1.9	51	1	AX164957
78	46.2	1.9	51	1	AX199318
79	45.8	1.9	51	1	AX116665
80	45.8	1.9	57	1	AX917839
81	45.8	1.9	57	1	BD053372
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83	45.2	1.9	51	1	AX160937
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94	43	1.8	51	1	AX163302
95	43	1.8	51	1	AX163480
96	43	1.8	51	1	AX189877
97	43	1.8	51	1	AX199154
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99	43	1.8	51	1	AX199357
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103	42.2	1.8	51	1	AX163126
104	42	1.8	51	1	AX156682
105	42	1.8	51	1	AX159128
106	42	1.8	51	1	AX163383

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C 158	39.8	1.7	51	1	AX161023	ACCESSION:AX161023
C 159	39.8	1.7	51	1	AX164908	ACCESSION:AX164908
C 160	39.8	1.7	51	1	AX190287	ACCESSION:AX190287
C 161	39.8	1.7	51	1	AX191556	ACCESSION:AX191556
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C 172	39.2	1.7	51	1	AX161914	ACCESSION:AX161914
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C 191	37.4	1.6	41	1	AX514746	ACCESSION:AX514746
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C 197	35.2	1.5	41	1	HUMALUANCA	ACCESSION:L36835
C 198	35.2	1.5	44	1	AX160004	ACCESSION:AX160004
C 199	35	1.5	43	1	HSLAS33	ACCESSION:X91548
C 200	34.8	1.5	41	1	AX516778	ACCESSION:AX516778
C 201	34.8	1.5	41	1	AX518941	ACCESSION:AX518941
C 202	34.2	1.4	35	1	A22672	ACCESSION:A22672
C 203	34.2	1.4	35	1	I21796	ACCESSION:I21796
C 204	34.2	1.4	39	1	AX709023	ACCESSION:AX709023
C 205	34.2	1.4	41	1	AX541485	ACCESSION:AX541485
C 206	34.2	1.4	41	1	AX520216	ACCESSION:AX520216
C 207	34	1.4	42	1	AX709009	ACCESSION:AX709009
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C 209	33.6	1.4	41	1	AX516379	ACCESSION:AX516379
C 210	33.6	1.4	44	1	AX160003	ACCESSION:AX160003
C 211	33.4	1.4	35	1	A25212	ACCESSION:A25212
C 212	33.4	1.4	35	1	E09140	ACCESSION:E09140
C 213	32.6	1.4	40	1	AX183780	ACCESSION:AX183780
C 214	32.6	1.4	41	1	AX514703	ACCESSION:AX514703
C 215	32.6	1.4	41	1	AX520711	ACCESSION:AX520711
C 216	32	1.3	41	1	AX327080	ACCESSION:AX327080
C 217	31.6	1.3	41	1	AX514160	ACCESSION:AX514160
C 218	31.6	1.3	40	1	AX520311	ACCESSION:AX520311
C 219	31	1.3	40	1	AX519117	ACCESSION:AX519117
C 220	31	1.3	41	1	AX513835	ACCESSION:AX513835
C 221	31	1.3	41	1	AX517711	ACCESSION:AX517711
C 222	31	1.3	41	1	AX519988	ACCESSION:AX519988
C 223	31	1.3	41	1	AX520856	ACCESSION:AX520856
C 224	29.8	1.3	33	1	AX709012	ACCESSION:AX709012
C 225	29	1.2	29	1	AX208404	ACCESSION:AX208404
C 226	28.4	1.2	30	1	BD169435	ACCESSION:BD169435
C 227	28.4	1.2	30	1	BD169436	ACCESSION:BD169436
C 228	28	1.2	28	1	AR089907	ACCESSION:AR089907
C 229	28	1.2	28	1	AR089908	ACCESSION:AR089908
C 230	28	1.2	28	1	AR196942	ACCESSION:AR196942
C 231	28	1.2	28	1	AR196943	ACCESSION:AR196943
C 232	28	1.2	28	1	AR208400	ACCESSION:AR208400
C 233	28	1.2	28	1	AR259096	ACCESSION:AR259096
C 234	28	1.2	28	1	AR259097	ACCESSION:AR259097
C 235	27.6	1.2	35	1	AX184110	ACCESSION:AX184110
C 236	27.4	1.2	32	1	A25214	ACCESSION:A25214
C 237	27.4	1.2	32	1	E09142	ACCESSION:E09142
C 238	26	1.1	26	1	AR208402	ACCESSION:AR208402
C 239	26	1.1	26	1	BD138344	ACCESSION:BD138344
C 240	25.8	1.1	30	1	AR214391	ACCESSION:AR214391
C 241	25.4	1.1	32	1	A72114	ACCESSION:A72114
C 242	25.4	1.1	32	1	BD003106	ACCESSION:BD003106
C 243	25	1.1	25	1	AR228262	ACCESSION:AR228262
C 244	25	1.1	25	1	AX116120	ACCESSION:AX116120
C 245	25	1.1	25	1	AX693020	ACCESSION:AX693020
C 246	25	1.1	25	1	AX693021	ACCESSION:AX693021
C 247	25	1.1	25	1	AX693022	ACCESSION:AX693022
C 248	25	1.1	25	1	AX693023	ACCESSION:AX693023
C 249	25	1.1	25	1	AX693024	ACCESSION:AX693024
C 250	25	1.1	25	1	AX693025	ACCESSION:AX693025
C 251	25	1.1	25	1	AX693026	ACCESSION:AX693026
C 252	25	1.1	25	1	AX693027	ACCESSION:AX693027

253	25	1.1	25	1	AX693028	ACCESSION:AX693028	326	21	0.9	21	1	AX800306	ACCESSION:AX800306
254	25	1.1	25	1	AX693029	ACCESSION:AX693029	327	21	0.9	21	1	BD073983	ACCESSION:BD073983
255	25	1.1	25	1	AX693030	ACCESSION:AX693030	328	21	0.9	21	1	BD074005	ACCESSION:BD074005
256	25	1.1	25	1	AX693031	ACCESSION:AX693031	329	21	0.9	21	1	BD138343	ACCESSION:BD138343
257	25	1.1	25	1	AX693032	ACCESSION:AX693032	330	21	0.9	22	1	AX092787	ACCESSION:AX092787
258	25	1.1	25	1	AX693033	ACCESSION:AX693033	331	21	0.9	25	1	AX693016	ACCESSION:AX693016
259	25	1.1	25	1	AX693034	ACCESSION:AX693034	332	20.8	0.9	24	1	CQ828992	ACCESSION:CQ828992
260	25	1.1	25	1	AX693035	ACCESSION:AX693035	333	20.8	0.9	24	1	AX092602	ACCESSION:AX092602
261	25	1.1	25	1	AX693036	ACCESSION:AX693036	334	20.8	0.9	24	1	AX092650	ACCESSION:AX092650
262	25	1.1	25	1	BD138345	ACCESSION:BD138345	335	20.8	0.9	24	1	AX662968	ACCESSION:AX662968
263	24.6	1.0	31	1	AX117259	ACCESSION:AX117259	336	20.8	0.9	24	1	AX797527	ACCESSION:AX797527
264	24.6	1.0	32	1	AX184256	ACCESSION:AX184256	337	20.8	0.9	24	1	AX817219	ACCESSION:AX817219
265	24.4	1.0	27	1	AX117744	ACCESSION:AX117744	338	20.8	0.9	25	1	AX115904	ACCESSION:AX115904
266	24.2	1.0	29	1	AR392160	ACCESSION:AR392160	339	20.8	0.9	25	1	AX116344	ACCESSION:AX116344
267	24.2	1.0	30	1	AR214384	ACCESSION:AR214384	340	20.8	0.9	25	1	AX692917	ACCESSION:AX692917
268	24.2	1.0	30	1	AX184136	ACCESSION:AX184136	341	20.8	0.9	25	1	AX692918	ACCESSION:AX692918
269	24	1.0	30	1	E40923	ACCESSION:E40923	342	20.8	0.9	25	1	AX692920	ACCESSION:AX692920
270	24	1.0	24	1	E40925	ACCESSION:E40925	343	20.8	0.9	25	1	AX692923	ACCESSION:AX692923
271	24	1.0	25	1	AX693019	ACCESSION:AX693019	344	20.8	0.9	25	1	AX692927	ACCESSION:AX692927
272	24	1.0	25	1	AX693037	ACCESSION:AX693037	345	20.8	0.9	25	1	AX692929	ACCESSION:AX692929
273	24	1.0	27	1	A72116	ACCESSION:A72116	346	20.8	0.9	25	1	AX692990	ACCESSION:AX692990
274	24	1.0	27	1	BD003108	ACCESSION:BD003108	347	20.8	0.9	25	1	AX692994	ACCESSION:AX692994
275	23.6	1.0	30	1	A68624	ACCESSION:A68624	348	20.8	0.9	25	1	AX692996	ACCESSION:AX692996
276	23.4	1.0	25	1	AX118472	ACCESSION:AX118472	349	20.8	0.9	25	1	AX692998	ACCESSION:AX692998
277	23.4	1.0	25	1	AX548255	ACCESSION:AX548255	350	20.8	0.9	27	1	AR381743	ACCESSION:AR381743
278	23.4	1.0	25	1	AX922581	ACCESSION:AX922581	351	20.8	0.9	27	1	AX116940	ACCESSION:AX116940
279	23.4	1.0	27	1	AX118000	ACCESSION:AX118000	352	20.8	0.9	27	1	AX183893	ACCESSION:AX183893
280	23.2	1.0	30	1	AX118407	ACCESSION:AX118407	353	20.6	0.9	21	1	AX095325	ACCESSION:AX095325
281	23	1.0	23	1	CQ766174	ACCESSION:CQ766174	354	20.6	0.9	27	1	AX709011	ACCESSION:AX709011
282	23	1.0	23	1	AR300897	ACCESSION:AR300897	355	20.4	0.9	22	1	E50641	ACCESSION:E50641
283	23	1.0	23	1	AR361046	ACCESSION:AR361046	356	20.4	0.9	22	1	AR242944	ACCESSION:AR242944
284	23	1.0	25	1	AX693018	ACCESSION:AX693018	357	20.4	0.9	22	1	AR242948	ACCESSION:AR242948
285	22.8	1.0	26	1	AR089946	ACCESSION:AR089946	358	20.4	0.9	22	1	AR393715	ACCESSION:AR393715
286	22.8	1.0	26	1	AR196981	ACCESSION:AR196981	359	20.4	0.9	22	1	AX384996	ACCESSION:AX384996
287	22.8	1.0	26	1	AR259135	ACCESSION:AR259135	360	20.4	0.9	22	1	AX385000	ACCESSION:AX385000
288	22.8	1.0	27	1	AX116952	ACCESSION:AX116952	361	20.4	0.9	22	1	AX674898	ACCESSION:AX674898
289	22.8	1.0	27	1	AX118160	ACCESSION:AX118160	362	20.4	0.9	22	1	AX674899	ACCESSION:AX674899
290	22.8	1.0	30	1	AX116662	ACCESSION:AX116662	363	20.2	0.9	25	1	AX115271	ACCESSION:AX115271
291	22.6	1.0	30	1	AR051440	ACCESSION:AR051440	364	20.2	0.9	25	1	AX115532	ACCESSION:AX115532
292	22.6	1.0	30	1	AR072580	ACCESSION:AR072580	365	20.2	0.9	25	1	AX116096	ACCESSION:AX116096
293	22.6	1.0	30	1	AR073125	ACCESSION:AR073125	366	20.2	0.9	25	1	AX116664	ACCESSION:AX116664
294	22.4	0.9	24	1	AX092647	ACCESSION:AX092647	367	20.2	0.9	25	1	AX117740	ACCESSION:AX117740
295	22.4	0.9	25	1	AR322085	ACCESSION:AR322085	368	20.2	0.9	25	1	AX118236	ACCESSION:AX118236
296	22.4	0.9	29	1	AX184030	ACCESSION:AX184030	369	20.2	0.9	25	1	AX692832	ACCESSION:AX692832
297	22	0.9	22	1	AR044033	ACCESSION:AR044033	370	20.2	0.9	25	1	AX692833	ACCESSION:AX692833
298	22	0.9	22	1	AR208403	ACCESSION:AR208403	371	20.2	0.9	25	1	AX692838	ACCESSION:AX692838
299	22	0.9	22	1	AR300896	ACCESSION:AR300896	372	20.2	0.9	25	1	AX692839	ACCESSION:AX692839
300	22	0.9	22	1	AR361045	ACCESSION:AR361045	373	20.2	0.9	25	1	AX692919	ACCESSION:AX692919
301	22	0.9	22	1	AR393736	ACCESSION:AR393736	374	20.2	0.9	25	1	AX692924	ACCESSION:AX692924
302	22	0.9	25	1	AX693017	ACCESSION:AX693017	375	20.2	0.9	25	1	AX692925	ACCESSION:AX692925
303	21.8	0.9	25	1	E50643	ACCESSION:E50643	376	20.2	0.9	25	1	AX692926	ACCESSION:AX692926
304	21.8	0.9	25	1	AX614112	ACCESSION:AX614112	377	20.2	0.9	25	1	AX692930	ACCESSION:AX692930
305	21.8	0.9	25	1	AX692921	ACCESSION:AX692921	378	20.2	0.9	25	1	AX692995	ACCESSION:AX692995
306	21.8	0.9	25	1	AX692922	ACCESSION:AX692922	379	20.2	0.9	25	1	AX692999	ACCESSION:AX692999
307	21.8	0.9	25	1	AX692928	ACCESSION:AX692928	380	20.2	0.9	25	1	AX693000	ACCESSION:AX693000
308	21.8	0.9	25	1	AX692991	ACCESSION:AX692991	381	20.2	0.9	26	1	AX183618	ACCESSION:AX183618
309	21.8	0.9	25	1	AX692992	ACCESSION:AX692992	382	20.2	0.9	26	1	AX183704	ACCESSION:AX183704
310	21.8	0.9	25	1	AX692993	ACCESSION:AX692993	383	20.2	0.9	20	1	AR154586	ACCESSION:AR154586
311	21.8	0.9	25	1	AX692997	ACCESSION:AX692997	384	20	0.8	20	1	AR154587	ACCESSION:AR154587
312	21.8	0.9	27	1	AX184125	ACCESSION:AX184125	385	20	0.8	20	1	AR154588	ACCESSION:AR154588
313	21.6	0.9	28	1	A49272	ACCESSION:A49272	386	20	0.8	20	1	AR154589	ACCESSION:AR154589
314	21.6	0.9	28	1	AR122136	ACCESSION:AR122136	387	20	0.8	20	1	AR154590	ACCESSION:AR154590
315	21.4	0.9	23	1	AR345149	ACCESSION:AR345149	388	20	0.8	20	1	AR154591	ACCESSION:AR154591
316	21.4	0.9	23	1	AX823487	ACCESSION:AX823487	389	20	0.8	20	1	AR154592	ACCESSION:AR154592
317	21.4	0.9	25	1	AB2465	ACCESSION:AB2465	390	20	0.8	20	1	AR154593	ACCESSION:AR154593
318	21.4	0.9	25	1	AX360029	ACCESSION:AX360029	391	20	0.8	20	1	AR154594	ACCESSION:AR154594
319	21.4	0.9	27	1	BD124526	ACCESSION:BD124526	392	20	0.8	20	1	AR154595	ACCESSION:AR154595
320	21.2	0.9	25	1	AX115732	ACCESSION:AX115732	393	20	0.8	20	1	AR154596	ACCESSION:AR154596
321	21.2	0.9	27	1	AX117196	ACCESSION:AX117196	394	20	0.8	20	1	AR154597	ACCESSION:AR154597
322	21.2	0.9	27	1	AX118476	ACCESSION:AX118476	395	20	0.8	20	1	AR154598	ACCESSION:AR154598
323	21	0.9	21	1	AR208405	ACCESSION:AR208405	396	20	0.8	20	1	AR154599	ACCESSION:AR154599
324	21	0.9	21	1	AX117999	ACCESSION:AX117999	397	20	0.8	20	1	AR154600	ACCESSION:AR154600
325	21	0.9	21	1	AX190635	ACCESSION:AX190635	398	20	0.8	20	1	AR154601	ACCESSION:AR154601

C 399	ACCSESSION:AR154602	20	0.8	20	1	BDI38062	C 472	20	0.8	20	1	BDI38083	ACCSESSION:BD138084
C 400	ACCSESSION:AR154603	20	0.8	20	1	BDI38084	C 473	20	0.8	20	1	BDI38085	ACCSESSION:BD138086
C 401	ACCSESSION:AR154604	20	0.8	20	1	BDI38085	C 474	20	0.8	20	1	BDI38086	ACCSESSION:BD138087
C 402	ACCSESSION:AR154605	20	0.8	20	1	BDI38086	C 475	20	0.8	20	1	BDI38087	ACCSESSION:BD138088
C 403	ACCSESSION:AR154608	20	0.8	20	1	BDI38087	C 476	20	0.8	20	1	BDI38088	ACCSESSION:BD138089
C 404	ACCSESSION:BD233827	20	0.8	20	1	BDI38088	C 477	20	0.8	20	1	BDI38089	ACCSESSION:BD138090
C 405	ACCSESSION:BD267626	20	0.8	20	1	BDI38089	C 478	20	0.8	20	1	BDI38090	ACCSESSION:BD138091
C 406	ACCSESSION:CQ784281	20	0.8	20	1	BDI38090	C 479	20	0.8	20	1	BDI38091	ACCSESSION:BD138092
C 407	ACCSESSION:CQ786097	20	0.8	20	1	BDI38091	C 480	20	0.8	20	1	BDI38092	ACCSESSION:BD138093
C 408	ACCSESSION:E31877	20	0.8	20	1	BDI38092	C 481	20	0.8	20	1	BDI38093	ACCSESSION:BD138094
C 409	ACCSESSION:AR208406	20	0.8	20	1	BDI38093	C 482	20	0.8	20	1	BDI38094	ACCSESSION:BD138095
C 410	ACCSESSION:AR236783	20	0.8	20	1	BDI38094	C 483	20	0.8	20	1	BDI38095	ACCSESSION:BD138096
C 411	ACCSESSION:AR305303	20	0.8	20	1	BDI38095	C 484	20	0.8	20	1	BDI38096	ACCSESSION:BD138097
C 412	ACCSESSION:AR309407	20	0.8	20	1	BDI38096	C 485	20	0.8	20	1	BDI38097	ACCSESSION:BD138098
C 413	ACCSESSION:AR310706	20	0.8	20	1	BDI38097	C 486	20	0.8	20	1	BDI38098	ACCSESSION:BD138099
C 414	ACCSESSION:AR310706	20	0.8	20	1	BDI38098	C 487	20	0.8	20	1	BDI38099	ACCSESSION:BD138100
C 415	ACCSESSION:AR321577	20	0.8	20	1	BDI38099	C 488	20	0.8	20	1	BDI38100	ACCSESSION:BD138101
C 416	ACCSESSION:AR337145	20	0.8	20	1	BDI38100	C 489	20	0.8	20	1	BDI38101	ACCSESSION:BD138102
C 417	ACCSESSION:AR370250	20	0.8	20	1	BDI38101	C 490	20	0.8	20	1	BDI38102	ACCSESSION:BD138103
C 418	ACCSESSION:AR370252	20	0.8	20	1	BDI38102	C 491	20	0.8	20	1	BDI38103	ACCSESSION:BD138104
C 419	ACCSESSION:AR435741	20	0.8	20	1	BDI38103	C 492	20	0.8	20	1	BDI38104	ACCSESSION:BD138105
C 420	ACCSESSION:AX115919	20	0.8	20	1	BDI38104	C 493	20	0.8	20	1	BDI38105	ACCSESSION:BD138106
C 421	ACCSESSION:AX116275	20	0.8	20	1	BDI38105	C 494	20	0.8	20	1	BDI38106	ACCSESSION:BD138107
C 422	ACCSESSION:AX146647	20	0.8	20	1	BDI38106	C 495	20	0.8	20	1	BDI38107	ACCSESSION:BD138108
C 423	ACCSESSION:AX657359	20	0.8	20	1	BDI38107	C 496	20	0.8	20	1	BDI38108	ACCSESSION:BD138109
C 424	ACCSESSION:BD073963	20	0.8	20	1	BDI38108	C 497	20	0.8	20	1	BDI38109	ACCSESSION:BD138110
C 425	ACCSESSION:BD073964	20	0.8	20	1	BDI38109	C 498	20	0.8	20	1	BDI38110	ACCSESSION:BD138111
C 426	ACCSESSION:BD073965	20	0.8	20	1	BDI38110	C 499	20	0.8	20	1	BDI38111	ACCSESSION:BD138112
C 427	ACCSESSION:BD073968	20	0.8	20	1	BDI38111	C 500	20	0.8	20	1	BDI38112	ACCSESSION:BD138113
C 428	ACCSESSION:BD073969	20	0.8	20	1	BDI38112	C 501	20	0.8	20	1	BDI38113	ACCSESSION:BD138114
C 429	ACCSESSION:BD073970	20	0.8	20	1	BDI38113	C 502	20	0.8	20	1	BDI38114	ACCSESSION:BD138115
C 430	ACCSESSION:BD073971	20	0.8	20	1	BDI38114	C 503	20	0.8	20	1	BDI38115	ACCSESSION:BD138116
C 431	ACCSESSION:BD073972	20	0.8	20	1	BDI38115	C 504	20	0.8	20	1	BDI38116	ACCSESSION:BD138117
C 432	ACCSESSION:BD073974	20	0.8	20	1	BDI38116	C 505	20	0.8	20	1	BDI38117	ACCSESSION:BD138118
C 433	ACCSESSION:BD073975	20	0.8	20	1	BDI38117	C 506	20	0.8	20	1	BDI38118	ACCSESSION:BD138119
C 434	ACCSESSION:BD073976	20	0.8	20	1	BDI38118	C 507	20	0.8	20	1	BDI38119	ACCSESSION:BD138120
C 435	ACCSESSION:BD073977	20	0.8	20	1	BDI38119	C 508	20	0.8	20	1	BDI38120	ACCSESSION:BD138121
C 436	ACCSESSION:BD073978	20	0.8	20	1	BDI38120	C 509	20	0.8	20	1	BDI38121	ACCSESSION:BD138122
C 437	ACCSESSION:BD073979	20	0.8	20	1	BDI38121	C 510	20	0.8	20	1	BDI38122	ACCSESSION:BD138123
C 438	ACCSESSION:BD073980	20	0.8	20	1	BDI38122	C 511	20	0.8	20	1	BDI38123	ACCSESSION:BD138124
C 439	ACCSESSION:BD073981	20	0.8	20	1	BDI38123	C 512	20	0.8	20	1	BDI38124	ACCSESSION:BD138125
C 440	ACCSESSION:BD073982	20	0.8	20	1	BDI38124	C 513	20	0.8	20	1	BDI38125	ACCSESSION:BD138126
C 441	ACCSESSION:BD073984	20	0.8	20	1	BDI38125	C 514	20	0.8	20	1	BDI38126	ACCSESSION:BD138127
C 442	ACCSESSION:BD073985	20	0.8	20	1	BDI38126	C 515	20	0.8	20	1	BDI38127	ACCSESSION:BD138128
C 443	ACCSESSION:BD073988	20	0.8	20	1	BDI38127	C 516	20	0.8	20	1	BDI38128	ACCSESSION:BD138129
C 444	ACCSESSION:BD073989	20	0.8	20	1	BDI38128	C 517	20	0.8	20	1	BDI38129	ACCSESSION:BD138130
C 445	ACCSESSION:BD073990	20	0.8	20	1	BDI38129	C 518	20	0.8	20	1	BDI38130	ACCSESSION:BD138131
C 446	ACCSESSION:BD073991	20	0.8	20	1	BDI38130	C 519	20	0.8	20	1	BDI38131	ACCSESSION:BD138132
C 447	ACCSESSION:BD073992	20	0.8	20	1	BDI38131	C 520	20	0.8	20	1	BDI38132	ACCSESSION:BD138133
C 448	ACCSESSION:BD073993	20	0.8	20	1	BDI38132	C 521	20	0.8	20	1	BDI38133	ACCSESSION:BD138134
C 449	ACCSESSION:BD073994	20	0.8	20	1	BDI38133	C 522	20	0.8	20	1	BDI38134	ACCSESSION:BD138135
C 450	ACCSESSION:BD073995	20	0.8	20	1	BDI38134	C 523	20	0.8	20	1	BDI38135	ACCSESSION:BD138136
C 451	ACCSESSION:BD073996	20	0.8	20	1	BDI38135	C 524	20	0.8	20	1	BDI38136	ACCSESSION:BD138137
C 452	ACCSESSION:BD073997	20	0.8	20	1	BDI38136	C 525	20	0.8	20	1	BDI38137	ACCSESSION:BD138138
C 453	ACCSESSION:BD073998	20	0.8	20	1	BDI38137	C 526	20	0.8	20	1	BDI38138	ACCSESSION:BD138139
C 454	ACCSESSION:BD073999	20	0.8	20	1	BDI38138	C 527	20	0.8	20	1	BDI38139	ACCSESSION:BD138140
C 455	ACCSESSION:BD074000	20	0.8	20	1	BDI38139	C 528	20	0.8	20	1	BDI38140	ACCSESSION:BD138141
C 456	ACCSESSION:BD074001	20	0.8	20	1	BDI38140	C 529	20	0.8	20	1	BDI38141	ACCSESSION:BD138142
C 457	ACCSESSION:BD074002	20	0.8	20	1	BDI38141	C 530	20	0.8	20	1	BDI38142	ACCSESSION:BD138143
C 458	ACCSESSION:BD074003	20	0.8	20	1	BDI38142	C 531	20	0.8	20	1	BDI38143	ACCSESSION:BD138144
C 459	ACCSESSION:BD074004	20	0.8	20	1	BDI38143	C 532	20	0.8	20	1	BDI38144	ACCSESSION:BD138145
C 460	ACCSESSION:BD074006	20	0.8	20	1	BDI38144	C 533	20	0.8	20	1	BDI38145	ACCSESSION:BD138146
C 461	ACCSESSION:BD074007	20	0.8	20	1	BDI38145	C 534	20	0.8	20	1	BDI38146	ACCSESSION:BD138147
C 462	ACCSESSION:BD074008	20	0.8	20	1	BDI38146	C 535	20	0.8	20	1	BDI38147	ACCSESSION:BD138148
C 463	ACCSESSION:BD088804	20	0.8	20	1	BDI38147	C 536	20	0.8	20	1	BDI38148	ACCSESSION:BD138149
C 464	ACCSESSION:BD089238	20	0.8	20	1	BDI38148	C 537	20	0.8	20	1	BDI38149	ACCSESSION:BD138150
C 465	ACCSESSION:BD106214	20	0.8	20	1	BDI38149	C 538	20	0.8	20	1	BDI38150	ACCSESSION:BD138151
C 466	ACCSESSION:BD128205	20	0.8	20	1	BDI38150	C 539	20	0.8	20	1	BDI38151	ACCSESSION:BD138152
C 467	ACCSESSION:BD138077	20	0.8	20	1	BDI38151	C 540	20	0.8	20	1	BDI38152	ACCSESSION:BD138153
C 468	ACCSESSION:BD138078	20	0.8	20	1	BDI38152	C 541	20	0.8	20	1	BDI38153	ACCSESSION:BD138154
C 469	ACCSESSION:BD138079	20	0.8	20	1	BDI38153	C 542	20	0.8	20	1	BDI38154	ACCSESSION:BD138155
C 470	ACCSESSION:BD138080	20	0.8	20	1	BDI38154	C 543	20	0.8	20	1	BDI38155	ACCSESSION:BD138156
C 471	ACCSESSION:BD138081	20	0.8	20	1	BDI38155	C 544	20	0.8	20	1	BDI38156	ACCSESSION:BD138157
C 472	ACCSESSION:BD138082	20	0.8	20	1	BDI38156	C 545	20	0.8	20	1	BDI38157	ACCSESSION:BD138158
C 473	ACCSESSION:BD138083	20	0.8	20	1	BDI38157	C 546	20	0.8	20	1	BDI38158	ACCSESSION:BD138159
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C 475	ACCSESSION:BD138085	20	0.8	20	1	BDI38159	C 548	20	0.8	20	1	BDI38160	ACCSESSION:BD138161
C 476	ACCSESSION:BD138086	20	0.8	20	1	BDI38160	C 549	20	0.8	20	1	BDI38161	ACCSESSION:BD138162
C 477	ACCSESSION:BD138087	20	0.8	20	1	BDI38161	C 550	20	0.8	20	1	BDI38162	ACCSESSION:BD138163
C 478	ACCSESSION:BD138088	20	0.8	20	1	BDI38162	C 551	20	0.8	20	1	BDI38163	ACCSESSION:BD138164
C 479	ACCSESSION:BD138089	20	0.8	20	1	BDI38163	C 552	20	0.8	20	1	BDI38164	ACCSESSION:BD138165
C 480	ACCSESSION:BD138090	20	0.8	20	1	BDI38164	C 553	20	0.8	20	1	BDI38165	ACCSESSION:BD138166
C 481	ACCSESSION:BD138091	20	0.8	20	1	BDI38165	C 554	20	0.8	20	1	BDI38166	ACCSESSION:BD138167
C 482	ACCSESSION:BD138092	20	0.8	20	1	BDI38166	C 555	20	0.8	20	1	BDI38167	ACCSESSION:BD138168
C 483	ACCSESSION:BD138093	20	0.8	20	1	BDI38167	C 556	20	0.8	20	1	BDI38168	ACCSESSION:BD138169
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C 486	ACCSESSION:BD138096	20	0.8	20	1	BDI38170	C 559	20	0.8	20	1	BDI38171	ACCSESSION:BD138172
C 487	ACCSESSION:BD138097	20	0.8	20	1	BDI38171	C 560	20	0.8	20	1	BDI38172	ACCSESSION:BD138173
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C 489	ACCSESSION:BD138099	20	0.8	20	1	BDI38173	C 562	20	0.8	20	1	BDI38174	ACCSESSION:BD138175
C 490	ACCSESSION:BD138100	20	0.8	20	1	BDI38174	C 563	20	0.8	20	1	BDI38175	ACCSESSION:BD138176
C 491	ACCSESSION:BD138101	20	0.8	20	1	BDI38175	C 564	20	0.8	20	1	BDI38176	ACCSESSION:BD138177
C 492	ACCSESSION:BD138102	20	0.8	20	1	BDI38176	C 565	20	0.8	20	1	BDI3	

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C 693	20	0.8	20	1	BD138313	ACCESSION:BD138313	C 766	19	0.8	19	1	CQ760691	ACCESSION:CQ760691
C 694	20	0.8	20	1	BD138314	ACCESSION:BD138314	767	19	0.8	19	1	IS2002	ACCESSION:IS2002
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C 697	20	0.8	20	1	BD138317	ACCESSION:BD138317	770	19	0.8	19	1	AX116350	ACCESSION:AX116350
C 698	20	0.8	20	1	BD138318	ACCESSION:BD138318	C 771	19	0.8	19	1	BD089274	ACCESSION:BD089274
C 699	20	0.8	20	1	BD138319	ACCESSION:BD138319	C 772	19	0.8	19	1	AR116725	ACCESSION:AR116725
C 700	20	0.8	20	1	BD138320	ACCESSION:BD138320	C 773	19	0.8	20	1	I89275	ACCESSION:I89275
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C 702	20	0.8	20	1	BD138322	ACCESSION:BD138322	C 775	19	0.8	20	1	AR208408	ACCESSION:AR208408
C 703	20	0.8	20	1	BD138323	ACCESSION:BD138323	C 776	19	0.8	20	1	AR208409	ACCESSION:AR208409
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C 705	20	0.8	20	1	BD138325	ACCESSION:BD138325	C 778	19	0.8	20	1	AR224472	ACCESSION:AR224472
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C 708	20	0.8	20	1	BD138328	ACCESSION:BD138328	C 781	19	0.8	25	1	AX693014	ACCESSION:AX693014
C 709	20	0.8	20	1	BD138329	ACCESSION:BD138329	C 782	18.8	0.8	22	1	AR066909	ACCESSION:AR066909
C 710	20	0.8	20	1	BD138330	ACCESSION:BD138330	C 783	18.8	0.8	22	1	AR088425	ACCESSION:AR088425
C 711	20	0.8	20	1	BD138331	ACCESSION:BD138331	C 784	18.8	0.8	22	1	AX116074	ACCESSION:AX116074
C 712	20	0.8	20	1	BD138332	ACCESSION:BD138332	785	18.8	0.8	22	1	AX817228	ACCESSION:AX817228
C 713	20	0.8	20	1	BD138333	ACCESSION:BD138333	786	18.8	0.8	23	1	CQ766173	ACCESSION:CQ766173
C 714	20	0.8	20	1	BD138334	ACCESSION:BD138334	C 787	18.8	0.8	24	1	AX183954	ACCESSION:AX183954
C 715	20	0.8	20	1	BD138335	ACCESSION:BD138335	788	18.8	0.8	25	1	AX042886	ACCESSION:AX042886
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C 719	20	0.8	20	1	BD138339	ACCESSION:BD138339	792	18.8	0.8	25	1	AX692988	ACCESSION:AX692988
C 720	20	0.8	20	1	BD138340	ACCESSION:BD138340	793	18.4	0.8	20	1	A83584	ACCESSION:A83584
C 721	20	0.8	20	1	BD138341	ACCESSION:BD138341	794	18.4	0.8	20	1	A83598	ACCESSION:A83598
C 722	20	0.8	20	1	BD138342	ACCESSION:BD138342	795	18.4	0.8	20	1	AR043282	ACCESSION:AR043282
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C 725	20	0.8	22	1	AX214484	ACCESSION:AX214484	C 798	18.4	0.8	20	1	AR154610	ACCESSION:AR154610
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C 728	19.8	0.8	23	1	CQ766177	ACCESSION:CQ766177	801	18.4	0.8	20	1	CQ784081	ACCESSION:CQ784081
C 729	19.8	0.8	23	1	AX115087	ACCESSION:AX115087	802	18.4	0.8	20	1	CQ801618	ACCESSION:CQ801618
C 730	19.8	0.8	24	1	AX124382	ACCESSION:AX124382	C 803	18.4	0.8	20	1	CQ819694	ACCESSION:CQ819694
C 731	19.8	0.8	24	1	AX093775	ACCESSION:AX093775	804	18.4	0.8	20	1	I21054	ACCESSION:I21054
C 732	19.8	0.8	25	1	AX612650	ACCESSION:AX612650	805	18.4	0.8	20	1	I31429	ACCESSION:I31429
C 733	19.8	0.8	25	1	AX692834	ACCESSION:AX692834	806	18.4	0.8	20	1	I82133	ACCESSION:I82133
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C 739	19.6	0.8	26	1	AR274339	ACCESSION:AR274339	812	18.4	0.8	20	1	AX938814	ACCESSION:AX938814
C 740	19.6	0.8	26	1	AX068482	ACCESSION:AX068482	813	18.4	0.8	20	1	BD128005	ACCESSION:BD128005
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C 743	19.4	0.8	21	1	AR148944	ACCESSION:AR148944	816	18.4	0.8	21	1	E31629	ACCESSION:E31629
C 744	19.4	0.8	21	1	AR182144	ACCESSION:AR182144	817	18.4	0.8	21	1	E31630	ACCESSION:E31630
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C 748	19.4	0.8	21	1	AX741033	ACCESSION:AX741033	821	18.4	0.8	22	1	E31632	ACCESSION:E31632
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C 750	19.4	0.8	21	1	AX800313	ACCESSION:AX800313	823	18.4	0.8	22	1	E31634	ACCESSION:E31634
C 751	19.4	0.8	21	1	BD056581	ACCESSION:BD056581	824	18.4	0.8	22	1	E31635	ACCESSION:E31635
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C 753	19.4	0.8	23	1	AX938799	ACCESSION:AX938799	826	18.4	0.8	22	1	E31637	ACCESSION:E31637
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C 762	19.2	0.8	25	1	AX692840	ACCESSION:AX692840	835	18.2	0.8	19	1	I29969	ACCESSION:I29969
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C 877	17.4	0.7	19	1	I31418	ACCESSION: I31418	C 950	17	0.7	17	1	AX692732	ACCESSION: AX692732
C 878	17.4	0.7	19	1	AR233457	ACCESSION: AR233457	C 951	17	0.7	17	1	AX692733	ACCESSION: AX692733
C 879	17.4	0.7	19	1	AR482557	ACCESSION: AR482557	C 952	17	0.7	17	1	AX692734	ACCESSION: AX692734
C 880	17.4	0.7	19	1	AX081966	ACCESSION: AX081966	C 953	17	0.7	17	1	AX692735	ACCESSION: AX692735
C 881	17.4	0.7	19	1	AX081968	ACCESSION: AX081968	C 954	17	0.7	17	1	AX692736	ACCESSION: AX692736
C 882	17.4	0.7	19	1	AX081972	ACCESSION: AX081972	C 955	17	0.7	17	1	AX692737	ACCESSION: AX692737
C 883	17.4	0.7	19	1	AX081974	ACCESSION: AX081974	C 956	17	0.7	17	1	AX692738	ACCESSION: AX692738
C 884	17.4	0.7	19	1	AX081978	ACCESSION: AX081978	C 957	17	0.7	17	1	AX692739	ACCESSION: AX692739
C 885	17.4	0.7	19	1	AX081980	ACCESSION: AX081980	C 958	17	0.7	17	1	AX692740	ACCESSION: AX692740
C 886	17.4	0.7	19	1	AX116142	ACCESSION: AX116142	C 959	17	0.7	17	1	AX732424	ACCESSION: AX732424
C 887	17.4	0.7	19	1	AX226138	ACCESSION: AX226138	C 960	17	0.7	17	1	AX734118	ACCESSION: AX734118
C 888	17.4	0.7	19	1	BD088699	ACCESSION: BD088699	C 961	17	0.7	17	1	AX741036	ACCESSION: AX741036
C 889	17.4	0.7	19	1	BD090072	ACCESSION: BD090072	C 962	17	0.7	17	1	AX741048	ACCESSION: AX741048
C 890	17.4	0.7	19	1	AB068733	ACCESSION: AB068733	C 963	17	0.7	19	1	AX081967	ACCESSION: AX081967
C 891	17.4	0.7	20	1	I31439	ACCESSION: I31439	C 964	17	0.7	19	1	AX081969	ACCESSION: AX081969
C 892	17.4	0.7	20	1	AR215877	ACCESSION: AR215877	C 965	17	0.7	19	1	AX081973	ACCESSION: AX081973
C 893	17.4	0.7	20	1	AR271152	ACCESSION: AR271152	C 966	17	0.7	19	1	AX081975	ACCESSION: AX081975
C 894	17.4	0.7	20	1	AR305332	ACCESSION: AR305332	C 967	17	0.7	19	1	AX081979	ACCESSION: AX081979
C 895	17.4	0.7	20	1	AR309436	ACCESSION: AR309436	C 968	17	0.7	19	1	AX081981	ACCESSION: AX081981
C 896	17.4	0.7	20	1	AX184102	ACCESSION: AX184102	C 969	17	0.7	19	1	AX081981	ACCESSION: AX081981
C 897	17.4	0.7	20	1	AX188411	ACCESSION: AX188411	C 970	17	0.7	19	1	AX081981	ACCESSION: AX081981
C 898	17.4	0.7	20	1	BD089312	ACCESSION: BD089312	C 971	17	0.7	19	1	AX081981	ACCESSION: AX081981
C 899	17.4	0.7	20	1	BD106243	ACCESSION: BD106243	C 972	17	0.7	19	1	AX081981	ACCESSION: AX081981
C 900	17.4	0.7	21	1	AR345147	ACCESSION: AR345147	C 973	17	0.7	19	1	AX081981	ACCESSION: AX081981
C 901	17.4	0.7	22	1	E31640	ACCESSION: E31640	C 974	17	0.7	19	1	AX081981	ACCESSION: AX081981
C 902	17.4	0.7	22	1	E31641	ACCESSION: E31641	C 975	17	0.7	19	1	AX081981	ACCESSION: AX081981
C 903	17.4	0.7	22	1	E31642	ACCESSION: E31642	C 976	17	0.7	19	1	AX081981	ACCESSION: AX081981
C 904	17.4	0.7	22	1	E31643	ACCESSION: E31643	C 977	17	0.7	19	1	AX081981	ACCESSION: AX081981
C 905	17.4	0.7	22	1	E31644	ACCESSION: E31644	C 978	17	0.7	20	1	AR152875	ACCESSION: AR152875
C 906	17.4	0.7	22	1	E31645	ACCESSION: E31645	C 979	17	0.7	20	1	AR162414	ACCESSION: AR162414
C 907	17.4	0.7	22	1	E31646	ACCESSION: E31646	C 980	17	0.7	20	1	AX477118	ACCESSION: AX477118
C 908	17.4	0.7	22	1	E31647	ACCESSION: E31647	C 981	17	0.7	20	1	AX526494	ACCESSION: AX526494
C 909	17.4	0.7	22	1	E31648	ACCESSION: E31648	C 982	17	0.7	20	1	AX811386	ACCESSION: AX811386

/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Best Local Similarity 93.6%; Score 86.4; DB 1; Length 100;
Matches 90; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db |||||
3 CCACATGCCCGCTAATTTTGTATTTTGTATTTTAGTAGACAGGGTTTCACAGTGTAGCC 62
Qy 2293 AGGATGCTCTCGATCTCTGACCTCGTATCCGCC 2328
Db |||||
63 AGGATGCTCTGATCTCTGACCTCGTATCCGCC 98

RESULT 2
AX902820
LOCUS AX902820 100 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 18683 from Patent EP1033401.
ACCESSION AX902820
VERSION AX902820.1 GI:40057777
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 18683 06-SEP-2000;
Genset (FR)

FEATURES
source
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 93.8%; Score 86.4; DB 1; Length 100;
Matches 90; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2233 CCACACACCTGGCTAATTTTGTACTTTTAGTAGACAGGGTTTCACCGTGTAGCC 2292
Db |||||
3 CCACATGCCCGCTAATTTTGTATTTTGTATTTTAGTAGACAGGGTTTCACAGTGTAGCC 62
Qy 2293 AGGATGCTCTCGATCTCTGACCTCGTATCCGCC 2328
Db |||||
63 AGGATGCTCTGATCTCTGACCTCGTATCCGCC 98

RESULT 3
BD037041
LOCUS BD037041 100 bp DNA linear PAT 27-AUG-2002
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD037041
VERSION BD037041.1 GI:22578783
KEYWORDS JP 2001269182-A/13287.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 13287 02-OCT-2001;
GENSET

COMMENT
OS Homo sapiens (human)
PN JP 2001269182-A/13287
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PI 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES

PI JORDAN
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
G06F15/40
CC

FEATURES
source
FH Key Location/Qualifiers
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 93.8%; Score 86.4; DB 1; Length 100;
Matches 90; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2233 CCACACACCTGGCTAATTTTGTACTTTTAGTAGACAGGGTTTCACCGTGTAGCC 2292
Db |||||
3 CCACATGCCCGCTAATTTTGTATTTTGTATTTTAGTAGACAGGGTTTCACAGTGTAGCC 62
Qy 2293 AGGATGCTCTCGATCTCTGACCTCGTATCCGCC 2328
Db |||||
63 AGGATGCTCTGATCTCTGACCTCGTATCCGCC 98

RESULT 4
BD038353
LOCUS BD038353 100 bp DNA linear PAT 27-AUG-2002
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD038353
VERSION BD038353.1 GI:22580095
KEYWORDS JP 2001269182-A/14599.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 100)
AUTHORS Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 14599 02-OCT-2001;
GENSET

COMMENT
OS Homo sapiens (human)
PN JP 2001269182-A/14599
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PI 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
PI JORDAN
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
G06F15/40
CC

FEATURES
source
FH Key Location/Qualifiers
1..100
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 93.8%; Score 86.4; DB 1; Length 100;
Matches 90; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2233 CCACACACCTGGCTAATTTTGTACTTTTAGTAGACAGGGTTTCACCGTGTAGCC 2292
Db |||||
3 CCACATGCCCGCTAATTTTGTATTTTGTATTTTAGTAGACAGGGTTTCACAGTGTAGCC 62
Qy 2293 AGGATGCTCTCGATCTCTGACCTCGTATCCGCC 2328
Db |||||
63 AGGATGCTCTGATCTCTGACCTCGTATCCGCC 98

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RESULT 5
AR421510/c
LOCUS AR421510 linear PAT 18-DEC-2003
DEFINITION Sequence 13007 from patent US 6639063.
ACCESSION AR421510
VERSION AR421510.1 GI:40176620
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 94)
AUTHORS Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
TITLE EST's and encoded human proteins
JOURNAL Patent: US 6639063-A 13007 28-OCT-2003;
FEATURES
source
1..94
/organism="unknown"
/mol_type="genomic DNA"

Query Match 3.6%; Score 85; DB 1; Length 94;
Best Local Similarity 94.6%; Pred. No. 1.3;
Matches 88; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2263 TAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGAT 2322
DB 94 TAGTAGAGACAGGGTTTCATCGTGTAGCCAGGATGGTCTTGATCTCTGACCTCATGAT 35
QY 2323 CCGCCACCTCGGCTCCCAAGTCTGGGATT 2355
DB 34 CCACCCACCTCGGCTCCCAAGTCTGGGATT 2

RESULT 6
AX982204/c
LOCUS AX982204 linear PAT 15-JAN-2004
DEFINITION Sequence 13007 from Patent EP1104808.
ACCESSION AX982204
VERSION AX982204.1 GI:40988344
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 94)
AUTHORS Dumas Milne Edwards,J.B., Jobert,S. and Giordano,J.Y.
TITLE ESTs and encoded human proteins
JOURNAL Patent: EP 1104808-A 13007 06-JUN-2001;
FEATURES
source
1..94
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 3.6%; Score 85; DB 1; Length 94;
Best Local Similarity 94.6%; Pred. No. 1.3;
Matches 88; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2263 TAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGAT 2322
DB 94 TAGTAGAGACAGGGTTTCATCGTGTAGCCAGGATGGTCTTGATCTCTGACCTCATGAT 35
QY 2323 CCGCCACCTCGGCTCCCAAGTCTGGGATT 2355
DB 34 CCACCCACCTCGGCTCCCAAGTCTGGGATT 2

RESULT 7
BD117063/c
LOCUS BD117063 linear PAT 18-SEP-2002
DEFINITION EST and encoded human protein.
ACCESSION BD117063

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VERSION BD117063.1 GI:23211967
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 94)
AUTHORS Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.
TITLE EST and encoded human protein
JOURNAL Patent: JP 2002010789-A 9140 15-JAN-2002;
COMMENT
OS Homo sapiens (human)
PN JP 2002010789-A/9140
PD 15-JAN-2002
PF 07-AUG-2000 JP 2000280989
PR 05-AUG-1999 US 60/147499
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE
GIORDANO
PC C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC
C12N1/21,
PC C12N5/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00, PC
C12N15/00
CC EST and encoded human protein
FH Key Location/Qualifiers
FT source 1..94
/organism="Homo sapiens (human)"
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/db_xref="taxon:9606"

Query Match 3.6%; Score 85; DB 1; Length 94;
Best Local Similarity 94.6%; Pred. No. 1.3;
Matches 88; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2263 TAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGAT 2322
DB 94 TAGTAGAGACAGGGTTTCATCGTGTAGCCAGGATGGTCTTGATCTCTGACCTCATGAT 35
QY 2323 CCGCCACCTCGGCTCCCAAGTCTGGGATT 2355
DB 34 CCACCCACCTCGGCTCCCAAGTCTGGGATT 2

RESULT 8
AX912163
LOCUS AX912163 94 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 28026 from Patent EP1033401.
ACCESSION AX912163
VERSION AX912163.1 GI:40205952
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 94)
AUTHORS Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 28026 06-SEP-2000;
FEATURES
source
1..94
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 3.4%; Score 81.2; DB 1; Length 94;
Best Local Similarity 91.5%; Pred. No. 2.1;
Matches 86; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2263 TAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGAT 2322

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Db 1 TAGTAGAGACGAGGTTTACCGCAATTAGCCAGAGATGCTTCGATCTCCTGACCTTGTGAT 60
QY 2323 CCGCCACCTCGGCTCCCAAAGTCTGGGATTA 2356
Db 61 CTGCGCGCTTGGCTCCCAAGTCTGGGATTA 94

RESULT 9
BD047696 94 bp DNA linear PAT 27-AUG-2002
LOCUS Sequence tag and encoded human protein.
DEFINITION BD047696
ACCESSION BD047696
VERSION BD047696.1 GI:22589438
KEYWORDS JP 2001269182-A/23942.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 94)
AUTHORS Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 23942 02-OCT-2001;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2001269182-A/23942
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTIST DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES
PI JORDAN
PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21,PC
C12N5/10,
PC C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00,PC
G06F15/40
CC
FH Key Location/Qualifiers.
FEATURES
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 3.4%; Score 81.2; DB 1; Length 94;
Best Local Similarity 91.5%; Pred. No. 2.1;
Matches 86; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2263 TAGTAGAGACGAGGTTTACCGCAATTAGCCAGAGATGCTTCGATCTCCTGACCTTGTGAT 2322
Db 1 TAGTAGAGACGAGGTTTACCGCAATTAGCCAGAGATGCTTCGATCTCCTGACCTTGTGAT 60

QY 2323 CCGCCACCTCGGCTCCCAAAGTCTGGGATTA 2356
Db 61 CTGCGCGCTTGGCTCCCAAGTCTGGGATTA 94

RESULT 10
AX197468/c 92 bp DNA linear PAT 29-AUG-2001
LOCUS Sequence 33 from Patent WO0151632.
DEFINITION AX197468
ACCESSION AX197468
VERSION AX197468.1 GI:15387840
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Padigaru,M., Prayaga,S.K., Taupier,R.J., Mishra,V., Tchernev,V.T.,
Szytek,K.A. and Li,L.
TITLE Odorant receptor polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0151632-A 33 19-JUL-2001;
Curagen Corporation (US)
FEATURES
source 1..94
Location/Qualifiers
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source 1..92
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 3.4%; Score 80.6; DB 1; Length 92;
Best Local Similarity 95.4%; Pred. No. 2.2;
Matches 83; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2286 GTTAGCCAGAGTGTCTCGATCTCCTGACCTCGTATCGCCACCTCGGCTCCCAAAG 2345
Db 92 GTTAGCCAGAGTGTCTCGATCTCCTGACCTCGTATCGCCACCTCGGCTCCCAAAG 33

QY 2346 TGCTGGGATTACAGGCATGAGCCACCG 2372
Db 32 TGCTGGGATTACAGGCGTGAGCCACCG 6

RESULT 11
AX197476/c 94 bp DNA linear PAT 29-AUG-2001
LOCUS Sequence 41 from Patent WO0151632.
DEFINITION AX197476
ACCESSION AX197476
VERSION AX197476.1 GI:15387843
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Padigaru,M., Prayaga,S.K., Taupier,R.J., Mishra,V., Tchernev,V.T.,
Szytek,K.A. and Li,L.
TITLE Odorant receptor polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0151632-A 41 19-JUL-2001;
Curagen Corporation (US)
FEATURES
source 1..94
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 3.4%; Score 80.6; DB 1; Length 94;
Best Local Similarity 95.4%; Pred. No. 2.2;
Matches 83; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2286 GTTAGCCAGAGTGTCTCGATCTCCTGACCTCGTATCGCCACCTCGGCTCCCAAAG 2345
Db 94 GTTAGCCAGAGTGTCTCGATCTCCTGACCTCGTATCGCCACCTCGGCTCCCAAAG 35

QY 2346 TGCTGGGATTACAGGCATGAGCCACCG 2372
Db 34 TGCTGGGATTACAGGCGTGAGCCACCG 8

RESULT 12
AX197483 94 bp DNA linear PAT 29-AUG-2001
LOCUS Sequence 48 from Patent WO0151632.
DEFINITION AX197483
ACCESSION AX197483
VERSION AX197483.1 GI:15387846
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Padigaru,M., Prayaga,S.K., Taupier,R.J., Mishra,V., Tchernev,V.T.,
Szytek,K.A. and Li,L.
TITLE Odorant receptor polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0151632-A 48 19-JUL-2001;
Curagen Corporation (US)
FEATURES
source 1..94
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 3.4%; Score 80.6; DB 1; Length 94;
Matches 83; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2286 GTTAGCCAGGATGCTCGATCTCTGACCTCGATCGGCGCCACCTCGGCGCTCCCAAAG 2345
Db 1 GTTAGCCAGGATGCTCGATCTCTGACCTCGATCGGCGCCACCTCGGCGCTCCCAAAG 60

QY 2346 TGCTGGATTACAGGCATGAGCCACCG 2372
Db 61 TGCTGGATTACAGGCATGAGCCACCG 87

RESULT 13
AX916923
LOCUS AX916923 95 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 32786 from Patent EP1033401.
ACCESSION AX916923
VERSION AX916923.1 GI:40210712
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 32786 06-SEP-2000;
Genset (FR)

FEATURES
source
1..95
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 3.4%; Score 80.6; DB 1; Length 95;
Matches 86; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2264 AGTAGACAGAGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATC 2323
Db 1 AGTAGACAGAGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCTGATCTCTTGATC 60

QY 2324 CGCCACCTCGGCTCCCAAAGTCTGGGATTACA 2358
Db 61 CGCTGCTTGATCTCTGAGTCTGGGATTACA 95

RESULT 14
BD052456
LOCUS BD052456 95 bp DNA linear PAT 27-AUG-2002
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD052456
VERSION BD052456.1 GI:22594198
KEYWORDS JP 2001269182-A/28702.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 28702 02-OCT-2001;
GENSET
COMMENT
OS Homo sapiens (human)
PN JP 2001269182-A/28702
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
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PI JEAN BAPTISTE DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES
PI JORDAN
PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21,PC
C12N5/10,
PC C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00,PC
G06F15/40
CC G06F15/40
FH Key Location/Qualifiers.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 3.4%; Score 80.6; DB 1; Length 95;
Matches 86; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2264 AGTAGACAGAGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATC 2323
Db 1 AGTAGACAGAGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCTGATCTCTTGATC 60

QY 2324 CGCCACCTCGGCTCCCAAAGTCTGGGATTACA 2358
Db 61 CGCTGCTTGATCTCTGAGTCTGGGATTACA 95

RESULT 15
AY003889
LOCUS AY003889 89 bp DNA linear PRI 01-APR-2004
DEFINITION Homo sapiens clone C317, HTLV-1 integration site flanking region.
ACCESSION AY003889
VERSION AY003889.1 GI:9438211
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Cavrois,M., Gessain,A., Gout,O., Wain-Hobson,S. and Wattel,E.
TITLE Common human T cell leukemia virus type 1 (HTLV-1) integration sites in cerebrospinal fluid and blood lymphocytes of patients with HTLV-1-associated myelopathy/tropical spastic paraparesis indicate that HTLV-1 crosses the blood-brain barrier via clonal HTLV-1-infected cells
JOURNAL J. Infect. Dis. 182 (4), 1044-1050 (2000)
MEDLINE 20435894
REFERENCE PUBMED 10979898
AUTHORS Cavrois,M., Gessain,A., Gout,O., Wain-Hobson,S. and Wattel,E.
TITLE Direct Submission
JOURNAL Submitted (26-JUN-2000) Unite d'Oncogenese Virale, Centre Leon Berard, Lyon, France
FEATURES
source
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/misc_feature
1..89
/note="downstream of HTLV-1 integration site"

Query Match
Best Local Similarity 3.4%; Score 80.2; DB 1; Length 89;
Matches 82; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2278 TTCCACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCTCGCCACCTCGGCC 2337
Db 1 TTCCACCGTGTAGCCAGGATGGTCTCGATCTCTGATCTCTGATCTCGCCACCTCGGCC 60

QY 2338 TCCCAAAGTCTGGGATTACAGGCA 2362
Db 61 TCCCAAAGTCTGGGATTACAGGCA 85
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RESULT 16
AY003892
LOCUS
DEFINITION Homo sapiens clone C307, HTLV-1 integration site flanking region.
ACCESSION AY003892
VERSION AY003892.1 GI:9438214
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Cavrois,M., Gessain,A., Gout,O., Wain-Hobson,S. and Wattel,E.
TITLE Common human T cell leukemia virus type 1 (HTLV-1) integration
sites in cerebrospinal fluid and blood lymphocytes of patients with
HTLV-1-associated myelopathy/tropical spastic paraparesis indicate
that HTLV-1 crosses the blood-brain barrier via clonal
HTLV-1-infected cells
J. Infect. Dis. 182 (4), 1044-1050 (2000)
MEDLINE 20435894
PUBMED 10979898
REFERENCE
AUTHORS Cavrois,M., Gessain,A., Gout,O., Wain-Hobson,S. and Wattel,E.
TITLE Direct Submission
JOURNAL Submitted (26-JUN-2000) Unite d'Oncogenese Virale, Centre Leon
Berard, Lyon, France
FEATURES
source Location/Qualifiers
1..89
/mol_type="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="C307"
misc_feature 1..89
/notes="downstream of HTLV-1 integration site"

Query Match 3.4%; Score 80.2; DB 1; Length 89;
Best Local Similarity 96.5%; Pred. No. 2.2;
Matches 82; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2278 TTCACCGTGTAGCCAGGATGCTCGATCTCTGACCTCGTATCGGCCACTCGGCC 2337
Db 1 TTCACCGTGTAGCCAGGATGCTCTGATCTCTGACCTCGTATCGGCCACTCGGCC 60

QY 2338 TCCCAAAGTCTGGATTACAGCA 2362
Db 61 TCCCAAAGTCTGGATTACAGCA 85

RESULT 17
AX899255/c
LOCUS
DEFINITION Sequence 15118 from Patent EP1033401.
ACCESSION AX899255
VERSION AX899255.1 GI:40054168
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 15118 06-SEP-2000;
Genset (FR)
FEATURES
source Location/Qualifiers
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/mol_type="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 3.4%; Score 80; DB 1; Length 100;

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Best Local Similarity 89.6%; Pred. No. 2.4;
Matches 86; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2250 TTTTGTGTTAGTAGACAGGTTTCACCGTGTAGCCAGGATGCTCTCGATCTC 2309
Db 96 TTTTGTGTTAGTAGACAGGTTTCACCGTGTAGCCAGGATGCTCTCGATCTC 37

QY 2310 CTGACCTCGTGATCCGCCACCTCGGCCTCCCAAAG 2345
Db 36 CTGACCTCGTGATCCATCCACCTCGGCCTCCCAAAG 1

RESULT 18
BD034788/c
LOCUS
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD034788
VERSION BD034788.1 GI:22576530
KEYWORDS JP 2001269182-A/11034.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 11034 02-OCT-2001;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2001269182-A/11034
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES
PC JORDAN
PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21,PC
C12N5/10,
PC C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00,PC
G06F15/40
CC Key Location/Qualifiers
FH source Location/Qualifiers
1..100
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 3.4%; Score 80; DB 1; Length 100;
Best Local Similarity 89.6%; Pred. No. 2.4;
Matches 86; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2250 TTTTGTGTTAGTAGACAGGTTTCACCGTGTAGCCAGGATGCTCTCGATCTC 2309
Db 96 TTTTGTGTTAGTAGACAGGTTTCACCGTGTAGCCAGGATGCTCTCGATCTC 37

QY 2310 CTGACCTCGTGATCCGCCACCTCGGCCTCCCAAAG 2345
Db 36 CTGACCTCGTGATCCATCCACCTCGGCCTCCCAAAG 1

RESULT 19
AX197487
LOCUS
DEFINITION Sequence 52 from Patent WO0151632.
ACCESSION AX197487
VERSION AX197487.1 GI:15387847
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Padigar,M., Prayaga,S.K., Taupier,R.J., Mishra,V., Tchernev,V.T.,

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Spvtek,K.A. and Li,L.
Odorant receptor polypeptides and nucleic acids encoding same
Patent: WO 0151632-A S2 19-JUL-2001;
Curagen Corporation (US)
Location/Qualifiers
source
1. .94
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 3.3%; Score 79; DB 1; Length 94;
Best Local Similarity 94.3%; Pred. No. 2.6;
Matches 82; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2286 GTTAGCCAGGATGCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTCCCAAAG 2345
|||||
Db 1 GTTAGCCAGGATGCTCTCAATCTCTGACCTCGTGATCCGCCCTGGCCTCCCAAAG 60
|||||

QY 2346 TGCTGGGATTACAGCATGAGCCACCG 2372
|||||
Db 61 TGCTGGGATTACAGCATGAGCCACTG 87
|||||

RESULT 20
AX911782/c
LOCUS AX911782 90 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 27645 from Patent EP1033401.
ACCESSION AX911782
VERSION AX911782.1 GI:40205571
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
Expressed sequence tags and encoded human proteins
Patent: EP 1033401-A 27645 06-SEP-2000;
Genset (FR)

FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 3.3%; Score 78.4; DB 1; Length 90;
Best Local Similarity 91.1%; Pred. No. 2.8;
Matches 82; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2250 TTTTGTGTTACTTTAGTAGACAGCGGTTTCACCGTTGTAGCCAGGATGGTCTCGATCTC 2309
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Db 90 TTTTGTGTTACTTTAGTAGACAGCGGTTTCACCGTTGTAGCCAGGATGGTCTCGATCTC 31
|||||

QY 2310 CTGACCTCGTGATCCGCCACCTCGGCCTC 2339
|||||
Db 30 CTGACCTCGTGATCCGCCACCTCGGCCTC 1
|||||

RESULT 21
BD047315/c
LOCUS BD047315 90 bp DNA linear PAT 27-AUG-2002
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD047315
VERSION BD047315.1 GI:22589057
KEYWORDS JP 2001269182-A/23561.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 90)
Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
Sequence tag and encoded human protein
Patent: JP 2001269182-A 23561 02-OCT-2001;

COMMENT GENSET
OS Homo sapiens (human)
PN JP 2001269182-A/23561
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES
FI JORDAN
PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10,
PC C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
G06F15/40
CC
FH Key Location/Qualifiers
1. .90
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 3.3%; Score 78.4; DB 1; Length 90;
Best Local Similarity 91.1%; Pred. No. 2.8;
Matches 82; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2250 TTTTGTGTTACTTTAGTAGACAGCGGTTTCACCGTTGTAGCCAGGATGGTCTCGATCTC 2309
|||||
Db 90 TTTTGTGTTACTTTAGTAGACAGCGGTTTCACCGTTGTAGCCAGGATGGTCTCGATCTC 31
|||||

QY 2310 CTGACCTCGTGATCCGCCACCTCGGCCTC 2339
|||||
Db 30 CTGACCTCGTGATCCGCCACCTCGGCCTC 1
|||||

RESULT 22
AX903206/c
LOCUS AX903206 86 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 19069 from Patent EP1033401.
ACCESSION AX903206
VERSION AX903206.1 GI:40058163
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
Expressed sequence tags and encoded human proteins
Patent: EP 1033401-A 19069 06-SEP-2000;
Genset (FR)

FEATURES
source
1. .86
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 3.3%; Score 78; DB 1; Length 86;
Best Local Similarity 94.2%; Pred. No. 2.8;
Matches 81; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2260 TTTTGTGTTACTTTAGTAGACAGCGGTTTCACCGTTGTAGCCAGGATGGTCTCGATCTC 2319
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Db 86 TTTTGTGTTACTTTAGTAGACAGCGGTTTCACCGTTGTAGCCAGGATGGTCTCGATCTC 27
|||||

QY 2320 GATCGCCGCCACCTCGGCCTCCCAAAG 2345
|||||
Db 26 GATCGCCGCCACCTCGGCCTCCCAAAG 1
|||||

RESULT 23
BD038739/c
LOCUS BD038739 86 bp DNA linear PAT 27-AUG-2002
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD038739

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VERSION      BD038739.1  GI:22580481
KEYWORDS     JP 2001269182-A/14985.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 86)
AUTHORS     Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
TITLE       Sequence tag and encoded human protein
JOURNAL     Patent: JP 2001269182-A 14985 02-OCT-2001;
GENSET
COMMENT     OS Homo sapiens (human)
            PN JP 2001269182-A/14985
            PD 22-OCT-2001
            PR 24-FEB-2000 JP 2000118773
            PR 26-FEB-1999 US 60/122487
            PI JEAN BAPTISTE DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES
            PI JORDAN
            PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21,PC
            PC C12N5/10,
            PC C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00,PC
            G06F15/40
            CC
            FH Key Location/Qualifiers.
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             /organism="Homo sapiens"
             /mol_type="genomic DNA"
             /db_xref="taxon:9606"
Query Match 3.3%; Score 78; DB 1; Length 86;
Best Local Similarity 94.2%; Pred. No. 2.8;
Matches 81; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2260 TTTTGTAGACAGAGGGTTTACCGTTGAGCAGAGTGTCTCGATCTCTGACCTCGT 2319
Db |||||
QY 2320 GATCCGCCACCTCGGCCTCCCAAAG 2345
Db |||||
RESULT 24
AX197472/c 92 bp DNA linear PAT 29-AUG-2001
LOCUS
DEFINITION Sequence 37 from Patent WO0151632.
ACCESSION AX197472
VERSION AX197472.1 GI:15387842
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE 1
AUTHORS Padigaru,M., Prayaga,S.K., Taupier,R.J., Mishra,V., Tchernev,V.T.,
        Spytek,K.A. and Li,L.
TITLE Odorant receptor polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0151632-A 37 19-JUL-2001;
        Curagen Corporation (US)
FEATURES     Location/Qualifiers
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             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"
Query Match 3.1%; Score 74.2; DB 1; Length 92;
Best Local Similarity 90.8%; Pred. No. 4.5;
Matches 79; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 2286 GTTAGCCAGATGGTCTCGATCTCCCTGACCTCGTGTATCGGCCACCTCGGCTCCCAAAG 2345
Db |||||
QY 92 GTTGACCAGGTTGGTCTCGAACAACCTGACCTCATGATCGGCCACCTCGGCTCCCAAAG 33

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QY 2346 TGTCTGGATTACAGGCATGAGCCACCG 2372
Db |||||
32 TGTCTGGATTACAGGCATGAGCCACCG 6
RESULT 25
BD074010/c 73 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD074010
VERSION BD074010.1 GI:22619613
KEYWORDS JP 2001513996-A/49.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 73)
AUTHORS Chen,J., Agrawal,S. and Zhang,R.
TITLE Antisense oligonucleotide specific to MDM2
JOURNAL Patent: JP 2001513996-A 49 11-SEP-2001;
        HYBRIDON INC
COMMENT     OS Unidentified
            PN JP 2001513996-A/49
            PD 11-SEP-2001
            PR 18-AUG-1998 JP 2000507794
            PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
            JIANDONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
            PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
            PC C12N15/00
            CC Strandedness: Both;
            CC Topology: Linear;
            CC Antisense oligonucleotide specific to MDM2
            FH Key Location/Qualifiers
            FT source
            FT 1..73
            /organism="Unidentified".
            /organism="Unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"
Query Match 3.1%; Score 73; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 665 AGGTACATCTGTGAGTGAGACAGGTGTCACTTGAGGTGGAGTGATCAAAAGACCT 724
Db |||||
73 AGGTACATCTGTGAGTGAGACAGGTGTCACTTGAGGTGGAGTGATCAAAAGACCT 14
QY 725 TGTACAAGAGCTT 737
Db |||||
13 TGTACAAGAGCTT 1
RESULT 26
AX901901/c 76 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 17764 from Patent EP1033401.
ACCESSION AX901901
VERSION AX901901.1 GI:40056815
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 17764 06-SEP-2000;
        Genset (FR)
FEATURES     Location/Qualifiers
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             /organism="Homo sapiens"

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 3.1%; Score 72.8; DB 1; Length 76;
Best Local Similarity 97.4%; Pred. No. 4.7;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2285 TGTTAGCAGGATGCTCTCGATCTCTGACCTCTGATCCGCGCCACCTCGGCTCCCAA 2344
|||||
Db 76 TGTTAGCAGGATGCTCTCGATCTCTGACCTCTGATCCGCGCCACCTCGGCTCCCAA 17
|||||

QY 2345 GTGCTGGGATTACAGG 2360
|||||
Db 16 GTGCTGGGATTACAGG 1

RESULT 27
BD037434/c
LOCUS
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD037434
VERSION BD037434.1 GI:22579176
KEYWORDS JP 2001269182-A/13680.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 13680 02-OCT-2001;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2001269182-A/13680
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES
PI JORDAN
PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10,
PC C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
G06F15/40
CC
FH Key Location/Qualifiers.
FEATURES
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 3.1%; Score 72.8; DB 1; Length 76;
Best Local Similarity 97.4%; Pred. No. 4.7;
Matches 74; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2285 TGTTAGCAGGATGCTCTCGATCTCTGACCTCTGATCCGCGCCACCTCGGCTCCCAA 2344
|||||
Db 76 TGTTAGCAGGATGCTCTCGATCTCTGACCTCTGATCCGCGCCACCTCGGCTCCCAA 17
|||||

QY 2345 GTGCTGGGATTACAGG 2360
|||||
Db 16 GTGCTGGGATTACAGG 1

RESULT 28
AX900729
LOCUS
DEFINITION Sequence 16592 from Patent EP1033401.
ACCESSION AX900729
VERSION AX900729.1 GI:40055643
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1
AUTHORS Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 16592 06-SEP-2000;
GENSET (FR)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 3.0%; Score 71.4; DB 1; Length 84;
Best Local Similarity 92.6%; Pred. No. 5.9;
Matches 75; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2248 AATTTTTGTACTTTTAGTAGACAGAGGGTTTCACCGTGTAGCCAGGATGCTCTCGATC 2307
|||||
Db 2 AATTTTTGTACTTTTAGTAGACAGAGGGTTTCACCGTGTAGCCAGGATGCTCTCGATC 61
|||||

QY 2308 TCCTGACCTCGTGATCCGCC 2328
|||||
Db 62 TCCTGACCTCGTGATCCGCC 82

RESULT 29
BD036262
LOCUS
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD036262
VERSION BD036262.1 GI:22578004
KEYWORDS JP 2001269182-A/12508.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 84)
AUTHORS Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 12508 02-OCT-2001;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2001269182-A/12508
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES
PI JORDAN
PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10,
PC C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
G06F15/40
CC
FH Key Location/Qualifiers.
FEATURES
source
1..84
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 3.0%; Score 71.4; DB 1; Length 84;
Best Local Similarity 92.6%; Pred. No. 5.9;
Matches 75; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2248 AATTTTTGTACTTTTAGTAGACAGAGGGTTTCACCGTGTAGCCAGGATGCTCTCGATC 2307
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Db 2 AATTTTTGTACTTTTAGTAGACAGAGGGTTTCACCGTGTAGCCAGGATGCTCTCGATC 61
|||||

QY 2308 TCCTGACCTCGTGATCCGCC 2328
|||||
Db 62 TCCTGACCTCGTGATCCGCC 82

QY 2251 TTTTGTACTTTTAGTAGACAGGGTTTACCGTGTGTAGCCAGGATGGTCTCGATCTCC 2310
 Db 1 TTTTGTATTTTAGTAGACAGGGTTTACCGTGTGTAGCCAGGATGGTCTCGATCTCC 60

QY 2311 TGACCTCGTGATCGGCCACCTCGGCCTCCC 2341
 Db 61 TGACCTGTGTATCCACCTCGCCTTGGCCTCCC 91

RESULT 34

BD035085
 LOCUS 92 bp DNA linear PAT 27-AUG-2002
 DEFINITION Sequence tag and encoded human protein.
 ACCESSION BD035085
 VERSION BD035085.1 GI:22576827
 KEYWORDS JP 2001269182-A/11331.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 92)
 AUTHORS Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
 TITLE Sequence tag and encoded human protein
 JOURNAL Patent: JP 2001269182-A 11331 02-OCT-2001;
 GENSET

COMMENT

OS Homo sapiens (human)
 PN JP 2001269182-A/11331
 PD 02-OCT-2001
 PF 24-FEB-2000 JP 2000118773
 PR 26-FEB-1999 US 60/122487
 PI JEAN BAPTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
 PC C12N15/09, C07K14/435, C12N1/15, C12N1/19, C12N1/21, PC
 C12N5/10,
 PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
 G06F15/40
 CC

FEATURES

source
 1..92
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

Query Match 3.0%; Score 70.2; DB 1; Length 92;
 Best Local Similarity 85.7%; Pred. No. 7.1;
 Matches 78; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2251 TTTTGTACTTTTAGTAGACAGGGTTTACCGTGTGTAGCCAGGATGGTCTCGATCTCC 2310
 Db 1 TTTTGTATTTTAGTAGACAGGGTTTACCGTGTGTAGCCAGGATGGTCTCGATCTCC 60

QY 2311 TGACCTCGTGATCGGCCACCTCGGCCTCCC 2341
 Db 61 TGACCTGTGTATCCACCTCGCCTTGGCCTCCC 91

RESULT 35

AR421270
 LOCUS 85 bp DNA linear PAT 18-DEC-2003
 DEFINITION Sequence 12767 from patent US 6639063.
 ACCESSION AR421270
 VERSION AR421270.1 GI:40176380
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 85)
 AUTHORS Edwards, J.-B.D.M., Jobert, S. and Giordano, J.-Y.
 TITLE EST's and encoded human proteins
 JOURNAL Patent: US 6639063-A 12767 28-OCT-2003;
 FEATURES Location/Qualifiers
 source 1..85

/organism="unknown"
 /mol_type="genomic DNA"

Query Match 2.8%; Score 66.6; DB 1; Length 85;
 Best Local Similarity 84.7%; Pred. No. 10;
 Matches 72; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 2258 ACTTTTAGTAGACAGAGGGTTTACCGTGTGTAGCCAGGATGGTCTCGATCTCTCGACCTC 2317
 Db 1 ATTTTTCATAGACATGGTTTCCACCATGTAGCCATGTGCTCGATCTCTCGACCTC 60

QY 2318 GTGATCGGCCACCTCGGCCTCCCA 2342
 Db 61 GTGATCCACATGCTTGGCCTCCYW 85

RESULT 36

AX981964
 LOCUS 85 bp DNA linear PAT 15-JAN-2004
 DEFINITION Sequence 12767 from Patent EP1104808.
 ACCESSION AX981964
 VERSION AX981964.1 GI:40988104
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Dumas Milne Edwards, J.B., Jobert, S. and Giordano, J.Y.
 TITLE ESTs and encoded human proteins
 JOURNAL Patent: EP 1104808-A 12767 06-JUN-2001;
 GENSET

FEATURES

source 1..85
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 2.8%; Score 66.6; DB 1; Length 85;
 Best Local Similarity 84.7%; Pred. No. 10;
 Matches 72; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 2258 ACTTTTAGTAGACAGAGGGTTTACCGTGTGTAGCCAGGATGGTCTCGATCTCTCGACCTC 2317
 Db 1 ATTTTTCATAGACATGGTTTCCACCATGTAGCCATGTGCTCGATCTCTCGACCTC 60

QY 2318 GTGATCGGCCACCTCGGCCTCCCA 2342
 Db 61 GTGATCCACATGCTTGGCCTCCYW 85

RESULT 37

BD116823
 LOCUS 85 bp DNA linear PAT 18-SEP-2002
 DEFINITION EST and encoded human protein.
 ACCESSION BD116823
 VERSION BD116823.1 GI:23211727
 KEYWORDS JP 2002010789-A/8900.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 85)
 AUTHORS Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.
 TITLE EST and encoded human protein
 JOURNAL Patent: JP 2002010789-A 8900 15-JAN-2002;
 GENSET CORP

OS Homo sapiens (human)
 PN JP 2002010789-A/8900
 PD 15-JAN-2002
 PF 07-AUG-2000 JP 2000280989
 PR 05-AUG-1999 US 60/147499
 PI JEAN BAPTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI

TITLE Neural thread protein gene expression and detection of Alzheimer's disease
JOURNAL Patent: US 5948634-A 91 07-SEP-1999;
FEATURES Location/Qualifiers
source 1..84
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 2.8%; Score 65.4; DB 1; Length 84;
Best Local Similarity 86.7%; Pred. No. 12;
Matches 72; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 2282 CCCTGTTAGCCAGATGGTCTCGATCTCTGACCTCTGTGATCGCCACCTCGGCTCCC 2341
Db 1 CCATGTTTCATCAGCGTGGTGTGCAACTCTCTGACCTCTGTGATCGCCGCGCTCAGCCTCCC 60

Qy 2342 AAAGTCTGGGATTACAGGCATG 2364
Db 61 AAAGTCTGGGATTACAGCGTG 83

RESULT 40
AR073206
LOCUS AR073206 84 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 91 from patent US 5948888.
ACCESSION AR073206
VERSION AR073206.1 GI:9999969
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 84)
AUTHORS de la Monte, S. and Wands, J.R.
TITLE Neural thread protein gene expression and detection of Alzheimer's disease
JOURNAL Patent: US 5948888-A 91 07-SEP-1999;
FEATURES Location/Qualifiers
source 1..84
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 2.8%; Score 65.4; DB 1; Length 84;
Best Local Similarity 86.7%; Pred. No. 12;
Matches 72; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 2282 CCCTGTTAGCCAGATGGTCTCGATCTCTGACCTCTGTGATCGCCACCTCGGCTCCC 2341
Db 1 CCATGTTTCATCAGCGTGGTGTGCAACTCTCTGACCTCTGTGATCGCCGCGCTCAGCCTCCC 60

Qy 2342 AAAGTCTGGGATTACAGGCATG 2364
Db 61 AAAGTCTGGGATTACAGCGTG 83

RESULT 41
AX900153
LOCUS AX900153 81 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 16016 from Patent EP1033401.
ACCESSION AX900153
VERSION AX900153.1 GI:40055067
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.
JOURNAL Expressed sequence tags and encoded human proteins
Patent: EP 1033401-A 16016 06-SEP-2000;
GenSet (FR)
FEATURES Location/Qualifiers
source 1..81
/organism="Homo sapiens"

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 2.6%; Score 62.2; DB 1; Length 81;
Matches 67; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 2253 TTGTACTTTTAGTAGACAGAGGTTTCACCGTGTAGCCAGGATGCTCGATCTCCTG 2312
Db 2 TATTNNNTTAAAGTAGACAGAGGTTTCATCGTGTGGCCAGGATGRTCTCAAACTCCTG 61

QY 2313 ACCTCGTATCGCCACC 2331
Db 62 ACCTCGTATCGCCGCC 80

RESULT 42
BD035686
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
TITLE
JOURNAL
Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
Sequence tag and encoded human protein
Patent: JP 2001269182-A 11932 02-OCT-2001;
GENSET
OS Homo sapiens (human)
PN JP 2001269182-A/11932
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
PI JORDAN
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
G06F15/40
CC
FH
Key Location/Qualifiers.
1..81
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 2.6%; Score 62.2; DB 1; Length 81;
Matches 67; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 2253 TTGTACTTTTAGTAGACAGAGGTTTCACCGTGTAGCCAGGATGCTCGATCTCCTG 2312
Db 2 TATTNNNTTAAAGTAGACAGAGGTTTCATCGTGTGGCCAGGATGRTCTCAAACTCCTG 61

QY 2313 ACCTCGTATCGCCACC 2331
Db 62 ACCTCGTATCGCCGCC 80

RESULT 43
CQ542955
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Sequence 12590 from Patent WO0210449.
CQ542955
CQ542955
CQ542955.1 GI:41509219
Homo sapiens (human)
Homo sapiens
```

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REFERENCE
AUTHORS
TITLE
JOURNAL
Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.
Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
Patent: WO 0210449-A 12590 07-FEB-2002;
Compugen Inc. (US)
FEATURES
source
1..60
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 2.5%; Score 60; DB 1; Length 60;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 TGACCCAGATCCTGCTGCTTTTCGACGACGAGCAGCGTCCCTCCCGGATTAGTGCCTA 157
Db 1 TGACCCAGATCCTGCTGCTTTTCGACGACGAGCAGCGTCCCTCCCGGATTAGTGCCTA 60

RESULT 44
AX523103/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AX523103
AX523103
AX523103.1 GI:24412057
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
TITLE
JOURNAL
Telerman, A., Amson, R., Tuijnder, M. and Susini, L.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
Patent: WO 02064731-A 773 22-AUG-2002;
Molecular Engines Laboratories (FR)
FEATURES
source
1..68
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 2.5%; Score 60; DB 1; Length 68;
Matches 63; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2256 GTACTTTTAGTAGACAGAGGTTTCACCGTGTAGCCAGGATGCTCGATCTCCTGACC 2315
Db 68 GTATTTTATAGACAGCGGTTTCACCATGTTAGTAGGATGCTCGATTTCTGACC 9

QY 2316 TCGTGATC 2323
Db 8 TCGTGATC 1

RESULT 45
AX523168/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AX523168
AX523168
AX523168.1 GI:24412122
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
TITLE
JOURNAL
Telerman, A., Amson, R., Tuijnder, M. and Susini, L.
```

<p>AUTHORS Meagher,M.J., Xu,J. and King,G.E.</p> <p>TITLE Compositions and methods for therapy and diagnosis of colon cancer</p> <p>JOURNAL Patent: WO 0173027-A 348 04-OCT-2001;</p> <p> CORIXA CORPORATION (US)</p>	
FEATURES	<p>source Location/Qualifiers</p> <p> 1..69</p> <p> /organism="Homo sapiens"</p> <p> /mol_type="unassigned DNA"</p> <p> /db_xref="taxon:9606"</p>
<p>Query Match 2.4%; Score 56.2; DB 1; Length 69;</p> <p>Best Local Similarity 88.4%; Pred. No. 29;</p> <p>Matches 61; Conservative 0; Mismatches 8; Indels 0; Gaps 0</p>	
Qy	2291 CCAGGATGGTCTCGATCTCTCGACTCGCTGATCCGCCACCTCGGCTCCCAAAGTGCTG 2350
Db	1 CCAGGCGGTCTCGACTCCAGACCTCATGATCCACCGCTTGCGCTCCCAAAGTGCTG 60
Qy	2351 GGATTACAG 2359
Db	61 GGATTACAG 69
<p>RESULT 48</p> <p>AX901137 65 bp DNA linear PAT 18-DEC-2003</p> <p>LOCUS Sequence 17000 from Patent EP1033401.</p> <p>DEFINITION AX901137</p> <p>ACCESSION AX901137.1 GI:40056051</p> <p>VERSION Homo sapiens (human)</p> <p>KEYWORDS Homo sapiens</p> <p>SOURCE Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi;</p> <p>ORGANISM Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p>	
REFERENCE	1 Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
AUTHORS	Expressed sequence tags and encoded human proteins
TITLE	Patent: EP 1033401-A 17000 06-SEP-2000;
JOURNAL	Genset (FR)
FEATURES	<p>source Location/Qualifiers</p> <p> 1..65</p> <p> /organism="Homo sapiens"</p> <p> /mol_type="unassigned DNA"</p> <p> /db_xref="taxon:9606"</p>
<p>Query Match 2.3%; Score 54.4; DB 1; Length 65;</p> <p>Best Local Similarity 90.6%; Pred. No. 34;</p> <p>Matches 58; Conservative 0; Mismatches 6; Indels 0; Gaps 0</p>	
Qy	2270 GACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCGGCCCA 2329
Db	1 GACGGGGTTTCCTCGTGTAGCCAGGATGGTCTCGATCTCTGACCTTGTAATCGGCCCA 60
Qy	2330 CCTC 2333
Db	61 CCGC 64
<p>RESULT 49</p> <p>BD036670 65 bp DNA linear PAT 27-AUG-2003</p> <p>LOCUS Sequence tag and encoded human protein.</p> <p>DEFINITION BD036670</p> <p>ACCESSION BD036670</p> <p>VERSION BD036670.1 GI:22578412</p> <p>KEYWORDS JP 2001269182-A/12916.</p> <p>SOURCE Homo sapiens (human)</p> <p>ORGANISM Homo sapiens</p> <p> Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi;</p> <p> Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p>	
REFERENCE	1 (bases 1 to 65)
AUTHORS	Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
TITLE	Sequence tag and encoded human protein
JOURNAL	Patent: JP 2001269182-A 12916 02-OCT-2001;

COMMENT OS Homo sapiens (human)
PN JP 2001269182-A/12916
PD 02-OCT-2001
PR 24-FEB-2000 JP 2000118773
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
PI JORDAN
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
G06F15/40
CC
FH Key Location/Qualifiers
FEATURES source
1.65
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 2.3%; Score 54.4; DB 1; Length 65;
Best Local Similarity 90.6%; Pred. No. 34;
Matches 58; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2270 GACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCCA 2329
Db 1 GACGGGGTTTCTGTGTAGCCAGGATGGTCTCGATCTCTGACCTGTGATTCGCCCA 60
QY 2330 CCTC 2333
Db 61 CGCG 64
RESULT 50
AX523219/c
LOCUS
DEFINITION Sequence 889 from Patent WO02064731.
ACCESSION AX523219
VERSION AX523219.1 GI:24412173
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman, A., Amson, R., Tuijnder, M. and Susini, L.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 02064731-A 889 22-AUG-2002;
Molecular Engines Laboratories (FR)
FEATURES source
1.60
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 2.2%; Score 52; DB 1; Length 60;
Best Local Similarity 91.7%; Pred. No. 43;
Matches 55; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2264 AGTAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATC 2323
Db 60 AGTAGATGGGGTTTCACTGTGTAGCCAGGATGTCTCCATCTCTGACCTCGTGATC 1
RESULT 51
AR416502/c
LOCUS
DEFINITION Sequence 7999 from patent US 6639063.
ACCESSION AR416502
VERSION AR416502.1 GI:40171612
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 68)
AUTHORS Edwards, J.-B.D.M., Jobert, S. and Giordano, J.-Y.
TITLE EST's and encoded human proteins
JOURNAL Patent: US 6639063-A 7999 28-OCT-2003;
FEATURES source
1.68
Location/Qualifiers
/organism="unknown DNA"
/mol_type="genomic DNA"
Query Match 2.2%; Score 52; DB 1; Length 68;
Best Local Similarity 85.3%; Pred. No. 46;
Matches 58; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 2189 TCTCCTGCCTCAGCCTCCCAATTAGCTTGCGCTACAGTCTCTGCCACACACCTGGCTA 2248
Db 68 TCTCCTGCCTCAGCCTCCCGAGTAGCTGGACTACAGGACCCGCCGCCGGCTA 9
QY 2249 ATTTTGTG 2256
Db 8 ATTTTGTG 1
RESULT 52
AX977196/c
LOCUS
DEFINITION Sequence 7999 from Patent EP1104808.
ACCESSION AX977196
VERSION AX977196.1 GI:40983336
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Dumas Milne Edwards, J.B., Jobert, S. and Giordano, J.Y.
TITLE ESTs and encoded human proteins
JOURNAL Patent: EP 1104808-A 7999 06-JUN-2001;
Genset (FR)
FEATURES source
1.68
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 2.2%; Score 52; DB 1; Length 68;
Best Local Similarity 85.3%; Pred. No. 46;
Matches 58; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 2189 TCTCCTGCCTCAGCCTCCCAATTAGCTTGCGCTACAGTCTCTGCCACACACCTGGCTA 2248
Db 68 TCTCCTGCCTCAGCCTCCCGAGTAGCTGGACTACAGGACCCGCCGCCGGCTA 9
QY 2249 ATTTTGTG 2256
Db 8 ATTTTGTG 1
RESULT 53
BD112055/c
LOCUS
DEFINITION EST and encoded human protein.
ACCESSION BD112055
VERSION BD112055.1 GI:23206873
KEYWORDS JP 2002010789-A/4132.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.

/gene="Scarlina"
/note="alternatively spliced epithelial sodium channel
alpha subunit containing intronic Alu sequence"

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PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTIST DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES
PC C12N15/09,C07K16/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10,
PC C12P21/02,C12P21/08,C12Q1/68/G06F17/30,C12N15/00,C12N5/00, PC
G06F15/40
CC
FH Key Location/Qualifiers.
FEATURES
    source
        1..64
        /organism="Homo sapiens"
        /mol_type="genomic DNA"
        /db_xref="taxon:9606"
Query Match 2.1%; Score 50.2; DB 1; Length 64;
Best Local Similarity 87.3%; Pred. No. 55;
Matches 55; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 2255 TGTACTTTTAGTAGACAGGGTTTCACCGTGTGTAGCCAGGATGGTCTCGATCTCTCGAC 2314
Db 2 TGTATTTTAGTAGACAGGGTTTCGCCATGTTGTCGGGCTGGTCTCGAACTCTCGAC 61
QY 2315 CTC 2317
Db 62 CTC 64
RESULT 59
AX322319
LOCUS
DEFINITION
ACCESSION AX322319
VERSION AX322319.1 GI:18093386
KEYWORDS
SOURCE
    ORGANISM
        Homo sapiens (human)
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
    1
    KRAMER,M.D., Winter,H. and Reinartz,J.
    Mrna molecules to be used as indicators of the functional and
    activation state of t-lymphocytes
    Patent: EP 1162276-A 192 12-DEC-2001;
    Lynx Therapeutics GmbH (DE)
FEATURES
    source
        1..63
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
Query Match 2.1%; Score 50; DB 1; Length 63;
Best Local Similarity 91.4%; Pred. No. 55;
Matches 53; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2250 TTTTGTACTTTTAGTAGACAGGGTTTCACCGTGTGTAGCCAGGATGGTCTCGATC 2307
Db 6 TTTTGTAAATTTTAGTAGATACGGGGTTTCACCGTGTGTAGCCAGGATGGTCTCGATC 63
RESULT 60
CQ006684/c
LOCUS
DEFINITION
ACCESSION CQ006684
VERSION CQ006684.1 GI:41013316
KEYWORDS
SOURCE
    ORGANISM
        Homo sapiens (human)
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTIST DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES
PC C12N15/09,C07K16/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10,
PC C12P21/02,C12P21/08,C12Q1/68/G06F17/30,C12N15/00,C12N5/00, PC
G06F15/40
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        /db_xref="taxon:9606"
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Best Local Similarity 85.1%; Pred. No. 52;
Matches 57; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 2251 TTTTGTACTTTTAGTAGACAGGGTTTCACCGTGTGTAGCCAGGATGGTCTCGATCTCC 2310
Db 67 TTTTGTATTTTAGCAGACAGGGTTTCACCATATTTGCCAGGTGGTCTCGAACTCC 8
QY 2311 TGACCTC 2317
Db 7 TGACCCC 1
RESULT 57
AX903935
LOCUS
DEFINITION
ACCESSION AX903935
VERSION AX903935.1 GI:40058892
KEYWORDS
SOURCE
    ORGANISM
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        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
    1
    Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
    Expressed sequence tags and encoded human proteins
    Patent: EP 1033401-A 19798 06-SEP-2000;
    Genset (FR)
FEATURES
    source
        1..64
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
Query Match 2.1%; Score 50.2; DB 1; Length 64;
Best Local Similarity 87.3%; Pred. No. 55;
Matches 55; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 2255 TGTACTTTTAGTAGACAGGGTTTCACCGTGTGTAGCCAGGATGGTCTCGATCTCTCGAC 2314
Db 2 TGTATTTTAGTAGACAGGGTTTCGCCATGTTGTCGGGCTGGTCTCGAACTCTCTGAC 61
QY 2315 CTC 2317
Db 62 CTC 64
RESULT 58
BD039468
LOCUS
DEFINITION
ACCESSION BD039468
VERSION BD039468.1 GI:22581210
KEYWORDS
SOURCE
    ORGANISM
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        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
    1 (bases 1 to 64)
    Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
    Sequence tag and encoded human protein
    Patent: JP 2001269182-A 15714 02-OCT-2001;
    Genset
COMMENT
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    PN JP 2001269182-A/15714

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REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
        methods of use thereof
JOURNAL Patent: WO 0147944-A 5324 05-JUL-2001;
        Curagen Corporation (US)
FEATURES
    source
        Location/Qualifiers
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                /db_xref="taxon:9606"
                /note="Accession number cg43287619"
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Best Local Similarity 98.0%; Pred. No. 53;
Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2292 CAGGATGGTCTCGATCTCCTGACCTCGTATCCGCCACCTCGGCTCCCA 2342
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||

51 CAGGATGGTCTCGATCTCCTGACCTCGTATCCGCCACCTCGGCTCCCA 1

RESULT 61
AR444760
LOCUS AR444760 51 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 1171 from patent US 6670464.
ACCESSION AR444760
VERSION AR444760.1 GI:42672539
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
        methods of use thereof
JOURNAL Patent: US 6670464-A 1171 30-DEC-2003;
FEATURES
    source
        Location/Qualifiers
            1..51
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                /mol_type="genomic DNA"
Query Match 2.0%; Score 48.4; DB 1; Length 51;
Best Local Similarity 98.0%; Pred. No. 59;
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2301 CTCGATCTCTGACCTCGATCCGCCACCTCGGCTCCCAAGTCTG 2350
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||

2 CTCGATCTCTGACCTCGATCCGCCACCTCGGCTCCCAAGTCTG 51

RESULT 62
HUMUT5223A/C
LOCUS HUMUT5223A 64 bp DNA linear STS 28-DEC-1994
DEFINITION Human STS 2223, 5' primer bind, sequence tagged site.
ACCESSION L31134
VERSION L31134.1 GI:604619
KEYWORDS STS; PCR primer; STS sequence; dinucleotide repeat; microsatellite
        DNA; microsatellite marker; sequence tagged site.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 64)
AUTHORS Gerken,S.C., Matsunami,N., Plaetke,R., Albertsen,H., Ballard,L.,
        Melis,R., Lawrence,E., Moore,M., Holik,P.R., Carlson,M., Zhao,X.,
        Robertson,M., Bradley,P., Elener,T., Tingey,A., Lalouel,J.-M. and
        White,R.
TITLE Genetic and physical mapping of simple sequence repeat containing
        sequence tagged sites from the human genome
JOURNAL Unpublished (1994)
COMMENT Original source text: Homo sapiens DNA.
        Submitted by: Utah Center for Human Genome Research University of

```

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Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
e-mail: sts@corona.med.utah.edu
Primer A: CACTGCACCTCCAGGCTGGG
Primer B: AGGTGAGGCTGCAGTGAGC
End to Label: Primer B
PCR Profile:
Initial Denaturation: 94C 300sec
Cycles Denaturation Annealing Extension 5 94
C 10 sec. 50 C 10 sec. 72 C 20 sec. 30
50 C 10 sec. 72 C 20 sec. Mg++: 0.00 mM
Gel: Acrylamide 7%, Formamide 32%, Urea 34%
Alleles: 0.
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Best Local Similarity 89.5%; Pred. No. 69;
Matches 51; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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59 TTTTATTTTTTTGGAGACAGAGCTCTGTCTCTGCCAGCTGGAGTGCAGTGGG 3

RESULT 63
AX161490
LOCUS AX161490 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 4818 from Patent WO0140521.
ACCESSION AX161490
VERSION AX161490.1 GI:14542821
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
        methods of use thereof
JOURNAL Patent: WO 0140521-A 4818 07-JUN-2001;
        Curagen Corporation (US)
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        Location/Qualifiers
            1..51
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Query Match 2.0%; Score 47.8; DB 1; Length 51;
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Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2292 CAGGATGGTCTCGATCTCCTGACCTCGTATCCGCCACCTCGGCTCCCA 2342
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||

1 CAGGATGGTCTCGATCTCCTGACCTCGTATCCGCCACCTCGGCTCCCA 51

RESULT 64
AX163313/C
LOCUS AX163313 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6641 from Patent WO0140521.
ACCESSION AX163313
VERSION AX163313.1 GI:14544644
KEYWORDS

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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE      1
JOURNAL    Shimkets,R.A. and Leach,M.
           Nucleic acids containing single nucleotide polymorphisms and
           methods of use thereof
           Patent: WO 0140521-A 6641 07-JUN-2001;
           Curagen Corporation (US)
FEATURES   Location/Qualifiers
source     1..51
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"
misc_feature 26
           /note="1 of 2 allelic variants (6642 is other entry)"
           Accession number cg42657675"

Query Match      2.0%; Score 47.8; DB 1; Length 51;
Best Local Similarity 96.1%; Pred. No. 63;
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2319 TGATCCGCCACCTCGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCA 2369
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Db 51 TGATCCGCCATCTCGGCTCCCAAATGCTGGGATTACAGGCATGAGCCA 1

RESULT 65
AX163451/c
LOCUS      AX163451
DEFINITION Sequence 6779 from Patent WO0140521.
ACCESSION  AX163451
VERSION    AX163451.1 GI:14544782
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Shimkets,R.A. and Leach,M.
TITLE     Nucleic acids containing single nucleotide polymorphisms and
           methods of use thereof
           Patent: WO 0140521-A 6779 07-JUN-2001;
           Curagen Corporation (US)
FEATURES   Location/Qualifiers
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           Accession number cg42657675"

Query Match      2.0%; Score 47.8; DB 1; Length 51;
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Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2318 GTGATCCGCCACCTCGGCTCCCAAAGTCTGGGATTACAGGCATGAGCC 2368
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Db 51 GTGATCCGCCATCTCGGCTCCCAAATGCTGGGATTACAGGCATGAGCC 1

RESULT 66
AX199317/c
LOCUS      AX199317
DEFINITION Sequence 247 from Patent WO0151670.
ACCESSION  AX199317
VERSION    AX199317.1 GI:15389696
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Shimkets,R.A. and Leach,M.D.
TITLE      Nucleic acids containing single nucleotide polymorphisms and
           methods of use thereof
           Patent: WO 0151670-A 247 19-JUL-2001;
           Curagen Corporation (US)
FEATURES   Location/Qualifiers
source     1..51
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           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"
misc_feature 26
           /note="1 of 2 allelic variants (248 is other entry)"
           Accession number cg39662754"

Query Match      2.0%; Score 47.8; DB 1; Length 51;
Best Local Similarity 96.1%; Pred. No. 63;
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2300 TCTGATCTCTGACCTCGATCGGCTCCGCCACCTCGGCTCCCAAAGTCTG 2350
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Db 51 TCTGATCTCTGACCTCGATCGGCTCCGCCACCTCGGCTCCCAAAGTCTG 1

RESULT 67
AX522922
LOCUS      AX522922
DEFINITION Sequence 592 from Patent WO02064731.
ACCESSION  AX522922
VERSION    AX522922.1 GI:24411876
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Telerman,A., Anson,R., Tuijnder,M. and Susini,L.
TITLE      Sequences involved in phenomena of tumour suppression, tumour
           reversion, apoptosis and/or virus resistance and their use as
           medicines
           Patent: WO 02064731-A 592 22-AUG-2002;
           Molecular Engines Laboratories (FR)
FEATURES   Location/Qualifiers
source     1..52
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Query Match      2.0%; Score 47.2; DB 1; Length 52;
Best Local Similarity 94.2%; Pred. No. 68;
Matches 49; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2256 GTACTTTTAGTAGACAGAGGTTTCACCGGTAGCCAGGATGCTCTCGATC 2307
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Db 1 GCATTTTAGTAGACAGAGGTTTCACCATGTTAGCCAGGATGCTCTCGATC 52

RESULT 68
AR444761
LOCUS      AR444761
DEFINITION Sequence 1172 from patent US 6670464.
ACCESSION  AR444761
VERSION    AR444761.1 GI:42672540
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
           1 (bases 1 to 51)
REFERENCE   Shimkets,R.A. and Leach,M.
AUTHORS    Nucleic acids containing single nucleotide polymorphisms and
TITLE      methods of use thereof
           Patent: US 6670464-A 1172 30-DEC-2003;
JOURNAL

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[illegible]

KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM
REFERENCE
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 012962-A 3124 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
Query Match 1.9%; Score 46.2; DB 1; Length 51;
Best Local Similarity 94.1%; Pred. No. 75;
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2304 GATCTCTGACCTGCTGATCGCCACCTCGGCTCCCAAGTCTGGAT 2354
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Db 51 GATCTCTGACCTGCTGATCGGCTCGGCTCCCAAGTCTGGAT 1
RESULT 74
AX161489
LOCUS AX161489 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 4817 from Patent WO0140521.
ACCESSION AX161489
VERSION AX161489.1 GI:14542820
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 4817 07-JUN-2001;
Curagen Corporation (US)
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Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2292 CAGGATGCTCGATCTCTGATCGGCTCGGCTCCCAAGTCTGGAT 2342
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Db 1 CAGGATGCTCGATCTCTGATCGGCTCGGCTCCCAAGTCTGGAT 51
RESULT 75
AX163314/c
LOCUS AX163314 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6642 from Patent WO0140521.
ACCESSION AX163314
VERSION AX163314.1 GI:14544645
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0138586-A 152 31-MAY-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
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Accession number CG42657675"
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Best Local Similarity 94.1%; Pred. No. 75;
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2319 TGATCGCCACCTCGGCTCCCAAGTCTGGATTCAGGCATGAGCCA 2369
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Db 51 TGATCGCCACCTCGGCTCCCAAGTCTGGATTCAGGCATGAGCCA 1
RESULT 76
AX163452/c
LOCUS AX163452 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6780 from Patent WO0140521.
ACCESSION AX163452
VERSION AX163452.1 GI:14544783
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 6780 07-JUN-2001;
Curagen Corporation (US)
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Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2318 GTGATCGCCACCTCGGCTCCCAAGTCTGGATTCAGGCATGAGCC 2368
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Db 51 GTGATCGCCACCTCGGCTCCCAAGTCTGGATTCAGGCATGAGCC 1
RESULT 77
AX164957
LOCUS AX164957 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 152 from Patent WO0138586.
ACCESSION AX164957
VERSION AX164957.1 GI:14545786
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0138586-A 152 31-MAY-2001;
Curagen Corporation (US)
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/db_xref="taxon:9606"
misc_feature
26
/note="2 of 2 allelic variants (6779 is other entry)
Accession number CG42657675"

TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 6642 07-JUN-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
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Best Local Similarity 94.1%; Pred. No. 75;
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|||||
Db 51 TGATCGCCACCTCGGCTCCCAAGTCTGGATTCAGGCATGAGCCA 1
RESULT 76
AX163452/c
LOCUS AX163452 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6780 from Patent WO0140521.
ACCESSION AX163452
VERSION AX163452.1 GI:14544783
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 6780 07-JUN-2001;
Curagen Corporation (US)
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QY 2318 GTGATCGCCACCTCGGCTCCCAAGTCTGGATTCAGGCATGAGCC 2368
|||||
Db 51 GTGATCGCCACCTCGGCTCCCAAGTCTGGATTCAGGCATGAGCC 1
RESULT 77
AX164957
LOCUS AX164957 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 152 from Patent WO0138586.
ACCESSION AX164957
VERSION AX164957.1 GI:14545786
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0138586-A 152 31-MAY-2001;
Curagen Corporation (US)
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/note="2 of 2 allelic variants (6779 is other entry)
Accession number CG42657675"

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FEATURES
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    /mol_type="unassigned DNA"
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variation
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Query Match
Best Local Similarity 1.9%; Score 46.2; DB 1; Length 51;
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2258 ACTTTAGTAGACAGGGTTTCCACCGTGTAGCCAGGATGGTCTCGATCT 2308
Db 1 ATTTTAGTAGACAGGGTTTCACTGTGTAGCCAGGATGGTCTCGATCT 51

RESULT 78
LOCUS AX199318/c 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 248 from Patent WO0151670.
ACCESSION AX199318
VERSION AX199318.1 GI:15389697
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shinkets, R.A. and Leach, M.D.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0151670-A 248 19-JUL-2001;
Curagen Corporation (US)
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    /db_xref="taxon:9606"
misc_feature
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    /notes="2 of 2 allelic variants (247 is other entry)"
    Accession number cg39662754"

Query Match
Best Local Similarity 1.9%; Score 46.2; DB 1; Length 51;
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2300 TCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTCCCAAGTGTG 2350
Db 51 TCTTGATCTCTGACCTCGTGATCCGCCACCTCGGCCTCCCAAGTGTG 1

RESULT 79
LOCUS AX116665 51 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 1788 from Patent WO0129262.
ACCESSION AX116665
VERSION AX116665.1 GI:14033607
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Picoult-Newburg, L. and Pohl, M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 1788 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES
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    /db_xref="taxon:9606"

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Best Local Similarity 1.9%; Score 45.8; DB 1; Length 51;
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QY 2300 TCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTCCCAAGTGTG 2350
Db 1 TCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCTCCCAAGTGTG 51

RESULT 80
LOCUS AX917839/c 57 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 33702 from Patent EP1033401.
ACCESSION AX917839
VERSION AX917839.1 GI:40211628
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 33702 06-SEP-2000;
Genset (FR)
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    /db_xref="taxon:9606"

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Best Local Similarity 1.9%; Score 45.8; DB 1; Length 57;
Matches 50; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2252 TTTTGTACTTTTAGTAGACAGGGTTTCCACCGTGTAGCCAGGATGGTCTCGATCT 2308
Db 57 TTTTGTACTTTTAGTAGACAGGGTTTCCACCGTGTAGCCAGGATGGTCTCGACT 1

RESULT 81
LOCUS BD053372/c 57 bp DNA linear PAT 27-AUG-2002
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD053372
VERSION BD053372.1 GI:22598978
KEYWORDS JP 2001269182-A/29618.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 29618 02-OCT-2001;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2001269182-A/29618
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
PI JORDAN
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

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Best Local Similarity 87.7%; Pred. No. 83;
Matches 50; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2552 TTTTGTTACTTTTAGTAGAGAGGGTTTCCACCGTGTAGCCAGGATGCTCGATCT 2308
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Db 57 TTTTGTTACTTTTAGTAGAGAGCGTGTTCACCGTGTTCACCGGATGCTCGAACT 1

RESULT 82
AY283614 50 bp DNA linear PRI 17-JUL-2003
LOCUS Homo sapiens KLK3 gene promoter region, partial sequence.
DEFINITION
ACCESSION AY283614
VERSION AY283614.1 GI:32879294
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Cramer,S.D., Cooke,B.-L., Rao,A., Hawkins,G.A., Chang,S.,
Wade,W.N., Cooke,R.T., Thomas,L.N., Bleecker,E.R., Catalona,W.J.,
Sterling,D.A., Meyers,D.A., Ohar,J. and Xu,J.
TITLE Association between Genetic Polymorphisms in the Prostate-specific
Antigen Gene Promoter and Serum Prostate-specific Antigen Levels
J. Natl. Cancer Inst. Monographs (2003) In press
REFERENCE 2 (bases 1 to 50)
AUTHORS Cramer,S.D., Xu,J. and Hawkins,G.A.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2003) Cancer Biology, Wake Forest University
School of Medicine, Medical Center Blvd, Winston-Salem, NC 27157,
USA
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Db 1 CGTGTAGCCAGGATGCTCGATCTCTGACCTCGTGATCTGCCACCT 50

RESULT 83
AX160937 51 bp DNA linear PAT 22-JUN-2001
LOCUS
DEFINITION Sequence 4265 from Patent WO0140521.
ACCESSION AX160937
VERSION AX160937.1 GI:14542268
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 4265 07-JUN-2001;
Curagen Corporation (US)
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/organism="Homo sapiens"
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Accession number cg3941567"

Query Match 1.9%; Score 45.2; DB 1; Length 51;
Best Local Similarity 94.0%; Pred. No. 84;
Matches 47; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2323 CGCCCCACCTCGGCCTCCCAAAGTGTGGGATTACAGGCATGAGCCACCG 2372
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Db 1 CTCTCCCGCTCGGCCTCCCAAAGTGTGGGATTACAGGCATGAGCCACCG 50

RESULT 84
AX163202 51 bp DNA linear PAT 22-JUN-2001
LOCUS
DEFINITION Sequence 6530 from Patent WO0140521.
ACCESSION AX163202
VERSION AX163202.1 GI:14544533
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 6530 07-JUN-2001;
Curagen Corporation (US)
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/db_xref="taxon:9606"
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Accession number cg38629253"

Query Match 1.9%; Score 45.2; DB 1; Length 51;
Best Local Similarity 94.0%; Pred. No. 84;
Matches 47; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2323 CGCCCCACCTCGGCCTCCCAAAGTGTGGGATTACAGGCATGAGCCACCG 2372
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Db 1 CCACCCACCTCGGCCTCCCAAAGTGTGGGATTACAGGCATGAGCCACCG 50

RESULT 85
AX117745/c 51 bp DNA linear PAT 11-MAY-2001
LOCUS
DEFINITION Sequence 2868 from Patent WO0129262.
ACCESSION AX117745
VERSION AX117745.1 GI:14034696
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 2868 26-APR-2001;
Orchid BioSciences, Inc. (US)
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Matches 47; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2306 TCTCCTGACCTCGTATCCGCCACCTCGGCCCTCCCAAGTGTGGGATTA 2356
|||||
Db 51 TCTCCTGACCTCGTATCCACCCACCCGCCCTCCCAAGGGGTGGATTA 1

RESULT 86
AX199153
LOCUS 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 83 from Patent WO0151670.
ACCESSION AX199153
VERSION AX199153.1 GI:15389504
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shinkets,R.A. and Leach,M.D.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0151670-A 83 19-JUL-2001;
Curagen Corporation (US)
FEATURES
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1. .51
/organism="Homo sapiens"
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Location/Qualifiers
misc_feature
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Query Match 1.9%; Score 44.6; DB 1; Length 51;
Best Local Similarity 92.2%; Pred. No. 90;
Matches 47; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2252 TTTTGTACTTTTATGATAGACAGGGTTTCAACCGTTGTAGCCAGGATGGTCT 2302
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Db 1 TTTTGTATTTTATGATAGACGGGGTTTCTCCGTGTATCCAGGATGGTCT 51

RESULT 87
AX160938
LOCUS 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 4266 from Patent WO0140521.
ACCESSION AX160938
VERSION AX160938.1 GI:14542269
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shinkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 4266 07-JUN-2001;
Curagen Corporation (US)
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1. .51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
Location/Qualifiers

REFERENCE 1
AUTHORS Shinkets,R.A. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 2868 26-APR-2001;
Orchid BioSciences, Inc. (US)
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Best Local Similarity 92.0%; Pred. No. 1e+02;
Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2323 CGGCCACCTCGGCCCTCCCAAGTGTGGGATTTACAGGCATGAGCCACCG 2372
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Db 1 CCTCCGCCCTCGGCCCTCCCAAGTGTGGGATTTACAGGCATGAGCCACCG 50

RESULT 88
AX163201
LOCUS 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6529 from Patent WO0140521.
ACCESSION AX163201
VERSION AX163201.1 GI:14544532
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shinkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 6529 07-JUN-2001;
Curagen Corporation (US)
FEATURES
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Location/Qualifiers
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QY 2323 CGGCCACCTCGGCCCTCCCAAGTGTGGGATTTACAGGCATGAGCCACCG 2372
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RESULT 89
AX157145/c
LOCUS 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 473 from Patent WO0140521.
ACCESSION AX157145
VERSION AX157145.1 GI:14538476
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shinkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 473 07-JUN-2001;
Curagen Corporation (US)
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Accession number cg44928115"

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QY 2324 CGCCACCTCGGCTCCCAAGTCTGGATTACGAGCATGAGCCACC 2371
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51 CGCGCGCTCGGCTCCCAAGTCTGGATTACGAGCTTGAGTCACC 4

Db

RESULT 90
AR444260/c
LOCUS AR444260 51 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 671 from patent US 6670464.
ACCESSION AR444260
VERSION AR444260.1 GI:42672039
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: US 6670464-A 671 30-DEC-2003;
FEATURES Location/Qualifiers
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Query Match 1.8%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 1.e+02;
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Db

RESULT 91
AR444714
LOCUS AR444714 51 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 1125 from patent US 6670464.
ACCESSION AR444714
VERSION AR444714.1 GI:42672493
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: US 6670464-A 1125 30-DEC-2003;
FEATURES Location/Qualifiers
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Query Match 1.8%; Score 43; DB 1; Length 51;
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Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2252 TTTTGACTTTTAGTAGACAGGGTTTCACCGTTAGCCAGATGGTCT 2302
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51 TTTTGATTTTATTAGTAGACGGGGTTTCACCATGTGGCCAGCGTGGTCT 1

Db

RESULT 92
AX159798/c
LOCUS AX159798 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 3126 from Patent WO0140521.
ACCESSION AX159798
VERSION AX159798.1 GI:14541129
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 3126 07-JUN-2001;
FEATURES Location/Qualifiers
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Accession number cg42920603"

Query Match 1.8%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 1.e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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RESULT 93
AX159805/c
LOCUS AX159805 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 3133 from Patent WO0140521.
ACCESSION AX159805
VERSION AX159805.1 GI:14541136
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 3133 07-JUN-2001;
FEATURES Location/Qualifiers
source 1..51
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Best Local Similarity 90.2%; Pred. No. 1.e+02;
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QY 2262 TTAGTAGACAGCGGTTTCACCGTTAGCCAGATGGTCTCGATCTCCTG 2312
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Db

RESULT 94
AX163302
LOCUS AX163302 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6630 from Patent WO0140521.

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Accession number cg44928115"

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Best Local Similarity 93.8%; Pred. No. 1.e+02;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db

RESULT 90
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LOCUS AR444260 51 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 671 from patent US 6670464.
ACCESSION AR444260
VERSION AR444260.1 GI:42672039
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: US 6670464-A 671 30-DEC-2003;
FEATURES Location/Qualifiers
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Db

RESULT 91
AR444714
LOCUS AR444714 51 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 1125 from patent US 6670464.
ACCESSION AR444714
VERSION AR444714.1 GI:42672493
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: US 6670464-A 1125 30-DEC-2003;
FEATURES Location/Qualifiers
source 1..51
/organism="unknown"
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Query Match 1.8%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 1.e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2252 TTTTGACTTTTAGTAGACAGGGTTTCACCGTTAGCCAGATGGTCT 2302
|||||
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Db

RESULT 92
AX163302
LOCUS AX163302 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6630 from Patent WO0140521.

ACCESSION AX163302
VERSION AX163302.1 GI:14544633
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 6630 07-JUN-2001;
Curagen Corporation (US)
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Db 1 TCTCGAACTCTGACCTCAAGATCGGCTCGCTCGGCTCCCAAAGTGCTG 51
RESULT 95
AX163480/c
LOCUS AX163480 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6808 from Patent WO0140521.
ACCESSION AX163480
VERSION AX163480.1 GI:14544811
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 6808 07-JUN-2001;
Curagen Corporation (US)
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/db_xref="taxon:9606"
misc_feature 26
/notes="2 of 2 allelic variants (6807 is other entry)
Accession number CG42487874"
Query Match 1.8%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 1.1e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2264 AGTAGAGACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCCTGAC 2314
|||||
Db 51 AGTAGAGACGGGGCTTACCGTGTAGCCAGGATGGTCTCAAACCTCCTGAC 1
RESULT 96
AX189877/c
LOCUS AX189877 51 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 56 from Patent WO0147942.
ACCESSION AX189877
VERSION AX189877.1 GI:15143248
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0147942-A 56 05-JUL-2001;
Curagen Corporation (US)
FEATURES
source
1. .51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="2 of 2 allelic variants (55 is other
entry)-Accession number CG42869755"
Query Match 1.8%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 1.1e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2308 TCTGACCTCGTGATCGGCCACCTCGGCTCCCAAAGTGCTGGATTACA 2358
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Db 51 TACTGACCTCGTGATCCACCTGCCACGGCTCCCAAAGTGCTGGATTACA 1
RESULT 97
AX199154
LOCUS AX199154 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 84 from Patent WO0151670.
ACCESSION AX199154
VERSION AX199154.1 GI:15389505
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shimkets, R.A. and Leach, M.D.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0151670-A 84 19-JUL-2001;
Curagen Corporation (US)
FEATURES
source
1. .51
/organism="Homo sapiens"
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/db_xref="taxon:9606"
misc_feature 26
/notes="2 of 2 allelic variants (83 is other entry)
Accession number CG44918284"
Query Match 1.8%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 1.1e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2252 TTTTGTACTTTTAGTAGACACAGGGTTTCACCGTGTAGCCAGGATGGTCT 2302
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Db 1 TTTTGTATTTTAGTAGACACGGGGCTTCTCCGTGTATTCCAGGATGGTCT 51
RESULT 98
AX199335/c
LOCUS AX199335 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 265 from Patent WO0151670.
ACCESSION AX199335
VERSION AX199335.1 GI:15389716
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.D.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0151670-A 265 19-JUL-2001;
AUTHORS Curagen Corporation (US)
TITLE Location/Qualifiers
FEATURES
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="1 of 2 allelic variants (266 is other entry)"
Accession number CG43011316"
Query Match 1.8%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 1.1e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2261 TTCTAGTACAGACGGGTTTACCGTGTAGCCAGGATGCTCGATCTCCT 2311
|||||
Db 51 TTCTAGTACAGACGGGTTTACCGTGTAGCCAGGATGCTCGATCTCCT 1
|||||
RESULT 99
LOCUS AX199357 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 287 from Patent WO0151670.
ACCESSION AX199357
VERSION AX199357.1 GI:15389742
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.D.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0151670-A 287 19-JUL-2001;
AUTHORS Curagen Corporation (US)
TITLE Location/Qualifiers
FEATURES
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="1 of 2 allelic variants (288 is other entry)"
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Query Match 1.8%; Score 43; DB 1; Length 51;
Best Local Similarity 90.2%; Pred. No. 1.1e+02;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2264 AGTAGAGACGGGTTTACCGTGTAGCCAGGATGCTCGATCTCCTGAC 2314
|||||
Db 1 AGTAGAGACGGGTTTACCGTGTAGCCAGGATGCTCGATCTCCTGAC 51
|||||
RESULT 100
LOCUS AY283615 50 bp DNA linear PRI 17-JUL-2003
DEFINITION Homo sapiens KLK3 gene promoter region, partial sequence.
ACCESSION AY283615
VERSION AY283615.1 GI:32879295
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Cramer,S.D., Chang,B.-L., Rao,A., Hawkins,G.A., Chang,S.,
Wade,W.N., Cooke,R.T., Thomas,L.N., Bleecker,E.R., Catalona,W.J.,

Sterling,D.A., Meyers,D.A., Ohar,J. and Xu,J.
TITLE Association between Genetic Polymorphisms in the Prostate-specific Antigen Gene Promoter and Serum Prostate-specific Antigen Levels
JOURNAL J. Natl. Cancer Inst. Monographs (2003) In press
AUTHORS Cramer,S.D., Xu,J. and Hawkins,G.A.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2003) Cancer Biology, Wake Forest University School of Medicine, Medical Center Blvd, Winston-Salem, NC 27157, USA
FEATURES
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/map="19q13.4"
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/notes="PSA"
<1..>50
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/note="in white population"
/frequency="0.02"
/replaces="g"
Query Match 1.8%; Score 42.6; DB 1; Length 50;
Best Local Similarity 91.8%; Pred. No. 1.1e+02;
Matches 45; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2319 TGATCGCCACCTCGCGCTCCCAAGTGTGGGATTACAGGATGAGC 2367
|||||
Db 2 TGATCGCCACCTCGCGCTCCCAAGTGTGGGATGACAGCGGTGAGC 50
|||||
RESULT 101
LOCUS AR288911/c 47 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 646 from patent US 6537751.
ACCESSION AR288911
VERSION AR288911.1 GI:31676195
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 47)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 646 25-MAR-2003;
FEATURES
source 1..47
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.8%; Score 42.4; DB 1; Length 47;
Best Local Similarity 93.5%; Pred. No. 1.1e+02;
Matches 43; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2261 TTCTAGTACAGACGGGTTTACCGTGTAGCCAGGATGCTCGAT 2306
|||||
Db 47 TTCTAGTACAGACGGGTTTACCTGTGTAGCCAGGATGCTCGAT 2
|||||
RESULT 102
LOCUS AX114379/c 47 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 48 from Patent WO0129257.
ACCESSION AX114379
VERSION AX114379.1 GI:14031343
KEYWORDS

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Schork, N. and Skierczynski, B.
 TITLE Methods of genetic cluster analysis and use thereof
 JOURNAL Patent: WO 0129257-A 48 26-APR-2001;
 GENSET (FR)
 FEATURES
 source Location/Qualifiers
 1. .47
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 variation 24
 /notes="99-1602-200 : polymorphic base G or C"
 Query Match 1.8%; Score 42.4; DB 1; Length 47;
 Best Local Similarity 93.5%; Pred. No. 1.1e+02;
 Matches 43; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2261 TTATGATAGACAGCGGTTTACCGTGTAGCCAGGATGGTCTCGAT 2306
 |||||
 Db 47 TTATGATAGACCGGGTTTCTCTGTAGCCAGGATGGTCTCGAT 2
 |||||
 RESULT 103
 AX156682/c
 LOCUS AX156682 51 bp DNA linear PAT 22-JUN-2001
 DEFINITION Sequence 6454 from Patent WO0140521.
 ACCESSION AX156682
 VERSION AX163126.1 GI:14544457
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Shinkets, R.A. and Leach, M.
 TITLE Nucleic acids containing single nucleotide polymorphisms and
 methods of use thereof
 JOURNAL Patent: WO 0140521-A 6454 07-JUN-2001;
 Curagen Corporation (US)
 FEATURES
 source Location/Qualifiers
 1. .51
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 Accession number cg43287601"
 Query Match 1.8%; Score 42.2; DB 1; Length 51;
 Best Local Similarity 93.8%; Pred. No. 1.2e+02;
 Matches 44; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2271 ACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTC 2317
 |||||
 Db 1 ACAGGGTTTACCGTGTAGCCAGGATGGTCTGAACTCTGACCTC 47
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 RESULT 104
 AX156682/c
 LOCUS AX156682 51 bp DNA linear PAT 22-JUN-2001
 DEFINITION Sequence 10 from Patent WO0140521.
 ACCESSION AX156682
 VERSION AX156682.1 GI:14537802
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1

AUTHORS Shinkets, R.A. and Leach, M.
 TITLE Nucleic acids containing single nucleotide polymorphisms and
 methods of use thereof
 JOURNAL Patent: WO 0140521-A 10 07-JUN-2001;
 Curagen Corporation (US)
 FEATURES
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 /db_xref="taxon:9606"
 misc_feature 26
 /notes="2 of 2 allelic variants (9 is other entry)"
 Accession number cg42918213"
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 Best Local Similarity 90.0%; Pred. No. 1.2e+02;
 Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 2089 TTATTTTGTGAGACCGAGTCTTGTCTGTATACCAGGCTGGAGTGCAG 2138
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 Db 50 TTCTTTTGTGAGACAGAGTCTCGCTCTGTGCCCGAGGCTGGAGTGCAG 1
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 RESULT 105
 AX159128
 LOCUS AX159128 51 bp DNA linear PAT 22-JUN-2001
 DEFINITION Sequence 2456 from Patent WO0140521.
 ACCESSION AX159128
 VERSION AX159128.1 GI:14540459
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Shinkets, R.A. and Leach, M.
 TITLE Nucleic acids containing single nucleotide polymorphisms and
 methods of use thereof
 JOURNAL Patent: WO 0140521-A 2456 07-JUN-2001;
 Curagen Corporation (US)
 FEATURES
 source Location/Qualifiers
 1. .51
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 /db_xref="taxon:9606"
 misc_feature 26
 /notes="2 of 2 allelic variants (2455 is other entry)"
 Accession number cg39602254"
 Query Match 1.8%; Score 42; DB 1; Length 51;
 Best Local Similarity 90.0%; Pred. No. 1.2e+02;
 Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 2268 GAGACAGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTC 2317
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 Db 1 GAGACAGGTTTACCATCTTGACCAGGCTGGTCTCGAACTCTGACCTC 50
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 RESULT 106
 AX163383
 LOCUS AX163383 51 bp DNA linear PAT 22-JUN-2001
 DEFINITION Sequence 6711 from Patent WO0140521.
 ACCESSION AX163383
 VERSION AX163383.1 GI:14544714
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Shinkets, R.A. and Leach, M.
 TITLE Nucleic acids containing single nucleotide polymorphisms and
 methods of use thereof

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source
1. .51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
26
misc_feature
notes="1 of 2 allelic variants (6588 is other entry)
Accession number cg43273813"
1.8%; Score 41.6; DB 1; Length 51;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2241 CCTGGCTAATTTTCTACTTTTAGTAGACAGCGGTTTCACCGTGT 2288
|||||
Db 48 CCTGGCTAATTTTATATATTTTAGTAGACGGGTTTCACCATGTT 1

RESULT 109
AX910629
LOCUS AX910629 52 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 26492 from Patent EP1033401.
ACCESSION AX910629
VERSION AX910629.1 GI:40066709
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 26492 06-SEP-2000;
Genset (FR)

FEATURES
source
1. .52
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
1.8%; Score 41.6; DB 1; Length 52;
Best Local Similarity 86.5%; Pred. No. 1.3e+02;
Matches 45; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2255 TGCTACTTTTAGTAGACAGCGTTTCACCGTGTAGCCAGGATGCTCGAT 2306
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Db 1 TGCTATTTTGBAGACAGCGGTTTCGCCATGTTGCCAGGATGGTCTCGAT 52

RESULT 110
BD046162
LOCUS BD046162 52 bp DNA linear PAT 27-AUG-2002
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD046162
VERSION BD046162.1 GI:22587904
KEYWORDS JP 2001269182-A/22408.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 52)
REFERENCE
AUTHORS Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 22408 02-OCT-2001;
GENSET
COMMENT
OS Homo sapiens (human)
PN JP 2001269182-A/22408
PD 02-OCT-2001
PE 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
PT JORDAN
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10.

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PC	C12P21/02	C12P21/08	C12Q1/68	/G06F17/30	C12N15/00	C12N5/00	FP
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				/db_xref="taxon:9606"			
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Best Local Similarity			86.5%;	Pred No. 1.3e+02;			
Matches	45;	Conservative	1;	Mismatches	6;	Indels	0; Gaps 0;
Qy	2255	TGTA	CTTTT	TTAGTAGAGACAGGGTTTCACCGTGT	TAGCCAGGATGGTCTCGAT	2306	
Db	1	TGTATTTT	TG	BAGAGACGGGGTTTCGCCATGTTG	CGCAGGATGGTCTCGAT	52	
RESULT 111							
AR444261/c							
LOCUS	AR444261			51 bp	DNA	linear	PAT 20-FEB-2004
DEFINITION	Sequence	672	from patent	US 6670464.			
ACCESSION	AR444261						
VERSION	AR444261.1	GI:42672040					
KEYWORDS							
SOURCE	Unknown.						
ORGANISM	Unclassified.						
REFERENCE	1	(bases 1 to 51)					
AUTHORS	Shimkets,R.A. and Leach,M.						
TITLE	Nucleic acids containing single nucleotide polymorphisms and						
	methods of use thereof						
JOURNAL	Patent: US 6670464-A	672 30-DEC-2003;					
FEATURES	Location/Qualifiers						
source	1..51			/organism="unknown"			
	/mol_type="genomic DNA"						
Query Match			1.7%;	Score 41.4;	DB 1;	Length 51;	
Best Local Similarity			88.2%;	Pred No. 1.3e+02;			
Matches	45;	Conservative	0;	Mismatches	6;	Indels	0; Gaps 0;
Qy	2252	TTTTGTACTTTT	TTAGTAGAGACAGGGTTTCACCGTGT	TAGCCAGGATGGTCT	2302		
Db	51	TTTTGTATTTT	TAGTAGAGACGGGGCTT	CACCATGTTGGCCAGGCTGTCT	1		
RESULT 112							
AR444502							
LOCUS	AR444502			51 bp	DNA	linear	PAT 20-FEB-2004
DEFINITION	Sequence	913	from patent	US 6670464.			
ACCESSION	AR444502						
VERSION	AR444502.1	GI:42672281					
KEYWORDS							
SOURCE	Unknown.						
ORGANISM	Unclassified.						
REFERENCE	1	(bases 1 to 51)					
AUTHORS	Shimkets,R.A. and Leach,M.						
TITLE	Nucleic acids containing single nucleotide polymorphisms and						
	methods of use thereof						
JOURNAL	Patent: US 6670464-A	913 30-DEC-2003;					
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	/mol_type="genomic DNA"						
Query Match			1.7%;	Score 41.4;	DB 1;	Length 51;	
Best Local Similarity			88.2%;	Pred No. 1.3e+02;			
Matches	45;	Conservative	0;	Mismatches	6;	Indels	0; Gaps 0;
Qy	2262	TTAGTAGAGACAGGGTTT	TACCGTGT	TAGCCAGGATGGTCTCGAT	2312		

REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 3125 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1..51
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misc_feature 26
/note="1 of 2 allelic variants (3126 is other entry)"
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Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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|||||
Db 51 TGTATTTTAGTAGACAGGGTTTACCATGTTGGCCAGGCTGGTCTCGA 1
RESULT 120
AX159806/c
LOCUS AX159806 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 3134 from Patent WO0140521.
ACCESSION AX159806
VERSION AX159806.1 GI:14541137
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 3134 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1..51
/organism="Homo sapiens"
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/db_xref="taxon:9606"
misc_feature 26
/note="2 of 2 allelic variants (3133 is other entry)"
Accession number cg42924993"
Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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|||||
Db 51 TTAGTAGACAGGGTTTACCATGCTGGCCAGGCTGGTCTCGAATCTCTG 1
RESULT 121
AX160263/c
LOCUS AX160263 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 3591 from Patent WO0140521.
ACCESSION AX160263
VERSION AX160263.1 GI:14541594
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 3591 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="1 of 2 allelic variants (3592 is other entry)"
Accession number cg43318557"
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Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2225 GTCATCTGCCACACACCTGGCTTAATTTTGTACTTTTAGTAGACACAGG 2275
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Db 51 GGCACCTGCCACCATCTGCTGAATTTTGTATTTTAGTAGACACAGG 1
RESULT 122
AX163301
LOCUS AX163301 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6629 from Patent WO0140521.
ACCESSION AX163301
VERSION AX163301.1 GI:14544632
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 6629 07-JUN-2001;
Curagen Corporation (US)
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1..51
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misc_feature 26
/note="1 of 2 allelic variants (6630 is other entry)"
Accession number cg43090974"
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Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2300 TCTCGATCTCCTGACCTCGTGATCCGCCACCTCGCCCTCCCAAGTGCTG 2350
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Db 1 TCTCGAATCTCCTGACCTCAAGATCCACCTGCTCGCCCTCCCAAGTGCTG 51
RESULT 123
AX163479/c
LOCUS AX163479 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6807 from Patent WO0140521.
ACCESSION AX163479
VERSION AX163479.1 GI:14544810
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 6807 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="1 of 2 allelic variants (6630 is other entry)"
Accession number cg43090974"

methods of use thereof
Patent: WO 0140521-A 3591 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="1 of 2 allelic variants (3592 is other entry)"
Accession number cg43318557"
Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2225 GTCATCTGCCACACACCTGGCTTAATTTTGTACTTTTAGTAGACACAGG 2275
|||||
Db 51 GGCACCTGCCACCATCTGCTGAATTTTGTATTTTAGTAGACACAGG 1
RESULT 122
AX163301
LOCUS AX163301 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6629 from Patent WO0140521.
ACCESSION AX163301
VERSION AX163301.1 GI:14544632
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 6629 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="1 of 2 allelic variants (6630 is other entry)"
Accession number cg43090974"
Query Match 1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2300 TCTCGATCTCCTGACCTCGTGATCCGCCACCTCGCCCTCCCAAGTGCTG 2350
|||||
Db 1 TCTCGAATCTCCTGACCTCAAGATCCACCTGCTCGCCCTCCCAAGTGCTG 51
RESULT 123
AX163479/c
LOCUS AX163479 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6807 from Patent WO0140521.
ACCESSION AX163479
VERSION AX163479.1 GI:14544810
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 6807 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="1 of 2 allelic variants (6630 is other entry)"
Accession number cg43090974"

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FEATURES
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    Location/Qualifiers
      1..51
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
      26
        misc_feature
          /note="1 of 2 allelic variants (6808 is other entry)"
          Accession number CG42487874"

Query Match
  Best Local Similarity 1.7%; Score 41.4; DB 1; Length 51;
  Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2264 AGTAGACAGCGGCTTACCGCTGTACCGAGGATGCTCGATCTCTGAC 2314
Db 51 AGTAGACAGCGGCTTACCGCTGTACCGCTGTGCGCAGGATGGTCTCAAACTCTGAC 1

RESULT 124
LOCUS AX164872 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 67 from Patent WO0138586.
ACCESSION AX164872
VERSION AX164872.1 GI:14545701
KEYWORDS
SOURCE
  ORGANISM
    Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 Shimkets, R.A. and Leach, M.
  Nucleic acids containing single nucleotide polymorphisms and
  methods of use thereof
  Patent: WO 0138586-A 67 31-MAY-2001;
  Curagen Corporation (US)
FEATURES
  source
    Location/Qualifiers
      1..51
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
      26
        variation
          /note="single nucleotide polymorphism"
          Accession number CG43957170"

Query Match
  Best Local Similarity 1.7%; Score 41.4; DB 1; Length 51;
  Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2218 GCCTACAGTCATCTGCCACACACCTGGCTAAATTTTGTACTTTTAGTAG 2268
Db 51 GACTACAGGATGCCACACACCGCTGCTAAATTTTGTACTTTTAGTAG 1

RESULT 125
LOCUS AX189876/c 51 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 55 from Patent WO0147942.
ACCESSION AX189876
VERSION AX189876.1 GI:15143247
KEYWORDS
SOURCE
  ORGANISM
    Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 Shimkets, R.A. and Leach, M.
  Nucleic acids containing single nucleotide polymorphisms and
  methods of use thereof
  Patent: WO 0147942-A 55 05-JUL-2001;
  Curagen Corporation (US)
FEATURES
  source
    Location/Qualifiers
      1..51
        /organism="Homo sapiens"

FEATURES
  source
    Location/Qualifiers
      1..51
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
      26
        misc_feature
          /note="1 of 2 allelic variants (6808 is other entry)"
          Accession number CG42487874"

Query Match
  Best Local Similarity 1.7%; Score 41.4; DB 1; Length 51;
  Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2308 TCCTGACCTCGTATCGCCACCTCGGCTCCCAAAAGTGTGGGATTACA 2358
Db 51 TACTGACCTCGTATCGCCACCTCGGCTCCCAAAAGTGTGGGATTACA 1

RESULT 126
LOCUS AX190286/c 51 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 465 from Patent WO0147942.
ACCESSION AX190286
VERSION AX190286.1 GI:15143665
KEYWORDS
SOURCE
  ORGANISM
    Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 Shimkets, R.A. and Leach, M.
  Nucleic acids containing single nucleotide polymorphisms and
  methods of use thereof
  Patent: WO 0147942-A 465 05-JUL-2001;
  Curagen Corporation (US)
FEATURES
  source
    Location/Qualifiers
      1..51
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
      26
        variation
          /note="1 of 2 allelic variants (466 is other entry)"
          Accession number CG43080072"

Query Match
  Best Local Similarity 1.7%; Score 41.4; DB 1; Length 51;
  Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2319 TGATCGCCACCTCGGCTCCCAAAAGTGTGGGATTACAGGATGAGCCA 2369
Db 51 TGATCCACTCGCTTCGGCTCCCAAAAGTGTGGGATTATAGCGTGAGCCA 1

RESULT 127
LOCUS AX199155 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 85 from Patent WO0151670.
ACCESSION AX199155
VERSION AX199155.1 GI:15389506
KEYWORDS
SOURCE
  ORGANISM
    Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 Shimkets, R.A. and Leach, M.D.
  Nucleic acids containing single nucleotide polymorphisms and
  methods of use thereof
  Patent: WO 0151670-A 85 19-JUL-2001;
  Curagen Corporation (US)
FEATURES
  source
    Location/Qualifiers
      1..51
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
      26
        misc_feature
          /note="1 of 2 allelic variants (86 is other entry)"
          Accession number CG43130275"
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Query Match          1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2245 GCTAAATTTTGTACTTTTAGTAGAGACAGGGTTTACCGGTGTAGCAGG 2295
Db 1 GCTAAATTTTGTATTTTAAATAGAGACGGGATTCACCATGTGTGGCCAGG 51

RESULT 128
AX199159/c
LOCUS AX199159 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 89 from Patent WO0151670.
ACCESSION AX199159
VERSION AX199159.1 GI:15389510
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.D.
TITLE Nucleic acids containing single nucleotide polymorphisms and
METHODS of use thereof
JOURNAL Patent: WO 0151670-A 89 19-JUL-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="1 of 2 allelic variants (90 is other entry)"
Accession number CG42657675"

Query Match          1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2279 TCACCGGTGTAGCAGGATGTTCTCGATCTCCGTGACCTCGATCGGCCCA 2329
Db 51 TCATCATGTGTTGCCAGGATGCTTGTGATTTCTTCCTGACCTCGTATCGGCCCA 1

RESULT 129
AX199336/c
LOCUS AX199336 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 266 from Patent WO0151670.
ACCESSION AX199336
VERSION AX199336.1 GI:15389717
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.D.
TITLE Nucleic acids containing single nucleotide polymorphisms and
METHODS of use thereof
JOURNAL Patent: WO 0151670-A 266 19-JUL-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="2 of 2 allelic variants (265 is other entry)"
Accession number CG43011316"

Query Match          1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;

QY 2261 TTTAGTAGACAGAGGTTTTCACCGTGTAGCCAGGATGGTCTCGATCTCCT 2311
Db 51 TTTAGTAGACAGAGGTTTTCACCATATTTGCCAGGCTGGTCTCAAACTCCT 1

RESULT 130
AX199358
LOCUS AX199358 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 288 from Patent WO0151670.
ACCESSION AX199358
VERSION AX199358.1 GI:15389743
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.D.
TITLE Nucleic acids containing single nucleotide polymorphisms and
METHODS of use thereof
JOURNAL Patent: WO 0151670-A 288 19-JUL-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="2 of 2 allelic variants (287 is other entry)"
Accession number CG41584420"

Query Match          1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2264 AGTAGAGACAGGAGGTTTTCACCGTGTAGCCAGGATGGTCTCGATCTCTGAC 2314
Db 1 AGTAGAGACAGGAGGTTTTCACCATGTTGCCAGGCTGGTCTCAAACTCTGAC 51

RESULT 131
AX199370/c
LOCUS AX199370 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 300 from Patent WO0151670.
ACCESSION AX199370
VERSION AX199370.1 GI:15389761
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.D.
TITLE Nucleic acids containing single nucleotide polymorphisms and
METHODS of use thereof
JOURNAL Patent: WO 0151670-A 300 19-JUL-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="2 of 2 allelic variants (299 is other entry)"
Accession number CG43973526"

Query Match          1.7%; Score 41.4; DB 1; Length 51;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2318 GTGATCCGCCACCTCGGCTCCCAAAGTGTCTGGGATTACAGGATGAGCC 2368

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Qy	2096	TTTGTGAGACCGAGTCTTGCTCTGTTATCCAGGGCTGGAGTGCACTGG	2141
Db	51	TTTAGAGACAGAGTCTTGCTCTGTTATCCAGGGCTGGAGTACACTGG	6
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RESULT	134		

PAT 24-OCT-2002
linear
DNA
52 bp
Sequence 184 from Patent WO02064731.
AX522514
AX522514
AX522514.1 GI:24411468
Homo sapiens (human)

AA522514/C
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

Accession number cg43287601"

Query Match 1.7%; Score 40.6; DB 1; Length 51;
Best Local Similarity 91.5%; Pred. No. 1.4e+02;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2271 ACAGGGTTTACCGGTTAGCAGGATGCTCGATCTCCGACCTC 2317
|||||
Db 1 ACAGGGTTTACCGGTTAGCAGGATGCTCGATCTCCGACCTC 47
|||||

RESULT 141
AX199684/c
LOCUS AX199684 50 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 614 from Patent WO0151670.
ACCESSION AX199684
VERSION AX199684.1 GI:15390125
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.D.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0151670-A 614 19-JUL-2001;
Curagen Corporation (US)

FEATURES
source
Location/Qualifiers
1..50

/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

misc_feature 25..26
/note="Nucleotide deleted between bases 25 and 26"

misc_feature 26
Accession number cg42925267"

/note="2 of 2 allelic variants (613 is other entry)"

Query Match 1.7%; Score 40.4; DB 1; Length 50;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2294 GGATGGTCTCGATCTCCTGACCTCGTGATCGGCCACCTCGGCTCCCAA 2343
|||||
Db 50 GGATGGTCTCGATCTCCTTACCTGATGATCACCCTCGGCTCCCAA 1
|||||

RESULT 142
AR444500
LOCUS AR444500 51 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 911 from patent US 6670464.
ACCESSION AR444500
VERSION AR444500.1 GI:42672279

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: US 6670464-A 911 30-DEC-2003;
Curagen Corporation (US)

FEATURES
source
Location/Qualifiers
1..51

/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.7%; Score 40.4; DB 1; Length 51;
Best Local Similarity 97.6%; Pred. No. 1.4e+02;
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2330 CCTCGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACC 2371

Db 1 CCTCAGCCTCCCAAGTCTGGGATTACAGGCATGAGCCACC 42
|||||

RESULT 143
AX156681/c
LOCUS AX156681 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 9 from Patent WO0140521.
ACCESSION AX156681
VERSION AX156681.1 GI:14537800

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 9 07-JUN-2001;
Curagen Corporation (US)

FEATURES
source
Location/Qualifiers
1..51

/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

misc_feature 26
/note="1 of 2 allelic variants (10 is other entry)"

Accession number cg42918213"

Query Match 1.7%; Score 40.4; DB 1; Length 51;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2089 TTATTTTTTTGAGACGAGTCTTGCTCTGTACCCAGGCTGGAGTGCAG 2138
|||||
Db 50 TTCTTTTTTTGAGACAGATCTCTCTGCTCGCCAGGCTGGAGTGCAG 1
|||||

RESULT 144
AX159127

LOCUS AX159127 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 2455 from Patent WO0140521.
ACCESSION AX159127

VERSION AX159127.1 GI:14540458
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 2455 07-JUN-2001;
Curagen Corporation (US)

FEATURES
source
Location/Qualifiers
1..51

/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

misc_feature 26
/note="1 of 2 allelic variants (2456 is other entry)"

Accession number cg39602254"

Query Match 1.7%; Score 40.4; DB 1; Length 51;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2268 GAGACAGGGTTTACCCTGTTACCGAGGATGGTCTCGATCTCTGACCTC 2317
|||||
Db 1 GAGACAGGGTTTACCCTGTTGACCGGCTGGTCTCGAACTCTCTGACCTC 50
|||||

KEYWORDS Homo sapiens (human)
SOURCE ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 246 07-JUN-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..51
/morganism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="2 of 2 allelic variants (245 is other entry)"
Accession number CG17872027"
Query Match 1.7%; Score 40; DB 1; Length 51;
Best Local Similarity 89.6%; Pred. No. 1.5e+02;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2318 GTGATCGGCCACTCGCCCTCCCAAGTCTCGGATTACAGGATGA 2365
|||||
Db 4 GTGATCCTCTCGCTCGGCCCTCCCAAGTCTCGGATTACAGATATGA 51
|||||
RESULT 148
LOCUS AX163260/c 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6588 from Patent WO0140521.
ACCESSION AX163260
VERSION AX163260.1 GI:14544591
KEYWORDS Homo sapiens (human)
SOURCE ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 6588 07-JUN-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..51
/morganism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="2 of 2 allelic variants (6587 is other entry)"
Accession number CG43273813"
Query Match 1.7%; Score 40; DB 1; Length 51;
Best Local Similarity 89.6%; Pred. No. 1.5e+02;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2241 CTTGGCTAATTTTGTACTTTAGTAGACAGGGTTTCACCGTGT 2288
|||||
Db 48 CTTGGCTAATTTTGTATTTTTCAGTAGACAGGGGTTTCACCATGTT 1
|||||
RESULT 149
LOCUS AX523088 51 bp DNA linear PAT 24-OCT-2002
DEFINITION Sequence 758 from Patent WO02064731.
ACCESSION AX523088
VERSION AX523088.1 GI:24412042
KEYWORDS Homo sapiens (human)
SOURCE ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Telerman, A., Amson, R., Tuijnder, M. and Susini, L.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines

JOURNAL

Patent: WO 02064731-A 758 22-AUG-2002;

FEATURES

source
Location/Qualifiers
1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.7%; Score 40; DB 1; Length 51;

Best Local Similarity 89.6%; Pred. No. 1.5e+02;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGACAGAGGTTTACCGTGTAGCCAGGATGCTCGATC 2307

Db 4 TTTTAGTAGAGATGGGGTTTCAACAATGTTGCCAGGATGCTCGATC 51

RESULT 150

AR444503 AR444503 51 bp DNA linear PAT 20-FEB-2004
LOCUS Sequence 914 from patent US 6670464.
DEFINITION AR444503
ACCESSION AR444503.1 GI:42672282
VERSION AR444503.1
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE

AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: US 6670464-A 914 30-DEC-2003;
FEATURES Location/Qualifiers
source
1..51
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.7%; Score 39.8; DB 1; Length 51;

Best Local Similarity 86.3%; Pred. No. 1.5e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2262 TTAGTAGACAGAGGTTTACCGTGTAGCCAGGATGCTCGATCCTG 2312

Db 1 TTAGTAGACAGCGGGTTTACCATGCTGTCAGGCTGCTCGAACTCCTG 51

RESULT 151

AX156683/c AX156683 51 bp DNA linear PAT 22-JUN-2001
LOCUS Sequence 11 from Patent WO0140521.
DEFINITION AX156683
ACCESSION AX156683.1 GI:14537804
VERSION AX156683.1
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 11 07-JUN-2001;

FEATURES

source
Location/Qualifiers
1..51
/organism="Homo sapiens"

/mol_type="unassigned DNA"
/db_xref="taxon:9606"

misc_feature

26
/notes="1 of 2 allelic variants (12 is other entry)
Accession number cg42918213"

Query Match 1.7%; Score 39.8; DB 1; Length 51;

Best Local Similarity 86.3%; Pred. No. 1.5e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2087 TATTATTTTTTTGAGACCGAGTCTTCTGTTTACCGAGCTGGAGTGCA 2137

Db 51 TTTTCTTTTTTTGAGACAGAGTCTCACTCTGTGCGCCGAGGCTGGAGTGCA 1

RESULT 152

AX158064/c AX158064 51 bp DNA linear PAT 22-JUN-2001
LOCUS Sequence 1392 from Patent WO0140521.
DEFINITION AX158064
ACCESSION AX158064
VERSION AX158064.1 GI:14539395
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 1392 07-JUN-2001;
FEATURES Curagen Corporation (US)
source
Location/Qualifiers
1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

misc_feature

26
/notes="2 of 2 allelic variants (1391 is other entry)
Accession number cg29337682"

Query Match 1.7%; Score 39.8; DB 1; Length 51;

Best Local Similarity 86.3%; Pred. No. 1.5e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2320 GATCCGCCACCTCGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCAC 2370

Db 51 GATCCTCTGCTCAGCCTCCCAAATTTGCTGGGATTACAGGCATGCCACCAC 1

RESULT 153

AX158592/c AX158592 51 bp DNA linear PAT 22-JUN-2001
LOCUS Sequence 1920 from Patent WO0140521.
DEFINITION AX158592
ACCESSION AX158592
VERSION AX158592.1 GI:14539923
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 1920 07-JUN-2001;

FEATURES

source
Location/Qualifiers
1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

misc_feature

26

/note="2 of 2 allelic variants (1919 is other entry)
Accession number cg36753762"

Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 1.5e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2262 TTAGTAGAGACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCCTG 2312
Db 51 TTAGTAGAGACAGGGTTTACCGTGTAGCCAGGATGGTCTTGAACCTCCTG 1

RESULT 154
AX159067/c
LOCUS AX159067 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 2395 from Patent WO0140521.
ACCESSION AX159067
VERSION AX159067.1 GI:14540398
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 2395 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source 1. .51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="1 of 2 allelic variants (2396 is other entry)
Accession number cg39574041"

Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 1.5e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2294 GGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGCGCTCCAAA 2344
Db 51 GGCTGGTCTCAAACTCTGATCTGTGTCATCCGCCCGCGCTCGGCTCCAAA 1

RESULT 155
AX159069/c
LOCUS AX159069 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 2397 from Patent WO0140521.
ACCESSION AX159069
VERSION AX159069.1 GI:14540400
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 2397 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source 1. .51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="1 of 2 allelic variants (2398 is other entry)
Accession number cg39574041"

/note="2 of 2 allelic variants (1919 is other entry)
Accession number cg36753762"

Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 1.5e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2262 TTAGTAGAGACAGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCCTG 2312
Db 51 TTAGTAGAGACAGGGTTTACCGTGTAGCCAGGATGGTCTTGAACCTCCTG 1

RESULT 154
AX159067/c
LOCUS AX159067 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 2395 from Patent WO0140521.
ACCESSION AX159067
VERSION AX159067.1 GI:14540398
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 2395 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source 1. .51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="1 of 2 allelic variants (2396 is other entry)
Accession number cg39574041"

Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 1.5e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2294 GGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGCGCTCCAAA 2344
Db 51 GGCTGGTCTCAAACTCTGATCTGTGTCATCCGCCCGCGCTCGGCTCCAAA 1

RESULT 155
AX159069/c
LOCUS AX159069 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 2397 from Patent WO0140521.
ACCESSION AX159069
VERSION AX159069.1 GI:14540400
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 2397 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source 1. .51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="1 of 2 allelic variants (2398 is other entry)
Accession number cg39574041"

QY 2320 GATCGCCACCTCGGCTCCCAAGTCTGGATTACAGCATGAGCCAC 2370
|||||
Db 51 GATCCTCTGCTTTGGCTCCCAAGTCTGGATTATAGGCATGAGCCGC 1

RESULT 158
AX161023/c
LOCUS AX161023 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 4351 from Patent WO0140521.
ACCESSION AX161023
VERSION AX161023.1 GI:14542354
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Shimkets, R.A. and Leach, M.
AUTHORS Nucleic acids containing single nucleotide polymorphisms and
TITLE Methods of use thereof
JOURNAL Patent: WO 0140521-A 4351 07-JUN-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="1 of 2 allelic variants (4352 is other entry)
Accession number CG43948257"

Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 1.5e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2202 CCTCCCAATTAGCTGGCTACGTCTGCCACACACCTGGCTAATTT 2252
|||||
Db 51 CCTCCCAATTAGCTGGCTACGTCTGCCACACACCTGGCTAATTT 1

RESULT 159
AX164908/c
LOCUS AX164908 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 103 from Patent WO0138586.
ACCESSION AX164908
VERSION AX164908.1 GI:14545737
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Shimkets, R.A. and Leach, M.
AUTHORS Nucleic acids containing single nucleotide polymorphisms and
TITLE Methods of use thereof
JOURNAL Patent: WO 0138586-A 103 31-MAY-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
variation 26
/note="single nucleotide polymorphism
Accession number CG43265754"

Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 1.5e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2254 TTGTACTTTTAGTAGACAGGGTTTCACCGTGTAGCCAGGATGGTCTCG 2304
|||||

Db 51 TTGTACTTTTAGTAGAGATGGGTTGCACCATGTGTGCCAGGCTGGTCTCG 1

RESULT 160
AX190287/c
LOCUS AX190287 51 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 466 from Patent WO0147942.
ACCESSION AX190287
VERSION AX190287.1 GI:15143666
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Shimkets, R.A. and Leach, M.
AUTHORS Nucleic acids containing single nucleotide polymorphisms and
TITLE Methods of use thereof
JOURNAL Patent: WO 0147942-A 466 05-JUL-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="2 of 2 allelic variants (465 is other entry) ~Accession number CG43080072"

Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 1.5e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2319 TGATCGCCACCTCGGCTCCCAAGTCTGGATTACAGCATGAGCCA 2369
|||||
Db 51 TGATCCACTCGCTCGCTCCCAAGTCTGGATTATAGCGGTGAGCCA 1

RESULT 161
AX199156/c
LOCUS AX199156 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 86 from Patent WO0151670.
ACCESSION AX199156
VERSION AX199156.1 GI:15389507
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Shimkets, R.A. and Leach, M.D.
AUTHORS Nucleic acids containing single nucleotide polymorphisms and
TITLE Methods of use thereof
JOURNAL Patent: WO 0151670-A 86 19-JUL-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="2 of 2 allelic variants (85 is other entry)
Accession number CG43130275"

Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 1.5e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2245 GCTAATTTTGTACTTTTAGTAGACAGCGGTTTACCGTGTAGCCAGG 2295
|||||
Db 1 GCTAATTTTGTATTTTAAATAGAAACGGGGATTACCATGTGTGGCCAGG 51

RESULT 162

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AX199160/c
LOCUS AX199160 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 90 from Patent WO0151670.
ACCESSION AX199160
VERSION AX199160.1 GI:15389511
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
misc_feature
26
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="2 of 2 allelic variants (89 is other entry)"
Accession number cg42657675"

Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 1.5e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2279 TCACCGGTGTAGCAGGATGCTCGATCTCCGACCTCGTATCGGCCCA 2329
|||||
DB 51 TCATCATGTGTCAGGATGCTCTTAATTTCTCGACCTCGTATCGGCCCA 1

RESULT 163
AX199168/c
LOCUS AX199168 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 98 from Patent WO0151670.
ACCESSION AX199168
VERSION AX199168.1 GI:15389520
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
misc_feature
26
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="2 of 2 allelic variants (97 is other entry)"
Accession number cg43273813"

Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 1.5e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2214 CTTGGCCTACGATCATCTGCCACACACCTGGCTAATTTTGTACTTTTA 2264
|||||
DB 51 CTGGGACTACAGGCATATGCCACACGCTGGCTAATTTTATATTTTA 1

RESULT 164
AX199369/c
LOCUS AX199369 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 299 from Patent WO0151670.

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ACCESSION AX199369
VERSION AX199369.1 GI:15389759
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
misc_feature
26
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="1 of 2 allelic variants (300 is other entry)"
Accession number cg43973526"

Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 1.5e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2318 GTGATCCGCCACCTCGGCTCCCAAAGTCTGGGATTACAGGCATGAGCC 2368
|||||
DB 51 GTGATCCATCCGCTTGGCTCCAGAGTCTGGGATTACAGCGGAGGCC 1

RESULT 165
AX199404/c
LOCUS AX199404 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 334 from Patent WO0151670.
ACCESSION AX199404
VERSION AX199404.1 GI:15389799
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
misc_feature
26
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="2 of 2 allelic variants (333 is other entry)"
Accession number cg43926000"

Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 1.5e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2267 AGAGACAGGTTTCACCGTGTAGCCAGGATGCTCGATCTCCTGACCTC 2317
|||||
DB 51 AGAGACGGGTTTCCACCAATTTGGCCAGGCTGGTCTTGAACCTCCTGACCTC 1

RESULT 166
AX199417/c
LOCUS AX199417 51 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 347 from Patent WO0151670.
ACCESSION AX199417
VERSION AX199417.1 GI:15389814
KEYWORDS

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Patent: JP 2001269182-A 14913 02-OCT-2001;

GENSET
OS Homo sapiens (human)
PN JP 2001269182-A/14913
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PI 26-FEB-1999 US 60/122487
PRI JEAN BAPTISTE DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES
PJ JORDAN
PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10,
PC C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
G06F15/40

CC
FH Key Location/Qualifiers.
source location/Qualifiers
1..51
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 1.7%; Score 39.8; DB 1; Length 51;
Best Local Similarity 86.3%; Pred. No. 1.5e+02;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2086 TTATTATTTTTTGGAGACCGAGTCCTGTCTGTACCAGGCTGGAGTGCC 2136
|||||
||| TTTTATTTTTTTGGAGATGGAGTCTCACTCTGTGCCAGGCTGGAGTGCC 1

Db 51 TTTTATTTTTTTGGAGATGGAGTCTCACTCTGTGCCAGGCTGGAGTGCC 1

RESULT 169
AX163311/c
LOCUS AX163311 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6639 from Patent WO0140521.
ACCESSION AX163311
VERSION AX163311.1 GI:14544642
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Shinkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 6639 07-JUN-2001;
Curagen Corporation (US)

FEATURES
source location/Qualifiers
1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

misc_feature
26
/note="1 of 2 allelic variants (6640 is other entry)"
Accession number cg38821538"

Query Match 1.7%; Score 39.6; DB 1; Length 51;
Best Local Similarity 91.3%; Pred. No. 1.5e+02;
Matches 42; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2096 TTTTAGACCGAGTCCTGTCTGTACCAGGCTGGAGTGCGAGTGG 2141
|||||
||| TTTTAGACAGAGCTCTGTCTGTGTGCCAGGCTGGAGTACAGTGG 6

Db 51 TTTTAGACAGAGCTCTGTCTGTGTGCCAGGCTGGAGTACAGTGG 6

RESULT 170
AX163193/c
LOCUS AX163193 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6521 from Patent WO0140521.
ACCESSION AX163193
VERSION AX163193.1 GI:14544524
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 5221 07-JUN-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/notes="1 of 2 allelic variants (6522 is other entry)"
Accession number cg39667665"

Query Match 1.7%; Score 39.4; DB 1; Length 51;
Best Local Similarity 97.6%; Pred. No. 1.6e+02;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 GTGATCGCCGCTCGGCTCCCAAGTCTGGGATTACA 2358
|||||
Db 41 GTGATCGCCGCTCGGCTCCCAAGTCTGGGATTACA 1
|||||

RESULT 171
AX199669 51 bp DNA linear PAT 29-AUG-2001
LOCUS
DEFINITION Sequence 599 from Patent WO0151670.
ACCESSION AX199669
VERSION AX199669.1 GI:15390109
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.D.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0151670-A 599 19-JUL-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/notes="1 of 2 allelic variants (600 is other entry)"
Accession number cg43130275"

Query Match 1.7%; Score 39.4; DB 1; Length 51;
Best Local Similarity 87.8%; Pred. No. 1.6e+02;
Matches 43; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2232 GCCACACACCTGGCTAATTTTGTACTTTTAGTAGACAGCGTTTC 2280
|||||
Db 3 GCCACACACCCAGCTAATTTTGTATTTTATATAGACGGGGATTC 51
|||||

RESULT 172
AX161914 51 bp DNA linear PAT 22-JUN-2001
LOCUS
DEFINITION Sequence 5242 from Patent WO0140521.
ACCESSION AX161914
VERSION AX161914.1 GI:14543245
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 5242 07-JUN-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/notes="2 of 2 allelic variants (5241 is other entry)"
Accession number cg43988015"

Query Match 1.7%; Score 39.2; DB 1; Length 51;
Best Local Similarity 93.2%; Pred. No. 1.6e+02;
Matches 41; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2329 ACCTCGGCTCCCAAGTCTGGGATTACAGGCATGAGCACCG 2372
|||||
Db 1 ACCTTGGCTCCCAAGTCTGGGACTACAGGCATGAGCACCG 44
|||||

RESULT 173
AX161651/c 51 bp DNA linear PAT 22-JUN-2001
LOCUS
DEFINITION Sequence 4979 from Patent WO0140521.
ACCESSION AX161651
VERSION AX161651.1 GI:14542982
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 4979 07-JUN-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/notes="1 of 2 allelic variants (4980 is other entry)"
Accession number cg43979411"

Query Match 1.6%; Score 39; DB 1; Length 51;
Best Local Similarity 89.4%; Pred. No. 1.6e+02;
Matches 42; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2326 CCCATCTCGGCTCCCAAGTCTGGGATTACAGGCATGAGCACCG 2372
|||||
Db 50 CTTGCTCAGCTCCCAAGTCTGAGGATTACAGGCATGAGCACCTG 4
|||||

RESULT 174
AX161487 51 bp DNA linear PAT 22-JUN-2001
LOCUS
DEFINITION Sequence 4815 from Patent WO0140521.
ACCESSION AX161487
VERSION AX161487.1 GI:14542818
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and

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methods of use thereof
Patent: WO 0140521-A 4815 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source
1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
26
misc_feature
/note="1 of 2 allelic variants (4816 is other entry)"
Accession number cg43971764"

Query Match
Best Local Similarity 1.6%; Score 38.9; DB 1; Length 51;
Matches 50; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2248 AATTTTGTACTTTTAGTAGACAGGGTTTCACCGTGTAGCCAGGATGG 2299
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Db 1 AATTTTGTATTTTATTAGTAGAC-GGGTTTCACCGTGTAGCCAGGATGG 51

RESULT 175
AX161488
LOCUS
DEFINITION
Sequence 4816 from Patent WO0140521.
ACCESSION
AX161488.1 GI:14542819
VERSION
AX161488.1
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
Curagen Corporation (US)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Shinkets, R.A. and Leach, M.
TITLE
Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL
Patent: WO 0140521-A 4816 07-JUN-2001;
Curagen Corporation (US)
FEATURES
Location/Qualifiers
source
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
26
misc_feature
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Accession number cg43971764"

Query Match
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Matches 50; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2248 AATTTTGTACTTTTAGTAGACAGGGTTTCACCGTGTAGCCAGGATGG 2299
|||||
Db 1 AATTTTGTATTTTATTAGTAGACA-GGTTTCACCGTGTAGCCAGGATGG 51

RESULT 176
AR444501
LOCUS
DEFINITION
Sequence 912 from patent US 6670464.
ACCESSION
AR444501
VERSION
AR444501.1 GI:42672280
KEYWORDS
Unknown.
SOURCE
Unknown.
Curagen Corporation (US)
ORGANISM
Unknown.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 51)
AUTHORS
Shinkets, R.A. and Leach, M.
TITLE
Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL
Patent: US 6670464-A 912 30-DEC-2003;
Curagen Corporation (US)
FEATURES
Location/Qualifiers
source
1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
26
misc_feature
/note="1 of 2 allelic variants (1826 is other entry)"
Accession number cg35097892"

methods of use thereof
Patent: WO 0140521-A 4815 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
26
misc_feature
/note="1 of 2 allelic variants (4816 is other entry)"
Accession number cg43971764"

Query Match
Best Local Similarity 1.6%; Score 38.8; DB 1; Length 51;
Matches 40; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2330 CCTGGCCTCCCAAGTGTGGGATTACAGGCATGAGCCACC 2371
|||||
Db 1 CCTCAGCCTCCCAAGTGTGGGATCAGAGGCATGAGCCACC 42

RESULT 177
AX158432
LOCUS
DEFINITION
Sequence 1760 from Patent WO0140521.
ACCESSION
AX158432
VERSION
AX158432.1 GI:14539763
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
Curagen Corporation (US)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Shinkets, R.A. and Leach, M.
TITLE
Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL
Patent: WO 0140521-A 1760 07-JUN-2001;
Curagen Corporation (US)
FEATURES
Location/Qualifiers
source
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
26
misc_feature
/note="2 of 2 allelic variants (1759 is other entry)"
Accession number cg34750113"

Query Match
Best Local Similarity 1.6%; Score 38.8; DB 1; Length 51;
Matches 43; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2089 TTATTTTGTGACACGAGTCTGCTCTGTTACCCAGGCTGGAGTGCAG 2138
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Db 2 TTTATTTGTTTGACACAGAGTCTGCTCTGTTGCTAGGCTGGAGTGCAG 51

RESULT 178
AX158497
LOCUS
DEFINITION
Sequence 1825 from Patent WO0140521.
ACCESSION
AX158497
VERSION
AX158497.1 GI:14539828
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
Curagen Corporation (US)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Shinkets, R.A. and Leach, M.
TITLE
Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL
Patent: WO 0140521-A 1825 07-JUN-2001;
Curagen Corporation (US)
FEATURES
Location/Qualifiers
source
1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
26
misc_feature
/note="1 of 2 allelic variants (1826 is other entry)"
Accession number cg35097892"
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Query Match	1.6%; Score 38.8; DB 1; Length 51;				
Best Local Similarity	86.0%; Pred. No. 1.7e+02;				
Matches	43; Conservative 0; Mismatches 7; Indels 0; Gaps 0;				
<hr/>					
Qy	2256 GTACTTTTAGTAGACAGCGGTTTTCCACGGTGTAGCCAGGATGCTTCGA 2305				
Dd	1 GTATTTTCAGTAGACAGCGGTTTTACCATGTTGCCAGGCTGGTCTCGA 50				
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RESULT 179					
AXI58578/c				PAT 22-JUN-2001	
LOCUS	AXI58578	51 bp DNA linear			
DEFINITION	Sequence 1906 from Patent WO0140521.				
ACCESSION	AXI58578				
VERSION	AXI58578.1 GI:14539909				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens (human)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
REFERENCE	1 Shimkets,R.A. and Leach,M.				
AUTHORS	Nucleic acids containing single nucleotide polymorphisms and methods of use thereof				
TITLE	Patent: WO 0140521-A 1906 07-JUN-2001;				
JOURNAL	Curagen Corporation (US)				
FEATURES	Location/Qualifiers				
source	1..51				
	/organism="Homo sapiens"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:9606"				
misc_feature	26				
	/note="2 of 2 allelic variants (1905 is other entry)"				
	Accession number cg36603177"				
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Query Match	1.6%; Score 38.8; DB 1; Length 51;				
Best Local Similarity	86.0%; Pred. No. 1.7e+02;				
Matches	43; Conservative 0; Mismatches 7; Indels 0; Gaps 0;				
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Qy	2268 GAGACAGGTTTTCACCGTGTTAGCCAGGATGGTCTCGATCCTCCGACCTC 2317				
Dd	51 GAGACAGGTTTTCATATGTGGTAGGCTGGTCTCGACTCTCATCTC 2				
<hr/>					
RESULT 180				PAT 22-JUN-2001	
AXI59264/c					
LOCUS	AXI59264	51 bp DNA linear			
DEFINITION	Sequence 2592 from Patent WO0140521.				
ACCESSION	AXI59264				
VERSION	AXI59264.1 GI:14540595				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
REFERENCE	1 Shimkets,R.A. and Leach,M.				
AUTHORS	Nucleic acids containing single nucleotide polymorphisms and methods of use thereof				
TITLE	Patent: WO 0140521-A 2592 07-JUN-2001;				
JOURNAL	Curagen Corporation (US)				
FEATURES	Location/Qualifiers				
source	1..51				
	/organism="Homo sapiens"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:9606"				
misc_feature	26				
	/note="2 of 2 allelic variants (2591 is other entry)"				
	Accession number cg40949022"				
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Query Match	1.6%; Score 38.8; DB 1; Length 51;				
Best Local Similarity	86.0%; Pred. No. 1.7e+02;				
Matches	43; Conservative 0; Mismatches 7; Indels 0; Gaps 0;				

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Db      2 CTACAGGCACGGCCACCAACCGCGCTAATTTTGTGTAATTTTAGTAGA 51

RESULT 183
LOCUS   AX159155
DEFINITION Sequence 2483 from Patent WO0140521.
ACCESSION AX159155
VERSION  AX159155.1 GI:14540486
KEYWORDS
SOURCE  Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS  Shinkets, R.A. and Leach, M.
TITLE    Nucleic acids containing single nucleotide polymorphisms and
         methods of use thereof
JOURNAL  Patent: WO 0140521-A 2483 07-JUN-2001;
         Curagen Corporation (US)
FEATURES
         source
         1..51
         /organism="Homo sapiens"
         /mol_type="unassigned DNA"
         /db_xref="taxon:9606"
         misc_feature
         26
         /note="1 of 2 allelic variants (2484 is other entry)"
         Accession number CG93704218"

Query Match 1.6%; Score 38.6; DB 1; Length 51;
Best Local Similarity 91.1%; Pred. No. 1.7e+02;
Matches 41; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2318 GTGATCCGCCACCTCGCGCTCCCAAAGTCTGGGATTACAGGCA 2362
Db      7 GCGATCCTCCAAACCCGCGCTCCCAAAGTCTGGGATTACAGGCA 51

RESULT 184
LOCUS   A68621/c
DEFINITION Sequence 1 from Patent WO9801573.
ACCESSION A68621
VERSION  A68621.1 GI:4759648
KEYWORDS
SOURCE  unidentified
         unidentified
         unclassified.
REFERENCE
AUTHORS  Resnick, M.A., Larionov, V.L., Koupriina, N.Y. and Perkins, E.L.
TITLE    TRANSFORMATION-ASSOCIATED RECOMBINATION CLONING
JOURNAL  Patent: WO 9801573-A 1 15-JAN-1998;
         US HEALTH (US)
FEATURES
         Location/Qualifiers
         source
         1..40
         /organism="unidentified"
         /mol_type="unassigned DNA"
         /db_xref="taxon:32644"

Query Match 1.6%; Score 38.4; DB 1; Length 40;
Best Local Similarity 97.5%; Pred. No. 1.6e+02;
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2332 TCGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACC 2371
Db      40 TCGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACC 1

RESULT 185
LOCUS   AR208401
DEFINITION Sequence 17 from patent US 6383752.
ACCESSION AR208401

Db      2 CTACAGGCACGGCCACCAACCGCGCTAATTTTGTGTAATTTTAGTAGA 51

VERSION AR208401.1 GI:21509546
KEYWORDS
SOURCE  Unknown.
ORGANISM
REFERENCE
AUTHORS  Agrawal, S. and Kandimala, E.R.
TITLE    Pseudo-cyclic oligonucleobases
JOURNAL  Patent: US 6383752-A 17 07-MAY-2002;
         Location/Qualifiers
FEATURES
         source
         1..40
         /organism="unknown"
         /mol_type="unassigned DNA"

Query Match 1.6%; Score 38.4; DB 1; Length 40;
Best Local Similarity 97.5%; Pred. No. 1.6e+02;
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 659 GGACTCAGGTACATCTGTGAGTCAGAACACAGGTGTCACTT 698
Db      1 GGACCCAGGTACATCTGTGAGTCAGAACACAGGTGTCACTT 40

RESULT 186
LOCUS   AX160116
DEFINITION Sequence 3444 from Patent WO0140521.
ACCESSION AX160116
VERSION  AX160116.1 GI:14541447
KEYWORDS
SOURCE  Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS  Shinkets, R.A. and Leach, M.
TITLE    Nucleic acids containing single nucleotide polymorphisms and
         methods of use thereof
JOURNAL  Patent: WO 0140521-A 3444 07-JUN-2001;
         Curagen Corporation (US)
FEATURES
         Location/Qualifiers
         source
         1..50
         /organism="Homo sapiens"
         /mol_type="unassigned DNA"
         /db_xref="taxon:9606"
         misc_feature
         25..26
         /note="Nucleotide deleted between bases 25 and 26"
         Accession number CG43271020"

Query Match 1.6%; Score 38.4; DB 1; Length 50;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2241 CTTGGCTAATTTTGTGTAATTTTAGTAGAGATGGAGTTTCACTGTT 2288
Db      3 CCCAGCTAATTTTGTGTAATTTTAGTAGAGATGGAGTTTCACTGTT 50

RESULT 187
LOCUS   AX156917
DEFINITION Sequence 245 from Patent WO0140521.
ACCESSION AX156917
VERSION  AX156917.1 GI:14538248
KEYWORDS
SOURCE  Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS  Shinkets, R.A. and Leach, M.

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TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 245 07-JUN-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="1 of 2 allelic variants (246 is other entry)"
Accession number CG17872027

Query Match 1.6%; Score 38.4; DB 1; Length 51;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2318 GTGATCGCCACCTCGGCTCCCAAGTCTGGATTACAGGATGA 2365
Db 4 GTGATCTCTGCTCGGCTCTCAAGTCTGGATTACAGATATGA 51

RESULT 188
AX160427
LOCUS AX160427 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 3755 from Patent WO0140521.
ACCESSION AX160427
VERSION AX160427.1 GI:14541758
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 3755 07-JUN-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="1 of 2 allelic variants (3756 is other entry)"
Accession number CG43919529

Query Match 1.6%; Score 38.4; DB 1; Length 51;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGACAGAGGTTTCACGGTTTACCGAGTGTCTCGATC 2307
Db 4 TTTTAGTAGACAGAGGTTTCACCGTGTGGCCAGGCTGTCTTGAAC 51

RESULT 189
AX514184/c
LOCUS AX514184 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 382 from Patent WO02052044.
ACCESSION AX514184
VERSION AX514184.1 GI:23560548
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Nakamura, Y., Sekine, A., Iida, A. and Saito, S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 382 04-JUL-2002;
Riken (JP)

FEATURES Location/Qualifiers
source 1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.6%; Score 37.4; DB 1; Length 41;
Best Local Similarity 92.7%; Pred. No. 1.8e+02;
Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2328 CACCTCGGCTCCCAAGTCTGGATTACAGCATGAGCC 2368
Db 41 CGCCTCGGCTCCCAAGTGTGGATTACAGCGTGAGCC 1

RESULT 190
AX514544
LOCUS AX514544 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 742 from Patent WO02052044.
ACCESSION AX514544
VERSION AX514544.1 GI:23561073
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Nakamura, Y., Sekine, A., Iida, A. and Saito, S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 742 04-JUL-2002;
Riken (JP)
FEATURES Location/Qualifiers
source 1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.6%; Score 37.4; DB 1; Length 41;
Best Local Similarity 92.7%; Pred. No. 1.8e+02;
Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2314 CTTCTGTGATCCGCCACCTCGGCTCCCAAGTGTGGAT 2354
Db 1 CTTCTGTGATTTGCCACCTCGGCTCCCAAGTGTGGAT 41

RESULT 191
AX514746
LOCUS AX514746 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 944 from Patent WO02052044.
ACCESSION AX514746
VERSION AX514746.1 GI:23561396
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Nakamura, Y., Sekine, A., Iida, A. and Saito, S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 944 04-JUL-2002;
Riken (JP)
FEATURES Location/Qualifiers
source 1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.6%; Score 37.4; DB 1; Length 41;
Best Local Similarity 92.7%; Pred. No. 1.8e+02;
Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2264 AGTAGACAGAGGTTTCACCGTGTAGCCAGGATGCTCG 2304

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Db      1 AGTAGAGACGGGTTTACCTGTTAGCCAGCATGGTCTCG 41
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RESULT 192
AX520135
LOCUS      41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 6333 from Patent WO02052044.
ACCESSION AX520135
VERSION    AX520135.1 GI:23570620
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Nakamura, Y., Sekine, A., Iida, A. and Saito, S.
TITLE      Detection of genetic polymorphisms
JOURNAL    Patent: WO 02052044-A 6333 04-JUL-2002;
            Riken (JP)
FEATURES   Location/Qualifiers
            source
            1..41
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      1.6%; Score 37.4; DB 1; Length 41;
Best Local Similarity 92.7%; Pred. No. 1.8e+02;
Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY      2314 CCTCGTATCGCCACCTCGGCTCCCAAGTCTGGAT 2354
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Db      1 CCTCGTATTCGCCACCTCGCTCCCAAGTCTGGAT 41
|||||
RESULT 193
AX520215/c
LOCUS      41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 6413 from Patent WO02052044.
ACCESSION AX520215
VERSION    AX520215.1 GI:23570721
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Nakamura, Y., Sekine, A., Iida, A. and Saito, S.
TITLE      Detection of genetic polymorphisms
JOURNAL    Patent: WO 02052044-A 6413 04-JUL-2002;
            Riken (JP)
FEATURES   Location/Qualifiers
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      1.6%; Score 37.4; DB 1; Length 41;
Best Local Similarity 92.7%; Pred. No. 1.8e+02;
Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY      2328 CACCTCGGCTCCCAAGTCTGGATTCAGGCATGAGCC 2368
|||||
Db      41 GCCTCGGCTCCCAAGTCTGGATTCAGGCATGAGCC 1
|||||
RESULT 194
AX520756
LOCUS      41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 6954 from Patent WO02052044.
ACCESSION AX520756
VERSION    AX520756.1 GI:23571411
KEYWORDS

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SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Nakamura, Y., Sekine, A., Iida, A. and Saito, S.
TITLE      Detection of genetic polymorphisms
JOURNAL    Patent: WO 02052044-A 6954 04-JUL-2002;
            Riken (JP)
FEATURES   Location/Qualifiers
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      1.6%; Score 37.4; DB 1; Length 41;
Best Local Similarity 92.7%; Pred. No. 1.8e+02;
Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY      2264 AGTAGAGACAGGGTTTACCGTGTAGCCAGGATGGTCTCG 2304
|||||
Db      1 AGTAGAGACGGGTTTACCTGTTAGCCAGCATGGTCTCG 41
|||||
RESULT 195
HUMALUANC/c
LOCUS      42 bp DNA linear PRI 08-OCT-1994
DEFINITION Homo sapiens 4000 year old remains from Nekht-anhk Alu repeat
            fragment 12.4.
ACCESSION L36838
VERSION    L36838.1 GI:556195
KEYWORDS   Alu repeat.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (sites)
AUTHORS    Paabo, S.
TITLE      Ancient DNA: extraction, characterization, molecular cloning, and
            enzymatic amplification
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 86 (6), 1939-1943 (1989)
MEDLINE    89184542
PUBMED     2928314
COMMENT    Original source text: Homo sapiens (individual isolate 4000 year
            old remains from Nekht-anhk) liver DNA.
FEATURES   Location/Qualifiers
            source
            1..42
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /isolate="4000 year old remains from Nekht-anhk"
            /db_xref="taxon:9606"
            /tissue_type="liver"
            repeat_region <1..>42
            /rpt_family="Alu"
Query Match      1.6%; Score 37.2; DB 1; Length 42;
Best Local Similarity 92.9%; Pred. No. 1.8e+02;
Matches 39; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      2311 TGACCTCGTGATCCGCCACCTCGGCTCCCAAGTCTGGG 2352
|||||
Db      42 TGACCTCGTGATCCGCCACCTCGGCTCCCAAGTCTGGG 1
|||||
RESULT 196
AR291264
LOCUS      47 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 2999 from patent US 6537751.
ACCESSION AR291264
VERSION    AR291264.1 GI:31678548
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unknown.

```

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Unclassified.
REFERENCE 1 (bases 1 to 47)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
        disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 2999 25-MAR-2003;
FEATURES
    source      Location/Qualifiers
        1..47
        /organism="unknown"
        /mol_type="genomic DNA"

Query Match      1.6%; Score 37; DB 1; Length 47;
Best Local Similarity 85.1%; Pred. No. 2e+02;
Matches 40; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2322 TCGCCACCTCGGCTCCCAAGTGTGGATTACAGGATGAGCC 2368
      |||||
Db 1 TCGCCCTGCTCAGCTCCCAAGTGTGGATTATAGGCTGAGCC 47

RESULT 197
LOCUS HUMALUANCA 41 bp DNA linear PRI 08-OCT-1994
DEFINITION Homo sapiens 4000 year old remains from Nekht-anKh Alu repeat
        fragment 11:2.
ACCESSION L36835
VERSION L36835.1 GI:556193
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Paabo,S.
TITLE Ancient DNA: extraction, characterization, molecular cloning, and
        enzymatic amplification
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 86 (6), 1939-1943 (1989)
MEDLINE 89184542
PUBMED 2928314
COMMENT Original source text: Homo sapiens (individual isolate 4000 year
        old remains from Nekht-anKh) liver DNA.
FEATURES
    source      Location/Qualifiers
        1..41
        /organism="Homo sapiens"
        /mol_type="genomic DNA"
        /isolate="4000 year old remains from Nekht-anKh"
        /db_xref="taxon:9606"
        /tissue_type="liver"
        repeat_region <1..>41
        /rpt_family="Alu"

Query Match      1.5%; Score 35.2; DB 1; Length 41;
Best Local Similarity 92.5%; Pred. No. 2.2e+02;
Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2312 GACCTCGTGTGCTCGCCACCTCGGCTCCCAAGTGTCTGG 2351
      |||||
Db 41 GACCTCGTGTGCTCGCTCGGCTCCCAAGTGTCTGG 2

RESULT 198
LOCUS AX160004 44 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 3332 from Patent WO0140521.
ACCESSION AX160004
VERSION AX160004.1 GI:14541335
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.

TITLE Nucleic acids containing single nucleotide polymorphisms and
        methods of use thereof
JOURNAL Patent: WO 0140521-A 3332 07-JUN-2001;
        Curagen Corporation (US)
FEATURES
    source      Location/Qualifiers
        1..44
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

misc_feature 19
        /note="2 of 2 allelic variants (3331 is other entry)"
        Accession number CG43247846"

Query Match      1.5%; Score 35.2; DB 1; Length 44;
Best Local Similarity 92.5%; Pred. No. 2.3e+02;
Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2316 TCGTGTGCTCGCCACCTCGGCTCCCAAGTGTCTGGATT 2355
      |||||
Db 5 TCATGATCGCGCGCTCGGCTCTCAAAAGTGTCTGGATT 44

RESULT 199
LOCUS HSLAS33 43 bp DNA linear PRI 22-APR-1996
DEFINITION H. sapiens DNA for loop attachment sequence (clone LAS33).
ACCESSION X91548
VERSION X91548.1 GI:987907
KEYWORDS loop attachment sequence.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 43)
AUTHORS Jackson,D.A., Bartlett,J. and Cook,P.R.
TITLE Sequences attaching loops of nuclear and mitochondrial DNA to
        underlying structures in human cells: the role of transcription
        unite
JOURNAL Nucleic Acids Res. 24 (7), 1212-1219 (1996)
MEDLINE 96188852
PUBMED 8614621
REFERENCE 2 (bases 1 to 43)
AUTHORS Cook,P.R.
TITLE Direct Submission
JOURNAL Submitted (14-SEP-1995) P.R. Cook, Sir William Dunn School of
        Pathology, University of Oxford, South Parks Road, Oxford, OX1 3RE,
        UK
COMMENT Related sequence: Proc.Natl.Acad.Sci. USA 85:4775-4778(1988).
FEATURES
    source      Location/Qualifiers
        1..43
        /organism="Homo sapiens"
        /mol_type="genomic DNA"
        /db_xref="taxon:9606"
        /clone="LAS33"
        /cell_line="HeLa"
        /clone_lib="DNA loop attachment sequences (LAS)"
        misc_feature 1..43
        /note="DNA loop attachment site (LAS)"
        repeat_region 1..43
        /rpt_family="Alu"

Query Match      1.5%; Score 35; DB 1; Length 43;
Best Local Similarity 88.4%; Pred. No. 2.3e+02;
Matches 38; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2292 CAGGATGGTCTCGATCTCCTGACCTCGTGTGATCGCCACCTCG 2334
      |||||
Db 1 CCGGATGGTCTTGATCTCTTGACCTTGATCGCCCGCTCG 43

RESULT 200
LOCUS AX516778 41 bp DNA linear PAT 05-OCT-2002

```

DEFINITION Sequence 2976 from Patent WO02052044.
ACCESSION AX516778
VERSION AX516778.1 GI:23564830
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Nakamura, Y., Sekine, A., Iida, A. and Saito, S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 2976 04-JUL-2002;
Riken (JP)
FEATURES
source Location/Qualifiers
1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1..5%; Score 34.8; DB 1; Length 41;
Best Local Similarity 90.0%; Pred. No. 2.3e+02;
Matches 36; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2092 TTTTGTGAGCCGAGCTTGTCTGTATCCAGGCTGG 2131
|||||
Db 1 TTTTGTGAGATGGAGCTGTGCTGTGTCGCCAGGCTGG 40
|||||
RESULT 201
AX518941
LOCUS AX518941
DEFINITION Sequence 5139 from Patent WO02052044.
ACCESSION AX518941
VERSION AX518941.1 GI:23568913
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Nakamura, Y., Sekine, A., Iida, A. and Saito, S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 5139 04-JUL-2002;
Riken (JP)
FEATURES
source Location/Qualifiers
1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1..5%; Score 34.8; DB 1; Length 41;
Best Local Similarity 90.0%; Pred. No. 2.3e+02;
Matches 36; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2092 TTTTGTGAGCCGAGCTTGTCTGTATCCAGGCTGG 2131
|||||
Db 1 TTTTGTGAGATGGAGCTGTGCTGTGTCGCCAGGCTGG 40
|||||
RESULT 202
A22672
LOCUS A22672
DEFINITION Oligonucleotide.
ACCESSION A22672
VERSION A22672.1 GI:1247933
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 35)
AUTHORS Anand, R.
TITLE Nucleotide sequences
JOURNAL Patent: EP 0518583-A 10 16-DEC-1992;
Riken (JP)

FEATURES
source Location/Qualifiers
1..35
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 1..4%; Score 34.2; DB 1; Length 35;
Best Local Similarity 94.3%; Pred. No. 2.3e+02;
Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2335 GCCTCCCAAAGTCTGGGATTACAGGCATGAGCCA 2369
|||||
Db 1 GCCTCCCAAAGTCTGGGATTACAGGYRTGAGCCA 35
|||||
RESULT 203
I21796
LOCUS I21796
DEFINITION Sequence 10 from patent US 5525467.
ACCESSION I21796
VERSION I21796.1 GI:1602150
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 35)
AUTHORS Anand, R.
TITLE Nucleotide sequences
JOURNAL Patent: US 5525467-A 10 11-JUN-1996;
Riken (JP)
FEATURES
source Location/Qualifiers
1..35
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1..4%; Score 34.2; DB 1; Length 35;
Best Local Similarity 94.3%; Pred. No. 2.3e+02;
Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2335 GCCTCCCAAAGTCTGGGATTACAGGCATGAGCCA 2369
|||||
Db 1 GCCTCCCAAAGTCTGGGATTACAGGYRTGAGCCA 35
|||||
RESULT 204
AX709023
LOCUS AX709023
DEFINITION Sequence 47 from Patent WO03008443.
ACCESSION AX709023
VERSION AX709023.1 GI:29564696
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Averback, P.A.
TITLE Peptides effective in the treatment of tumors and other conditions
JOURNAL Patent: WO 03008443-A 47 30-JAN-2003;
Nymox Corporation (CA)
FEATURES
source Location/Qualifiers
1..39
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"
Query Match 1..4%; Score 34.2; DB 1; Length 39;
Best Local Similarity 92.3%; Pred. No. 2.4e+02;
Matches 36; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2326 CCCACCTCGGCTCCCAAGTCTGGGATTACAGGCATG 2364
|||||


```
Db 1 CCTCCCTCGGCCTCCCAAAGTGTGGGATTACAGGCGTG 39

RESULT 205
AX514185/c
LOCUS AX514185 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 383 from Patent WO02052044.
ACCESSION AX514185
VERSION AX514185.1 GI:23560550
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 383 04-JUL-2002;
Riken (JP)
FEATURES
source Location/Qualifiers
1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.4%; Score 34.2; DB 1; Length 41;
Best Local Similarity 87.8%; Pred. No. 2.5e+02;
Matches 36; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2307 CTCCTGACCTCGTGATCGGCCACCTCGGCTCCCAAAGTG 2347
Db 41 CTCCTGACTTTGTGATGCACGCGCTCGGCTCCCAAAGTG 1

RESULT 206
AX520216/c
LOCUS AX520216 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 6414 from Patent WO02052044.
ACCESSION AX520216
VERSION AX520216.1 GI:23570722
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 6414 04-JUL-2002;
Riken (JP)
FEATURES
source Location/Qualifiers
1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.4%; Score 34.2; DB 1; Length 41;
Best Local Similarity 87.8%; Pred. No. 2.5e+02;
Matches 36; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2307 CTCCTGACCTCGTGATCGGCCACCTCGGCTCCCAAAGTG 2347
Db 41 CTCCTGACTTTGTGATGCACGCGCTCGGCTCCCAAAGTG 1

RESULT 207
AX709009
LOCUS AX709009 42 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 33 from Patent WO03008443.
ACCESSION AX709009
VERSION AX709009.1 GI:29564682
KEYWORDS
SOURCE synthetic construct

Db 1 CCTCCCTCGGCCTCCCAAAGTGTGGGATTACAGGCGTG 39

ORGANISM synthetic construct
REFERENCE 1
AUTHORS Averbach, P.A.
TITLE Peptides effective in the treatment of tumors and other conditions requiring the removal or destruction of cells
JOURNAL Patent: WO 0308443-A 33 30-JAN-2003;
Nymox Corporation (CA)
FEATURES
source Location/Qualifiers
1..42
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Synthetic oligonucleotide"

Query Match 1.4%; Score 34; DB 1; Length 42;
Best Local Similarity 88.1%; Pred. No. 2.6e+02;
Matches 37; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2322 TCCGCCACCTCGGCTCCCAAAGTGTGGGATTACAGGCAT 2363
Db 1 TCCACCTGCTCAGCTCCCAAAGTGTGGGATTACAGGCCT 42

RESULT 208
CO760643
LOCUS CO760643 45 bp DNA linear PAT 03-MAR-2004
DEFINITION Sequence 85 from Patent WO2004003229.
ACCESSION CO760643
VERSION CO760643.1 GI:44904146
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Nex,B.R., Vogel,U., Rockenbauer,E. and Bukowy,Z.K.
TITLE Disease risk estimating method using sequence polymorphisms in a specific region of chromosome 19
JOURNAL Patent: WO 2004003229-A 85 08-JAN-2004;
Aarhus University (DK); Arbejdsmiljø Instituttet (National Institute of Occupational Health) (DK)
FEATURES
source Location/Qualifiers
1..45
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Probe"

Query Match 1.4%; Score 34; DB 1; Length 45;
Best Local Similarity 84.1%; Pred. No. 2.6e+02;
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2252 TTTTGTACTTTTAGTAGACAGAGGTTTCACTGTTAGCCAGG 2295
Db 1 TTTTGTACTTTTAGTAGACAGAGGTTTCTCCATGTTGGTCAGG 44

RESULT 209
AX516379/c
LOCUS AX516379 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 2577 from Patent WO02052044.
ACCESSION AX516379
VERSION AX516379.1 GI:23564062
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 2577 04-JUL-2002;
Riken (JP)
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FEATURES
  source
    Location/Qualifiers
      1..41
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
  Best Local Similarity 1.4%; Score 33.6; DB 1; Length 41;
  Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2326 CCACCTGGCTCCCAAGTCTGGGATTACAGGCATGA 2365
  |||||
Db 40 CCACCTTGGCTCCCAAGTCTGGGATTACAGGTATGA 1

RESULT 210
LOCUS AX160003 44 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 3331 from Patent WO0140521.
ACCESSION AX160003
VERSION AX160003.1 GI:14541334
KEYWORDS
  ORGANISM Homo sapiens (human)
  SOURCE Homo sapiens
  ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  AUTHORS Shinkets, R.A. and Leach, M.
  TITLE Nucleic acids containing single nucleotide polymorphisms and
  methods of use thereof
  JOURNAL Patent: WO 0140521-A 3331 07-JUN-2001;
  Curagen Corporation (US)
FEATURES
  source
    Location/Qualifiers
      1..44
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
      19
        /note="1 of 2 allelic variants (3332 is other entry)
        Accession number CG43247846"
      misc_feature
        1.44
          /organism="unidentified"
          /mol_type="genomic DNA"
          /db_xref="taxon:32644"

Query Match
  Best Local Similarity 1.4%; Score 33.6; DB 1; Length 44;
  Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2316 TCGTATCGCCACCTCGGCTCCCAAGTCTGGGATT 2355
  |||||
Db 5 TCATGATCGCCCGTCTCGGCTCTCAAAAGTCTGGGATT 44

RESULT 211
A25212
LOCUS A25212 35 bp DNA linear PAT 11-APR-1995
DEFINITION inter-Alu specific primer DNA (pdj33) from patent WO9213101.
ACCESSION A25212
VERSION A25212.1 GI:904592
KEYWORDS
  SOURCE synthetic construct
  ORGANISM synthetic construct
  ORGANISM artificial sequences.
  REFERENCE
    1 (bases 1 to 35)
  AUTHORS
  TITLE METHOD OF DETECTING DNA SEQUENCE VARIATION
  JOURNAL Patent: WO 9213101-A 3 06-AUG-1992;
  Location/Qualifiers
  FEATURES
    source
      1..35
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"

Query Match
  Best Local Similarity 1.4%; Score 33.4; DB 1; Length 35;
  Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAGTCTGGGATTACAGGCATGAGCCA 2369
  |||||
Db 1 GCCTCCCAAGTCTGGGATTACAGGCATGAGCCA 35

RESULT 212
LOCUS E09140 35 bp DNA linear PAT 29-SEP-1997
DEFINITION Synthetic DNA for Alu specific primer.
ACCESSION E09140
VERSION E09140.1 GI:22025766
KEYWORDS
  SOURCE unidentified
  ORGANISM unidentified
  ORGANISM unclassified.
  REFERENCE
    1 (bases 1 to 35)
  AUTHORS Andureau, H.A. and Yan, F.
  TITLE DETECTING METHOD FOR DNA ARRANGEMENT VARIATION
  JOURNAL Patent: JP 1995115999-A 3 09-MAY-1995;
  INGENII BV
  COMMENT
    OS None
    OC Artificial sequences.
    PN JP 1995115999-A/3
    PD 09-MAY-1995
    PF 22-MAY-1992 JP 1992130668
    PI ANDOREASU HERARDOUSU AITSUTERURINDEN, YAN FUEIKU PC
    CI2Q1/68, C12N15/00, G01N27/447, G01N27/447;
    CC strandedness: Single;
    CC topology: Linear;
    FH Key Location/Qualifiers
    FH Key Location/Qualifiers
    FT source 1..35
    FT misc_feature 1..35 /organism='Artificial sequences' FT
    FT /note='Alu specific primer'.
FEATURES
  source
    Location/Qualifiers
      1..35
        /organism="unidentified"
        /mol_type="genomic DNA"
        /db_xref="taxon:32644"

Query Match
  Best Local Similarity 1.4%; Score 33.4; DB 1; Length 35;
  Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAGTCTGGGATTACAGGCATGAGCCA 2369
  |||||
Db 1 GCCTCCCAAGTCTGGGATTACAGGCATGAGCCA 35

RESULT 213
LOCUS AX183780 40 bp DNA linear PAT 06-AUG-2001
DEFINITION Sequence 1533 from Patent WO0142511.
ACCESSION AX183780
VERSION AX183780.1 GI:15135106
KEYWORDS
  SOURCE Homo sapiens (human)
  ORGANISM Homo sapiens
  ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  AUTHORS Daly, M., Hudson, T.J., Lander, E.S., Rioux, J. and Siminovitch, K.
  TITLE Ibd-related polymorphisms
  JOURNAL Patent: WO 0142511-A 1533 14-JUN-2001;
  WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipse
  Biotherapeutics Corporation (CA)
  Location/Qualifiers
  FEATURES
    source
      1..40
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

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Query Match
Best Local Similarity 1.4%; Score 32.6; DB 1; Length 40;
Matches 35; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2277 TTTCCACGCTGTAGCCAGGATGGTCTCGATCTCTGACCT 2316
Db 40 TTTCCACGATGTAGTCAGGCTGGTCTCNAACTCTCTGACCT 1

RESULT 214
AX514703/c
LOCUS AX514703 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 901 from Patent WO02052044.
ACCESSION AX514703
VERSION AX514703.1 GI:23561309
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE
AUTHORS Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 901 04-JUL-2002;
Riken (JP)
FEATURES
source Location/Qualifiers
1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 1.4%; Score 32.6; DB 1; Length 41;
Matches 35; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2252 TTTTGTACTTTTAGTAGAGACAGGGTTTCACCGTTAGCC 2292
Db 41 TTTTGTATTTTAGTAGAGAYGGGTTTCGCCATGTTGGCC 1

RESULT 215
AX520711/c
LOCUS AX520711 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 6909 from Patent WO02052044.
ACCESSION AX520711
VERSION AX520711.1 GI:23571362
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE
AUTHORS Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 6909 04-JUL-2002;
Riken (JP)
FEATURES
source Location/Qualifiers
1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 1.4%; Score 32.6; DB 1; Length 41;
Matches 35; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2252 TTTTGTACTTTTAGTAGAGACAGGGTTTCACCGTTAGCC 2292
Db 41 TTTTGTATTTTAGTAGAGAYGGGTTTCGCCATGTTGGCC 1

RESULT 216
AX520711/c
LOCUS AX520711 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 6909 from Patent WO02052044.
ACCESSION AX520711
VERSION AX520711.1 GI:23571362
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE
AUTHORS Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 6909 04-JUL-2002;
Riken (JP)
FEATURES
source Location/Qualifiers
1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 1.4%; Score 32.6; DB 1; Length 41;
Matches 35; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2252 TTTTGTACTTTTAGTAGAGACAGGGTTTCACCGTTAGCC 2292
Db 41 TTTTGTATTTTAGTAGAGAYGGGTTTCGCCATGTTGGCC 1

RESULT 217
AX514160/c
LOCUS AX514160 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 358 from Patent WO02052044.
ACCESSION AX514160
VERSION AX514160.1 GI:23560520
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE
AUTHORS Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 358 04-JUL-2002;
Riken (JP)
FEATURES
source Location/Qualifiers
1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 1.3%; Score 32; DB 1; Length 41;
Matches 35; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2315 CTGCTGATCGCCACCTCGGCCTCCAAAGTCTGGGAT 2354
Db 40 CTGCTGATCTCTCTACCCGGCTTCCAAAGTCTGGGAT 1

RESULT 218
AX520311/c
LOCUS AX520311 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 6509 from Patent WO02052044.
ACCESSION AX520311
VERSION AX520311.1 GI:23570855
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE
AUTHORS Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 6509 04-JUL-2002;
Riken (JP)
FEATURES
source Location/Qualifiers
1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 1.3%; Score 31.6; DB 1; Length 41;
Matches 34; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2263 TAGTAGACACGGGTTTCACCGTTAGCCAGGATGGTCT 2302
Db 41 TAGTAGAGACGGGGTTTCACYGTGTTGGTCAGGCTGGTCT 2

RESULT 219
AX520311/c
LOCUS AX520311 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 6509 from Patent WO02052044.
ACCESSION AX520311
VERSION AX520311.1 GI:23570855
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE
AUTHORS Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 6509 04-JUL-2002;
Riken (JP)
FEATURES
source Location/Qualifiers
1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 1.3%; Score 31.6; DB 1; Length 41;
Matches 34; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2263 TAGTAGACACGGGTTTCACCGTTAGCCAGGATGGTCT 2302
Db 41 TAGTAGAGACGGGGTTTCACYGTGTTGGTCAGGCTGGTCT 2

RESULT 220
AX520311/c
LOCUS AX520311 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 6509 from Patent WO02052044.
ACCESSION AX520311
VERSION AX520311.1 GI:23570855
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE
AUTHORS Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 6509 04-JUL-2002;
Riken (JP)
FEATURES
source Location/Qualifiers
1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 1.3%; Score 31.6; DB 1; Length 41;
Matches 34; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2263 TAGTAGACACGGGTTTCACCGTTAGCCAGGATGGTCT 2302
Db 41 TAGTAGAGACGGGGTTTCACYGTGTTGGTCAGGCTGGTCT 2
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REFERENCE 1
AUTHORS Nakamura, Y., Sekine, A., Iida, A. and Saito, S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 6509 04-JUL-2002;
Riken (JP)
FEATURES
source
Location/Qualifiers
1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.3%; Score 31.6; DB 1; Length 41;
Best Local Similarity 85.0%; Pred. No. 3.2e+02;
Matches 34; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 2263 TAGTAGACAGCGGTTTACCGTGTACCCAGGATGGTCT 2302
DB 41 TAGTAGACAGCGGTTTACCGTGTACCCAGGATGGTCT 2
RESULT 219
AX519117
LOCUS AX519117 40 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 5315 from Patent WO02052044.
ACCESSION AX519117
VERSION AX519117.1 GI:23569187
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Nakamura, Y., Sekine, A., Iida, A. and Saito, S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 5315 04-JUL-2002;
Riken (JP)
FEATURES
source
Location/Qualifiers
1..40
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.3%; Score 31; DB 1; Length 40;
Best Local Similarity 87.2%; Pred. No. 3.4e+02;
Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2257 TACTTTTAGTAGACAGCGGTTTACCGTGTAGCCAGG 2295
DB 1 TACTTTTAGTAGACAGCGGTTTACCATATTGCCAGG 39
RESULT 220
AX513835/c
LOCUS AX513835 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 33 from Patent WO02052044.
ACCESSION AX513835
VERSION AX513835.1 GI:23560039
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Nakamura, Y., Sekine, A., Iida, A. and Saito, S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 33 04-JUL-2002;
Riken (JP)
FEATURES
source
Location/Qualifiers
1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.3%; Score 31; DB 1; Length 41;
Best Local Similarity 82.9%; Pred. No. 3.4e+02;
Matches 34; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 2092 TTTTGTGAGACCGAGTCTTGTCTGTACCCAGGCTGGA 2132
DB 41 TTTTGTGAGATGAAGTCTTACTGTCTACCCAGGCTGGA 1
RESULT 221
AX517711/c
LOCUS AX517711 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 3909 from Patent WO02052044.
ACCESSION AX517711
VERSION AX517711.1 GI:23566615
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Nakamura, Y., Sekine, A., Iida, A. and Saito, S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 3909 04-JUL-2002;
Riken (JP)
FEATURES
source
Location/Qualifiers
1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.3%; Score 31; DB 1; Length 41;
Best Local Similarity 82.9%; Pred. No. 3.4e+02;
Matches 34; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 2092 TTTTGTGAGACCGAGTCTTGTCTGTACCCAGGCTGGA 2132
DB 41 TTTTGTGAGATGAAGTCTTACTGTCTACCCAGGCTGGA 1
RESULT 222
AX519988
LOCUS AX519988 41 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 6186 from Patent WO02052044.
ACCESSION AX519988
VERSION AX519988.1 GI:23570430
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Nakamura, Y., Sekine, A., Iida, A. and Saito, S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 6186 04-JUL-2002;
Riken (JP)
FEATURES
source
Location/Qualifiers
1..41
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.3%; Score 31; DB 1; Length 41;
Best Local Similarity 82.9%; Pred. No. 3.4e+02;
Matches 34; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 2272 CAGGGTTTACCGTGTAGCCAGGATGGTCTGCTCCTG 2312
DB 1 CAGAGTTTCACCATGTGGCYAGGCTGTCTTGAACCTCTG 41
RESULT 223
AX520856

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LOCUS       AX520856               41 bp    DNA             linear      PAT 05-OCT-2002
DEFINITION   Sequence 7054 from Patent WO02052044.
ACCESSION    AX520856
VERSION      AX520856.1  GI:23571532
KEYWORDS
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE        Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
JOURNAL      Detection of Genetic Polymorphisms
              Patent: WO 02052044-A 7054 04-JUL-2002;
              Riken (JP)
FEATURES     Location/Qualifiers
             source             1..41
                                 /organism="Homo sapiens"
                                 /mol_type="unassigned DNA"
                                 /db_xref="taxon:9606"
             Query Match       1.3%; Score 31; DB 1; Length 41;
             Best Local Similarity 82.9%; Pred. No. 3.4e+02;
             Matches 34; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2195 GCCTCAGCCTCCCAATTAGCTTGCCCTACAGTACATCTGCCA 2235
Db 1 GCCTCAGCCTCCCAAGTAGCGGAGCTACAGGCGCTGCCA 41

RESULT 224
AX709012
LOCUS       AX709012               33 bp    DNA             linear      PAT 04-APR-2003
DEFINITION   Sequence 36 from Patent WO03008443.
ACCESSION    AX709012
VERSION      AX709012.1  GI:29564685
KEYWORDS     synthetic construct
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1
AUTHORS      Averbach,P.A.
TITLE        Peptides effective in the treatment of tumors and other conditions
              requiring the removal or destruction of cells
JOURNAL      Patent: WO 03008443-A 36 30-JAN-2003;
              Nymox Corporation (CA)
FEATURES     Location/Qualifiers
             source             1..33
                                 /organism="synthetic construct"
                                 /mol_type="unassigned DNA"
                                 /db_xref="taxon:32630"
                                 /note="Synthetic oligonucleotide"
             Query Match       1.3%; Score 29.8; DB 1; Length 33;
             Best Local Similarity 93.9%; Pred. No. 3.6e+02;
             Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2331 CTCGGCCTCCCAAGTCTGCGATTACAGGCAT 2363
Db 1 CTCAGCCTCCCAAGTCTGCGATTACAGCGT 33

RESULT 225
AR208404/c
LOCUS       AR208404               29 bp    DNA             linear      PAT 20-JUN-2002
DEFINITION   Sequence 20 from patent US 6383752.
ACCESSION    AR208404
VERSION      AR208404.1  GI:21509549
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 29)
              Agrawal,S. and Kandimalla,E.R.

LOCUS       Pseudo-cyclic oligonucleobases
DEFINITION   Patent: US 6383752-A 20 07-MAY-2002;
              Location/Qualifiers
              source             1..29
                                 /organism="unknown"
                                 /mol_type="unassigned DNA"
             Query Match       1.2%; Score 29; DB 1; Length 29;
             Best Local Similarity 100.0%; Pred. No. 3.7e+02;
             Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 649 AGGAATCATCGGACTCAGGTACATCTGTG 677
Db 29 AGGAATCATCGGACTCAGGTACATCTGTG 1

RESULT 226
BD169435
LOCUS       BD169435               30 bp    DNA             linear      PAT 17-JAN-2003
DEFINITION   Genomes participating in rheumatoid arthritis, method of diagnosing
              the same, method of judging the onset risk thereof, kit for
              detecting and diagnosing the same, method of treating rheumatoid
              arthritis and remedies therefor.
ACCESSION    BD169435
VERSION      BD169435.1  GI:27875247
KEYWORDS     synthetic construct
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 (bases 1 to 30)
              Shiozawa,S. and Konishi,Y.
              Genomes participating in rheumatoid arthritis, method of diagnosing
              the same, method of judging the onset risk thereof, kit for
              detecting and diagnosing the same, method of treating rheumatoid
              arthritis and remedies therefor
JOURNAL      Patent: WO 0234912-A 12 02-MAY-2002;
              SHUNICHI SHIOZAWA,YOSHITAKE KONISHI
              OS Artificial Sequence
              PN WO 0234912-A/12
              PD 02-MAY-2002
              PP 24-OCT-2001 WO 2001JP009313
              PR 24-OCT-2000 JP 00P 324296,27-MAR-2001 JP 01P 090546 PR
              30-MAR-2001 JP 01P 099990
              PI SHUNICHI SHIOZAWA,YOSHITAKE KONISHI
              PC C12N15/12,C07K14/47,C12Q1/68,G01N33/50,A61K38/17,A61K48/00 CC
              Synthesized oligonucleotide
              FH Key Location/Qualifiers
              FT source             1..30
                                 /organism="Artificial Sequence".
              FEATURES
              source             1..30
                                 /organism="synthetic construct"
                                 /mol_type="genomic DNA"
                                 /db_xref="taxon:32630"
             Query Match       1.2%; Score 28.4; DB 1; Length 30;
             Best Local Similarity 96.7%; Pred. No. 4e+02;
             Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2295 GATGGTCTCGATCTCCTGACCTCGTGATCC 2324
Db 1 GATGGTCTTGATCTCCTGACCTCGTGATCC 30

RESULT 227
BD169436/c
LOCUS       BD169436               30 bp    DNA             linear      PAT 17-JAN-2003
DEFINITION   Genomes participating in rheumatoid arthritis, method of diagnosing
              the same, method of judging the onset risk thereof, kit for
              detecting and diagnosing the same, method of treating rheumatoid
              arthritis and remedies therefor.
ACCESSION    BD169436
VERSION      BD169436.1  GI:27875248

```

KEYWORDS WO 0234912-A/13.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1 (bases 1 to 30)
 AUTHORS Shiozawa, S. and Konishi, Y.
 TITLE Genomes participating in rheumatoid arthritis, method of diagnosing the same, method of judging the onset risk thereof, kit for detecting and diagnosing the same, method of treating rheumatoid arthritis and remedies therefor
 JOURNAL Patent: WO 0234912-A 13 02-MAY-2002;
 COMMENT SHUNICHI SHIOZAWA, YOSHITAKE KONISHI
 OS Artificial Sequence
 PN WO 0234912-A/13
 PD 02-MAY-2002
 PF 24-OCT-2001 WO 2001JP009313
 PR 24-OCT-2000 JP 00P 324296, 27-MAR-2001 JP 01P 090546 PR
 30-MAR-2001 JP 01P 099990
 PI SHUNICHI SHIOZAWA, YOSHITAKE KONISHI
 PC C12N15/12, C07K14/47, C12Q1/68, G01N33/50, A61K38/17, A61K48/00 CC
 Synthesized oligonucleotide
 FH key Location/Qualifiers
 FT source 1..30
 FT Location/Qualifiers
 FEATURES
 source 1..30
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 Query Match 1..2%; Score 28.4; DB 1; Length 30;
 Best Local Similarity 96.7%; Pred. No. 4e+02;
 Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2295 GATGCTCTGATCTCTCGACCTCGTGATCC 2324
 |||||
 Db 30 GATGCTCTGATCTCTCGACCTCGTGATCC 1
 RESULT 228
 AR089907
 LOCUS 28 bp DNA linear PAT 07-SEP-2000
 DEFINITION Sequence 27 from patent US 5994076.
 ACCESSION AR089907
 VERSION AR089907.1 GI:10016662
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 28)
 AUTHORS Chenchik, A., Jokhadze, G. and Bibilashvili, R.
 TITLE Methods of assaying differential expression
 JOURNAL Patent: US 5994076-A 27 30-NOV-1999;
 FEATURES Location/Qualifiers
 source 1..28
 /organism="unknown"
 /mol_type="unassigned DNA"
 Query Match 1..2%; Score 28; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 920 GGAGATATGTTGTGAAAGACGATAGC 947
 |||||
 Db 1 GGAGATATGTTGTGAAAGACGATAGC 28
 RESULT 229
 AR089908/c
 LOCUS 28 bp DNA linear PAT 07-SEP-2000
 DEFINITION Sequence 28 from patent US 5994076.
 ACCESSION AR089908
 VERSION AR089908.1 GI:10016663
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 28)
 AUTHORS Chenchik, A., Jokhadze, G. and Bibilashvili, R.
 TITLE Methods of assaying differential expression
 JOURNAL Patent: US 5994076-A 27 30-NOV-1999;
 FEATURES Location/Qualifiers
 source 1..28
 /organism="unknown"
 /mol_type="unassigned DNA"
 Query Match 1..2%; Score 28; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 920 GGAGATATGTTGTGAAAGACGATAGC 947
 |||||
 Db 1 GGAGATATGTTGTGAAAGACGATAGC 28
 RESULT 229
 AR089908/c
 LOCUS 28 bp DNA linear PAT 07-SEP-2000
 DEFINITION Sequence 28 from patent US 5994076.
 ACCESSION AR089908
 VERSION AR089908.1 GI:10016663

KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 28)
 AUTHORS Chenchik, A., Jokhadze, G. and Bibilashvili, R.
 TITLE Methods of assaying differential expression
 JOURNAL Patent: US 5994076-A 28 30-NOV-1999;
 FEATURES Location/Qualifiers
 source 1..28
 /organism="unknown"
 /mol_type="unassigned DNA"
 Query Match 1..2%; Score 28; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1204 CCTAGCTGACTATTGGAAATGCATTC 1231
 |||||
 Db 28 CCTAGCTGACTATTGGAAATGCATTC 1
 RESULT 230
 AR196942
 LOCUS 28 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 27 from patent US 6352829.
 ACCESSION AR196942
 VERSION AR196942.1 GI:20246791
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 28)
 AUTHORS Chenchik, A., Jokhadze, G. and Bibilashvili, R.
 TITLE Methods of assaying differential expression
 JOURNAL Patent: US 6352829-A 27 05-MAR-2002;
 FEATURES Location/Qualifiers
 source 1..28
 /organism="unknown"
 /mol_type="unassigned DNA"
 Query Match 1..2%; Score 28; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 920 GGAGATATGTTGTGAAAGACGATAGC 947
 |||||
 Db 1 GGAGATATGTTGTGAAAGACGATAGC 28
 RESULT 231
 AR196943/c
 LOCUS 28 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 28 from patent US 6352829.
 ACCESSION AR196943
 VERSION AR196943.1 GI:20246792
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 28)
 AUTHORS Chenchik, A., Jokhadze, G. and Bibilashvili, R.
 TITLE Methods of assaying differential expression
 JOURNAL Patent: US 6352829-A 28 05-MAR-2002;
 FEATURES Location/Qualifiers
 source 1..28
 /organism="unknown"
 /mol_type="unassigned DNA"
 Query Match 1..2%; Score 28; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1204 CCTTAGCTGACTATTGGAATGCACCTTC 1231
Db 28 CCTTAGCTGACTATTGGAATGCACCTTC 1

RESULT 232
AR208400
LOCUS AR208400 28 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 16 from patent US 6383752.
ACCESSION AR208400
VERSION AR208400.1 GI:21509544
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE Pseudo-cyclic oligonucleobases
JOURNAL Patent: US 6383752-A 16 07-MAY-2002;
FEATURES
source
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 671 ATCTGTGAGTGAGAACAGGTTGCACCTT 698
Db 1 ATCTGTGAGTGAGAACAGGTTGCACCTT 28

RESULT 233
AR259096
LOCUS AR259096 28 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 27 from patent US 6489455.
ACCESSION AR259096
VERSION AR259096.1 GI:27309607
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6489455-A 27 03-DEC-2002;
FEATURES
source
/mol_type="unknown"
/mol_type="genomic DNA"

Query Match 1.2%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 920 GGAGATATGTTGTGAAGAGCAGCTAGC 947
Db 1 GGAGATATGTTGTGAAGAGCAGCTAGC 28

RESULT 234
AR259097/c
LOCUS AR259097 28 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 28 from patent US 6489455.
ACCESSION AR259097
VERSION AR259097.1 GI:27309608
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6489455-A 27 03-DEC-2002;
FEATURES
source
/mol_type="unknown"
/mol_type="genomic DNA"

Query Match 1.2%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2233 CCACCACACCTGGCTAAATTTTGTACTTTAGTA 2267
Db 35 CCACAACGCCGCGCTAAATTTTGTACTTTTGGTA 1

RESULT 236
A25214
LOCUS A25214 32 bp DNA linear PAT 11-APR-1995
DEFINITION Inter-Alu specific primer DNA (pdj33a) from patent WO9213101.
ACCESSION A25214
VERSION A25214.1 GI:904594
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 27.6; DB 1; Length 35;
Best Local Similarity 85.7%; Pred. No. 4.6e+02;
Matches 30; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2233 CCACCACACCTGGCTAAATTTTGTACTTTAGTA 2267
Db 35 CCACAACGCCGCGCTAAATTTTGTACTTTTGGTA 1

RESULT 236
A25214
LOCUS A25214 32 bp DNA linear PAT 11-APR-1995
DEFINITION Inter-Alu specific primer DNA (pdj33a) from patent WO9213101.
ACCESSION A25214
VERSION A25214.1 GI:904594
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 27.4; DB 1; Length 32;
Best Local Similarity 96.8%; Pred. No. 4.5e+02;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2332 TCGGCCTCCCAAGTGTGGATTACAGG 2360

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TITLE Methods of assaying differential expression
JOURNAL Patent: US 6489455-A 28 03-DEC-2002;
FEATURES
source
/mol_type="unknown"
/mol_type="genomic DNA"

Query Match 1.2%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1204 CCTTAGCTGACTATTGGAATGCACCTTC 1231
Db 28 CCTTAGCTGACTATTGGAATGCACCTTC 1

RESULT 235
AX184110/c
LOCUS AX184110 35 bp DNA linear PAT 06-AUG-2001
DEFINITION Sequence 1863 from Patent WO0142511.
ACCESSION AX184110
VERSION AX184110.1 GI:15135450
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Daly,M., Hudson,T.J., Lander,E.S., Rioux,J. and Siminovitch,K.
TITLE Ibd-related polymorphisms
JOURNAL Patent: WO 0142511-A 1863 14-JUN-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
Biotherapeutics Corporation (CA)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 27.6; DB 1; Length 35;
Best Local Similarity 85.7%; Pred. No. 4.6e+02;
Matches 30; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2233 CCACCACACCTGGCTAAATTTTGTACTTTAGTA 2267
Db 35 CCACAACGCCGCGCTAAATTTTGTACTTTTGGTA 1

RESULT 236
A25214
LOCUS A25214 32 bp DNA linear PAT 11-APR-1995
DEFINITION Inter-Alu specific primer DNA (pdj33a) from patent WO9213101.
ACCESSION A25214
VERSION A25214.1 GI:904594
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 27.4; DB 1; Length 32;
Best Local Similarity 96.8%; Pred. No. 4.5e+02;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2332 TCGGCCTCCCAAGTGTGGATTACAGG 2360

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Db      4 TCCGCTCCCAAGTCTGGGATTACAG 32
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RESULT 237
E09142
LOCUS      32 bp DNA linear PAT 29-SEP-1997
DEFINITION Synthetic DNA for Alu specific primer.
ACCESSION E09142
VERSION    E09142.1 GI:22025768
KEYWORDS   JP 1995115999-A/5.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 32)
AUTHORS    Andressu,H.A. and Yan,P.
TITLE      DETECTING METHOD FOR DNA ARRANGEMENT VARIATION
JOURNAL    INGENII BV
COMMENT     OS None
           OC Artificial sequences.
           PN JP 1995115999-A/5
           PD 09-MAY-1995
           PF 22-MAY-1992 JP 1992130668
           PI ANDOREASU HERARUDOUSU AITSUTERURINDEN, YAN FUEIKU PC
           C12Q1/68.C12N15/00.G01N27/447.G01N27/447;
           CC strandedness: Single;
           CC topology: Linear;
           FH Key Location/Qualifiers
           FT source 1..32
           FT misc_feature 1..32 /notes='Artificial sequences' FT
           FT misc_feature 1..32 /notes='Alu specific primer'.

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/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 1.2%; Score 27.4; DB 1; Length 32;
Best Local Similarity 96.6%; Pred. No. 4.5e+02;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2332 TCGGCTCCCAAGTCTGGGATTACAG 2360
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Db      4 TCCGCTCCCAAGTCTGGGATTACAG 32
|||||

RESULT 238
AR208402
LOCUS      26 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 18 from patent US 6383752.
ACCESSION AR208402
VERSION    AR208402.1 GI:21509547
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 26)
AUTHORS    Agrawal,S. and Kandimalla,E.R.
TITLE      Pseudo-cyclic oligonucleobases
JOURNAL    Patent: US 6383752-A 18 07-MAY-2002;
FEATURES   Location/Qualifiers
source     1..26
           /organism='unknown'
           /mol_type='unassigned DNA'

Query Match 1.1%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 622 ACAGGAAGTCTGGTAGTCAATCAG 647
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Db      1 ACAGGAAGTCTGGTAGTCAATCAG 26
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RESULT 239
BD138344/c
LOCUS      26 bp DNA linear PAT 18-SEP-2002
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138344
VERSION    BD138344.1 GI:23233289
KEYWORDS   JP 2002508944-A/270.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 26)
AUTHORS    Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsert,L.M.
TITLE      Antisense modulation of human MDM2 expression
JOURNAL    Patent: JP 2002508944-A 270 26-MAR-2002;
           ISIS PHARMACEUTICALS INC
COMMENT     OS Unidentified
           PN JP 2002508944-A/270
           PD 26-MAR-2002
           PF 26-MAR-1999 JP 2000538025
           PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M
           PI COWSERT
           PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//
           PC C12Q1/68,
           PC C12N15/00
           CC Strandedness: Single;
           CC Topology: Linear;
           CC Antisense modulation of human MDM2 expression FH Key
           CC Location/Qualifiers
           FT source 1..26
           FT Location/Qualifiers
           FT source 1..26
           /organism='Unidentified'.

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/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 1.1%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 415 TGAAGTTATTAAAGTCTGTTGGTGCA 440
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Db      26 TGAAGTTATTAAAGTCTGTTGGTGCA 1
|||||

RESULT 240
AR214391
LOCUS      30 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 35 from patent US 6407062.
ACCESSION AR214391
VERSION    AR214391.1 GI:23312044
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 30)
AUTHORS    Sherr,C.J., Quelle,D., Rousnel,M.F., Zindy,F. and Weber,J.D.
TITLE      ARF-P19, a novel regulator of the mammalian cell cycle
JOURNAL    Patent: US 6407062-A 35 18-JUN-2002;
FEATURES   Location/Qualifiers
source     1..30
           /organism='unknown'
           /mol_type='genomic DNA'

Query Match 1.1%; Score 25.8; DB 1; Length 30;
Best Local Similarity 93.1%; Pred. No. 5.1e+02;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 312 ATGTGCAATACCAACATGCTGTACCTAC 340
Db 1 ATGTGCAATACCAACATGCTGTCTCTAC 29

/db_xref="taxon:32644"

Query Match 1.1%; Score 25.4; DB 1; Length 32;
Best Local Similarity 96.3%; Pred. No. 5.5e+02;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 241
A72114/c
LOCUS A72114 Sequence 69 from Patent WO9801467. 32 bp DNA linear PAT 11-MAY-1999
DEFINITION A72114
ACCESSION A72114
VERSION A72114.1 GI:4808071
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Lane,D., Boettger,V., Boettger,A., Picklesley,S., Hochkeppel,H.,
TITLE INHIBITORS OF THE INTERACTION BETWEEN P53 AND MDM2
JOURNAL Patent: WO 9801467-A 69 15-JAN-1998;
FEATURES
source Location/Qualifiers
1..32
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.1%; Score 25.4; DB 1; Length 32;
Best Local Similarity 96.3%; Pred. No. 5.5e+02;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1764 ATGTGCTAACTTATTTCCCTAGTTG 1790
Db 32 ATGTGCTAACTTATTTCCCTAGCTG 6

/db_xref="taxon:32644"

Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2335 GCCTCCCAAAGTCTGGATTACAG 2359
Db 1 GCCTCCCAAAGTCTGGATTACAG 25

/db_xref="taxon:32644"

Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2185 CCATTCTCTGCTCAGCTCCCAA 2209
Db 25 CCATTCTCTGCTCAGCTCCCAA 1

/db_xref="taxon:32630"
/notes="Primer"

Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 245
AX693020
LOCUS AX693020 25 bp DNA linear PAT 31-MAR-2003

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DEFINITION Sequence 5752 from Patent EP1281758.
ACCESSION AX693020
VERSION AX693020.1 GI:29415983
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5752 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred.No. 5.2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2274 GGGTTTCACCGTGTAGCCAGGATG 2298
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Db 1 GGGTTTCACCGTGTAGCCAGGATG 25
Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred.No. 5.2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2274 GGGTTTCACCGTGTAGCCAGGATG 2298
|||||
Db 1 GGGTTTCACCGTGTAGCCAGGATG 25
RESULT 246
AX693021
LOCUS AX693021 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5753 from Patent EP1281758.
ACCESSION AX693021
VERSION AX693021.1 GI:29415984
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5753 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
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Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred.No. 5.2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2275 GGTTCACCGTGTAGCCAGGATG 2299
|||||
Db 1 GGTTCACCGTGTAGCCAGGATG 25
RESULT 247
AX693022
LOCUS AX693022 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5754 from Patent EP1281758.
ACCESSION AX693022
VERSION AX693022.1 GI:29415985
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1

AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5754 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred.No. 5.2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2276 GTTTCACCGTGTAGCCAGGATGT 2300
|||||
Db 1 GTTTCACCGTGTAGCCAGGATGT 25
RESULT 248
AX693023
LOCUS AX693023 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5755 from Patent EP1281758.
ACCESSION AX693023
VERSION AX693023.1 GI:29415986
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5755 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred.No. 5.2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2277 TTTCACCGTGTAGCCAGGATGTGC 2301
|||||
Db 1 TTTCACCGTGTAGCCAGGATGTGC 25
RESULT 249
AX693024
LOCUS AX693024 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5756 from Patent EP1281758.
ACCESSION AX693024
VERSION AX693024.1 GI:29415987
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5756 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
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/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2278 TTCACCGTGTAGCCAGGATGGTCT 2302
|||||
Db 1 TTCACCGTGTAGCCAGGATGGTCT 25

RESULT 250
AX693025
LOCUS 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5757 from Patent EPI281758.
ACCESSION AX693025
VERSION AX693025.1 GI:29415988
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5757 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2279 TCACCGTGTAGCCAGGATGGTCTC 2303
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Db 1 TCACCGTGTAGCCAGGATGGTCTC 25

RESULT 251
AX693026
LOCUS 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5758 from Patent EPI281758.
ACCESSION AX693026
VERSION AX693026.1 GI:29415989
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5758 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2280 CACCGTGTAGCCAGGATGGTCTCG 2304
|||||
Db 1 CACCGTGTAGCCAGGATGGTCTCG 25

RESULT 252
AX693027
LOCUS 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5759 from Patent EPI281758.
ACCESSION AX693027
VERSION AX693027.1 GI:29415990
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5759 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2281 ACCGTGTAGCCAGGATGGTCTCGA 2305
|||||
Db 1 ACCGTGTAGCCAGGATGGTCTCGA 25

RESULT 253
AX693028
LOCUS 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5760 from Patent EPI281758.
ACCESSION AX693028
VERSION AX693028.1 GI:29415991
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5760 05-FEB-2003;
Aeomica, Inc. (US)
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2282 CCGTGTAGCCAGGATGGTCTCGAT 2306
|||||
Db 1 CCGTGTAGCCAGGATGGTCTCGAT 25

RESULT 254
AX693029
LOCUS 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5761 from Patent EPI281758.
ACCESSION AX693029
VERSION AX693029.1 GI:29415992
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5761 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2283 CGTGTAGCCAGGATGGTCTCGATC 2307
|||||
Db 1 CGTGTAGCCAGGATGGTCTCGATC 25
RESULT 255
AX693030
LOCUS AX693030 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5762 from Patent EP1281758.
ACCESSION AX693030
VERSION AX693030.1 GI:29415993
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5762 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2284 GTGTTAGCCAGGATGGTCTCGATCT 2308
|||||
Db 1 GTGTTAGCCAGGATGGTCTCGATCT 25
RESULT 256
AX693031
LOCUS AX693031 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5763 from Patent EP1281758.
ACCESSION AX693031
VERSION AX693031.1 GI:29415994
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5763 05-FEB-2003;

FEATURES Aeomica, Inc. (US)
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2285 TGTAGCCAGGATGGTCTCGATCTC 2309
|||||
Db 1 TGTAGCCAGGATGGTCTCGATCTC 25
RESULT 257
AX693032
LOCUS AX693032 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5764 from Patent EP1281758.
ACCESSION AX693032
VERSION AX693032.1 GI:29415995
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5764 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2286 GTTAGCCAGGATGGTCTCGATCTCC 2310
|||||
Db 1 GTTAGCCAGGATGGTCTCGATCTCC 25
RESULT 258
AX693033
LOCUS AX693033 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5765 from Patent EP1281758.
ACCESSION AX693033
VERSION AX693033.1 GI:29415996
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5765 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.1%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2287 GTTAGCCAGGATGGTCTCGATCTCC 2310
|||||
Db 1 GTTAGCCAGGATGGTCTCGATCTCC 25
RESULT 259
AX693034
LOCUS AX693034 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5766 from Patent EP1281758.
ACCESSION AX693034
VERSION AX693034.1 GI:29415997
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5766 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source
1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2287 TTAGCCAGGATGGTCTCGATCTCCT 2311
 |||||
 Db 1 TTAGCCAGGATGGTCTCGATCTCCT 25

RESULT 259
 AX693034
 LOCUS 25 bp DNA linear PAT 31-MAR-2003
 DEFINITION Sequence 5766 from Patent EP1281758.
 ACCESSION AX693034
 VERSION AX693034.1 GI:29415997
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 REFERENCE Shannon,M., Gu,Y. and Nguyen,C.T.
 AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
 TITLE mdz12
 JOURNAL Patent: EP 1281758-A 5766 05-FEB-2003;
 Aeomica, Inc. (US)
 FEATURES Location/Qualifiers
 source 1..25
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 1.1%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2288 TAGCCAGGATGGTCTCGATCTCCTG 2312
 |||||
 Db 1 TAGCCAGGATGGTCTCGATCTCCTG 25

RESULT 260
 AX693035
 LOCUS 25 bp DNA linear PAT 31-MAR-2003
 DEFINITION Sequence 5767 from Patent EP1281758.
 ACCESSION AX693035
 VERSION AX693035.1 GI:29415998
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 REFERENCE Shannon,M., Gu,Y. and Nguyen,C.T.
 AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
 TITLE mdz12
 JOURNAL Patent: EP 1281758-A 5767 05-FEB-2003;
 Aeomica, Inc. (US)
 FEATURES Location/Qualifiers
 source 1..25
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 1.1%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2289 AGCCAGGATGGTCTCGATCTCCTGA 2313
 |||||
 Db 1 AGCCAGGATGGTCTCGATCTCCTGA 25

RESULT 261
 AX693036

LOCUS AX693036 25 bp DNA linear PAT 31-MAR-2003
 DEFINITION Sequence 5768 from Patent EP1281758.
 ACCESSION AX693036
 VERSION AX693036.1 GI:29415999
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE Shannon,M., Gu,Y. and Nguyen,C.T.
 AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
 TITLE mdz12
 JOURNAL Patent: EP 1281758-A 5768 05-FEB-2003;
 Aeomica, Inc. (US)
 FEATURES Location/Qualifiers
 source 1..25
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 1.1%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2290 GCCAGGATGGTCTCGATCTCCTGAC 2314
 |||||
 Db 1 GCCAGGATGGTCTCGATCTCCTGAC 25

RESULT 262
 BD138345
 LOCUS 25 bp DNA linear PAT 18-SEP-2002
 DEFINITION Antisense modulation of human MDM2 expression.
 ACCESSION BD138345
 VERSION BD138345.1 GI:23233290
 KEYWORDS JP 2002508944-A/271.
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.

REFERENCE 1 (bases 1 to 25)
 AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
 TITLE Antisense modulation of human MDM2 expression
 JOURNAL Patent: JP 2002508944-A 271 26-MAR-2002;
 ISIS PHARMACEUTICALS INC
 COMMENT OS Unidentified
 EN JP 2002508944-A/271
 PD 26-MAR-2002
 PF 26-MAR-1999 JP 2000538025
 PR 26-MAR-1998 US 09/048810

PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M
 COWSEERT
 PC C12N15/09, A61K48/00, A61P9/10, A61P17/06, A61P35/00, C07H21/04//
 PC C12Q1/68,
 PC C12N15/00
 CC Strandedness: Single;
 CC Topology: Linear;
 CC Antisense modulation of human MDM2 expression FH Key
 Location/Qualifiers
 FT source 1..25
 /organism='Unidentified'.
 FT Location/Qualifiers
 source 1..25
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

Query Match 1.1%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CCACCTCACAGATTCACGCTCGGA 379

Db 1 CCACCTCACAGATCCAGCTTCGGA 25
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RESULT 263
AX117259/c
LOCUS AX117259 31 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 2382 from Patent WO0129262.
ACCESSION AX117259
VERSION AX117259.1 GI:14034210
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 2382 26-APR-2001;
Orchid BioSciences, Inc. (US)
FEATURES
source 1..31
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="caxon:32630"
/note="Primer"
Query Match 1.0%; Score 24.6; DB 1; Length 31;
Best Local Similarity 87.1%; Pred. No. 5.9e+02;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2256 GTACTTTTAGTAGACAGAGGGTTTCACCGTG 2286
|||||
Db 31 GTAGTTTAGTAGACAGAGGGTTTCATTATG 1
Query Match 1.0%; Score 24.6; DB 1; Length 31;
Best Local Similarity 87.1%; Pred. No. 5.9e+02;
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
LOCUS AX184256/c
AX184256 32 bp DNA linear PAT 06-AUG-2001
DEFINITION Sequence 2009 from Patent WO0142511.
ACCESSION AX184256
VERSION AX184256.1 GI:15135601
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Daly,M., Hudson,T.J., Lander,E.S., Rioux,J. and Siminovitch,K.
TITLE Ibd-related polymorphisms
JOURNAL Patent: WO 0142511-A 2009 14-JUN-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
FEATURES
source 1..32
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.0%; Score 24.6; DB 1; Length 32;
Best Local Similarity 84.4%; Pred. No. 5.9e+02;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2300 TCTCGATCTCTGACCTCGTGATCGGCCACC 2331
|||||
Db 32 TCTCGATCTCTGACCTCTGATCGGCTGCC 1
Query Match 1.0%; Score 24.6; DB 1; Length 32;
Best Local Similarity 84.4%; Pred. No. 5.9e+02;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
LOCUS AX117744
AX117744 27 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 2867 from Patent WO0129262.
ACCESSION AX117744
VERSION AX117744.1 GI:14034695
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 2382 26-APR-2001;
Orchid BioSciences, Inc. (US)
FEATURES
source 1..27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"
misc_feature 1..27
/notes="n = C3 linker"
Query Match 1.0%; Score 24.4; DB 1; Length 27;
Best Local Similarity 92.8%; Pred. No. 5.7e+02;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2304 GATCTCTGACCTCGTGATCGGCCAC 2330
|||||
Db 1 GATCTCTGACCTCGTGATCGGCCAC 27
RESULT 266
AR392160
LOCUS AR392160 29 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6613750.
ACCESSION AR392160
VERSION AR392160.1 GI:40116136
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 29)
AUTHORS DePinho,R.A.
TITLE Method of inhibiting cell proliferation using an anti-oncogene protein
JOURNAL Patent: US 6613750-A 1 02-SEP-2003;
FEATURES
source 1..29
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.0%; Score 24.2; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 6e+02;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 964 CGCCATCGAATCCGGATCTTGATGCTGGT 992
|||||
Db 1 CGCCATCTAGACCGGATCTTGATGCTGGT 29
RESULT 267
AR214384
LOCUS AR214384 30 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 28 from patent US 6407062.
ACCESSION AR214384
VERSION AR214384.1 GI:23312037
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Sherr,C.J., Quelle,D., Rousset,M.F., Zindy,F. and Weber,J.D.
TITLE ARF-P19, a novel regulator of the mammalian cell cycle
JOURNAL Patent: US 6407062-A 28 18-JUN-2002;
FEATURES
source 1..30
/organism="unknown"

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Query Match      1.0%; Score 24.2; DB 1; Length 30;
Best Local Similarity 89.7%; Pred. No. 6e+02;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

/mol_type="genomic DNA"

QY 934 AAGAAGCAGTAGCAGTGAATCTACAGG 962
Db 2 ATATGACGAGTAGCAGTGAATCTACAGG 30

RESULT 268
LOCUS AX184136/c
DEFINITION Sequence 1889 from Patent WO0142511.
ACCESSION AX184136
VERSION AX184136.1 GI:15135477
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
TOSHIHORI IDE
OS Artificial Sequence
PN JP 2001095586-A/1
PD 10-APR-2001
PF 30-SEP-1999 JP 1999279948
PI TOSHIHORI IDE, YASUHIRO NAKAMURA, MINORU HIROSE PC
C12N15/09, C12Q1/68, G01N33/50, C12N15/00 CC Synthetic DNA
FH Key Location/Qualifiers
FEATURES
source
1..30
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match      1.0%; Score 24.2; DB 1; Length 30;
Best Local Similarity 86.7%; Pred. No. 6e+02;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2090 TATTTTTTTTGAGACCGAGTCTGCTCTGT 2119
Db 30 TTTTITTTTNGAGACCGAGTCTGCTCTGT 1

RESULT 269
LOCUS E40923
DEFINITION Method for measuring telomeric size.
ACCESSION E40923
VERSION E40923.1 GI:22553151
KEYWORDS JP 2001095586-A/1.
SOURCE synthetic construct
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
TOSHIHORI IDE
OS Artificial Sequence
PN JP 2001095586-A/1
PD 10-APR-2001
PF 30-SEP-1999 JP 1999279948
PI TOSHIHORI IDE, YASUHIRO NAKAMURA, MINORU HIROSE PC
C12N15/09, C12Q1/68, G01N33/50, C12N15/00 CC Synthetic DNA
FH Key Location/Qualifiers
FEATURES
source
1..24
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      1.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAGTCTGGATTACA 2358
Db 24 GCCTCCCAAGTCTGGATTACA 1

RESULT 270
LOCUS E40925/c
DEFINITION Method for measuring telomeric size.
ACCESSION E40925
VERSION E40925.1 GI:22553153
KEYWORDS JP 2001095586-A/3.
SOURCE synthetic construct
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
TOSHIHORI IDE
OS Artificial Sequence
PN JP 2001095586-A/3
PD 10-APR-2001
PF 30-SEP-1999 JP 1999279948
PI TOSHIHORI IDE, YASUHIRO NAKAMURA, MINORU HIROSE PC
C12N15/09, C12Q1/68, G01N33/50, C12N15/00 CC Synthetic DNA
FH Key Location/Qualifiers
FEATURES
source
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      1.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAGTCTGGATTACA 2358
Db 24 GCCTCCCAAGTCTGGATTACA 1

RESULT 271
LOCUS AX693019
DEFINITION Sequence 5751 from Patent EP1281758.
ACCESSION AX693019
VERSION AX693019.1 GI:29415982
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Shannon, M., Gu, Y. and Nguyen, C. T.
Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
Patent: EP 1281758-A 5751 05-FEB-2003;
Neomica, Inc. (US)
FH Key Location/Qualifiers
FEATURES
source
1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      1.0%; Score 24; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GCGTTTCACCGTGTAGCCAGGAT 2297
Db 2274 GCGTTTCACCGTGTAGCCAGGAT 2297

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Db      2  GGGTTTACCGTGTTAGCCAGAT 25

RESULT 272
AX693037
LOCUS      25 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 5769 from Patent EPI281758.
ACCESSION  AX693037
VERSION     AX693037.1  GI:29416000
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL   Patent: EP 1281758-A 5769 05-FEB-2003;
          mdz12
FEATURES   source
            location/Qualifiers
            1..25
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      1.0%; Score 24; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2291  CCAGGATGGTCTCGATCTCCTGAC 2314
          |||||
          1  CCAGGATGGTCTCGATCTCCTGAC 24

Db

RESULT 273
A72116
LOCUS      27 bp      DNA      linear      PAT 11-MAY-1999
DEFINITION Sequence 71 from Patent WO9801467.
ACCESSION  A72116
VERSION     A72116.1  GI:4808073
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 27)
AUTHORS   Lane,D., Boettger,V., Boettger,A., Picksley,S., Hochkeppel,H.,
          Garcia-Echeverria,C., Chene,P. and Furet,P.
TITLE     INHIBITORS OF THE INTERACTION BETWEEN P53 AND MDM2
JOURNAL   Patent: WO 9801467-A 71 15-JAN-1998;
          CIBA GEIGY AG (CH)
FEATURES   location/Qualifiers
            source
            1..27
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match      1.0%; Score 24; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1191  GATCCTGAAATTCCTTAGCTGAC 1214
          |||||
          4  GATCCTGAAATTCCTTAGCTGAC 27

Db

RESULT 274
BD003108
LOCUS      27 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION Inhibitor of interaction between P53 and MDM2.
ACCESSION  BD003108
VERSION     BD003108.1  GI:18631069
KEYWORDS   JP 2001500365-A/5.

SOURCE     unidentified
            unclassified.
            1 (bases 1 to 27)
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match      1.0%; Score 24; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1191  GATCCTGAAATTCCTTAGCTGAC 1214
          |||||
          4  GATCCTGAAATTCCTTAGCTGAC 27

Db

RESULT 275
A68624
LOCUS      30 bp      DNA      linear      PAT 06-MAY-1999
DEFINITION Sequence 4 from Patent WO9801573.
ACCESSION  A68624
VERSION     A68624.1  GI:4759651
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 30)
AUTHORS   Resnick,M.A., Lariouov,V.L., Kouprina,N.Y. and Perkins,E.L.
TITLE     TRANSFORMATION-ASSOCIATED RECOMBINATION CLONING
JOURNAL   Patent: WO 9801573-A 4 15-JAN-1998;
          US HEALTH (US)
FEATURES   location/Qualifiers
            source
            1..30
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match      1.0%; Score 23.6; DB 1; Length 30;
Best Local Similarity 86.7%; Pred. No. 6.4e+02;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2097  TTTGAGACCGAGTCTGCTGTACCCAG 2126
          |||||
          1  TTTGAGACCGAGTCTGCTGTACCCAG 30

Db

RESULT 276
AX118472
LOCUS      25 bp      DNA      linear      PAT 11-MAY-2001

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SOURCE     unidentified
            unclassified.
            1 (bases 1 to 27)
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

REFERENCE  1
AUTHORS   Lane,D., Boettger,V., Boettger,A., Picksley,S., Hochkeppel,H.K.,
          Echeverria,C.G., Chene,P. and Furet,P.
TITLE     Inhibitor of interaction between P53 and MDM2
JOURNAL   Patent: JP 2001500365-A 5 16-JAN-2001;
          NOVARTIS AG,CANCER RESEARCH CAMPAIGN TECHNOLOGY LTD
COMMENT    OS Unidentified
            PN JP 2001500365-A/5
            PD 16-JAN-2001
            PR 04-JUL-1996 GB 9614197.3,07-APR-1997 GB 9707041.1 PI
            DAVID LANE,VOLKER BOETTGER,ANGELIKA ECHEVERRIA,PATRICK CHENE, PI
            HEINZ KURT HOCHKEPPEL,CARLOS GARCIA ECHEVERRIA,PATRICK CHENE, PI
            PASCAL FURET
            PC C12N15/09,A61K38/00,A61K45/00,A61P35/00,C07K7/06,C07K7/08, PC
            C12Q1/68,
            PC G01N33/53//C07K14/82,C12N15/00,A61K37/02
            CC Strandedness: Single;
            CC Topology: Linear;
            FH Key Location/Qualifiers
            FT source 1..27
            /organism="Unidentified".
            FT Location/Qualifiers
            1..27
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

Query Match      1.0%; Score 24; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1191  GATCCTGAAATTCCTTAGCTGAC 1214
          |||||
          4  GATCCTGAAATTCCTTAGCTGAC 27

Db

RESULT 275
A68624
LOCUS      30 bp      DNA      linear      PAT 06-MAY-1999
DEFINITION Sequence 4 from Patent WO9801573.
ACCESSION  A68624
VERSION     A68624.1  GI:4759651
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 30)
AUTHORS   Resnick,M.A., Lariouov,V.L., Kouprina,N.Y. and Perkins,E.L.
TITLE     TRANSFORMATION-ASSOCIATED RECOMBINATION CLONING
JOURNAL   Patent: WO 9801573-A 4 15-JAN-1998;
          US HEALTH (US)
FEATURES   location/Qualifiers
            source
            1..30
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match      1.0%; Score 23.6; DB 1; Length 30;
Best Local Similarity 86.7%; Pred. No. 6.4e+02;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2097  TTTGAGACCGAGTCTGCTGTACCCAG 2126
          |||||
          1  TTTGAGACCGAGTCTGCTGTACCCAG 30

Db

RESULT 276
AX118472
LOCUS      25 bp      DNA      linear      PAT 11-MAY-2001

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FEATURES	source	Curagen Corporation (US)	Location/Qualifiers	1. .25	/organism="synthetic construct"	/mol_type="unassigned DNA"	/db_xref="taxon:32630"	/note="Description of Artificial Sequence: NOV22c Primer"
Query Match				1.0%; Score 23.4; DB 1; Length 25;				
Best Local Similarity				96.0%; Pred. NO. 6.1e+02;				
Matches	24; Conservative	0; Mismatches	1; Indels	0; Gaps				
Qy	2295	GATGGTCTCGATCTCTGACCTCGT	2319					
Db	1	GATGGTCTCGATCTCTGACCTCTT	25					
RESULT 279								
AX118000								
LOCUS		AX118000	27 bp	DNA				linear PAT 11-MAY-2000
DEFINITION		Sequence 3123 from Patent WO0129262.						
ACCESSION		AX118000						
VERSION		AX118000.1	GI:14034951					
KEYWORDS								
SOURCE		synthetic construct						
ORGANISM		synthetic construct						
REFERENCE	1	artificial sequences.						
AUTHORS		Picoult-Newburg,L. and Pohl,M.						
TITLE		Genotyping reagents, kits and methods of use thereof						
JOURNAL		Patent: WO 0129262-A 3123 26-APR-2001;						
		Orchid Biosciences, Inc. (US)						
FEATURES								
source		Location/Qualifiers						
misc_feature	1. .27	/organism="synthetic construct"						
		/mol_type="unassigned DNA"						
		/db_xref="taxon:32630"						
		/note="Primer"						
	1. .27	/note="n = C3 linker"						
Query Match				1.0%; Score 23.4; DB 1; Length 27;				
Best Local Similarity				88.9%; Pred. NO. 6.3e+02;				
Matches	24; Conservative	0; Mismatches	3; Indels	0; Gaps				
Qy	2302	TGATCTCTCGACCTCGTGATCCGCC	2328					
Db	1	TGATCTCTCGACCTCGTGATCCGCC	27					
RESULT 280								
AX118407								
LOCUS		AX118407	30 bp	DNA				linear PAT 11-MAY-2000
DEFINITION		Sequence 3530 from Patent WO0129262.						
ACCESSION		AX118407						
VERSION		AX118407.1	GI:14035358					
KEYWORDS								
SOURCE		synthetic construct						
ORGANISM		synthetic construct						
REFERENCE	1	artificial sequences.						
AUTHORS		Picoult-Newburg,L. and Pohl,M.						
TITLE		Genotyping reagents, kits and methods of use thereof						
JOURNAL		Patent: WO 0129262-A 3530 26-APR-2001;						
		Orchid Biosciences, Inc. (US)						
FEATURES								
source		Location/Qualifiers						
misc_feature	1. .30	/organism="synthetic construct"						
		/mol_type="unassigned DNA"						
		/db_xref="taxon:32630"						
		/note="Primer"						
Query Match				1.0%; Score 23.2; DB 1; Length 30;				

Best Local Similarity 89.3%; Pred. No. 6.6e+02;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2249 ATTCTTTCTACTTTTGTAGTAGACAGGG 2276
| | | | | | | | | | | | | | | | | | | | |
Db 3 AATTTTGTATTTTGTAGTAGACAGGG 30

RESULT 281
LOCUS CQ766174 23 bp DNA PAT 03-MAR-2004
DEFINITION Sequence 135 from Patent WO2004/005547.
ACCESSION CQ766174
VERSION CQ766174.1 GI:44908434
KEYWORDS synthetic construct
ORGANISM synthetic construct
SOURCE artificial sequences.
REFERENCE 1
AUTHORS Weinzierl, R.
TITLE Method
JOURNAL IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES
source
1. .23
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="HS consensus sequence"

Query Match 1.0%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2345 GTGCTGGGATTACAGGCATGAGC 2367
| | | | | | | | | | | | | | | | | | | | |
Db 1 GTGCTGGGATTACAGGCATGAGC 23

RESULT 282
LOCUS AR300897/c 23 bp DNA PAT 12-JUN-2003
DEFINITION Sequence 4 from patent US 6537984.
ACCESSION AR300897
VERSION AR300897.1 GI:31688464
KEYWORDS Unknown.
ORGANISM Unknown.
SOURCE Unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Rosen, G.D., Lennox, E.S. and Musser, J.H.
TITLE Uses of diterpenoid triepoxides as an anti-proliferative agent
JOURNAL Patent: US 6537984-A 4 25-MAR-2003;
FEATURES Location/Qualifiers
source
1. .23
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1374 GAGGCGTTTGATGTTCTGATTG 1396
| | | | | | | | | | | | | | | | | | | | |
Db 23 GAGGCGTTTGATGTTCTGATTG 1

RESULT 283
LOCUS AR361046/c 23 bp DNA PAT 17-AUG-2003
DEFINITION Sequence 4 from patent US 6599499.
ACCESSION AR361046
VERSION AR361046.1 GI:33768613

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Rosen, G.D., Lennox, E.S. and Musser, J.H.
TITLE Uses of diterpenoid triepoxides as an anti-proliferative agent
JOURNAL Patent: US 6599499-A 4 29-JUL-2003;
FEATURES Location/Qualifiers
source
1. .23
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1374 GAGGCGTTTGATGTTCTGATTG 1396
| | | | | | | | | | | | | | | | | | | | |
Db 23 GAGGCGTTTGATGTTCTGATTG 1

RESULT 284
LOCUS AX693018 25 bp DNA PAT 31-MAR-2003
DEFINITION Sequence 5750 from Patent EPI281758.
ACCESSION AX693018
VERSION AX693018.1 GI:29415981
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5750 05-FEB-2003;
FEATURES Location/Qualifiers
source
1. .25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 23; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGTTTCACCGTGTAGCCAGGA 2296
| | | | | | | | | | | | | | | | | | | | |
Db 3 GGTTTCACCGTGTAGCCAGGA 25

RESULT 285
LOCUS AR089946 26 bp DNA PAT 07-SEP-2000
DEFINITION Sequence 66 from patent US 5994076.
ACCESSION AR089946
VERSION AR089946.1 GI:10016701
KEYWORDS Unknown.
ORGANISM Unknown.
SOURCE Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Chenchik, A., Jokhadze, G. and Bibilashvili, R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 66 30-NOV-1999;
FEATURES Location/Qualifiers
source
1. .26
/organism="unknown"
/mol_type="unassigned DNA"

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Query Match      1.0%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 6.6e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2342 AAAGTCTGGGATTACAGGCATGAGC 2367
||||| ||||||| ||||||| ||||||| |||||||
Db 1 AAAGTCTAGGATTACAGGCGTGAGC 26

RESULT 286
LOCUS AR196981 26 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 66 from patent US 6352829.
ACCESSION AR196981
VERSION AR196981.1 GI:20246830
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 66 05-MAR-2002;
FEATURES
Location/Qualifiers
source
1..26
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      1.0%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 6.6e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2342 AAAGTCTGGGATTACAGGCATGAGC 2367
||||| ||||||| ||||||| ||||||| |||||||
Db 1 AAAGTCTAGGATTACAGGCGTGAGC 26

RESULT 287
LOCUS AR259135 26 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 66 from patent US 6489455.
ACCESSION AR259135
VERSION AR259135.1 GI:27309646
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6489455-A 66 03-DEC-2002;
FEATURES
Location/Qualifiers
source
1..26
/organism="unknown"
/mol_type="genomic DNA"

Query Match      1.0%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 6.6e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2342 AAAGTCTGGGATTACAGGCATGAGC 2367
||||| ||||||| ||||||| ||||||| |||||||
Db 1 AAAGTCTAGGATTACAGGCGTGAGC 26

RESULT 288
LOCUS AX116952 27 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 2075 from Patent WO0129262.
ACCESSION AX116952
VERSION AX116952.1 GI:14033894
KEYWORDS
SOURCE synthetic construct
```

```
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 2075 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES
Location/Qualifiers
source
1..27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"
misc_feature
1..27
/note="n = C3 linker"

Query Match      1.0%; Score 22.8; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 6.7e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2344 AGTCTGGGATTACAGGCATGAGCCAC 2370
||||| ||||||| ||||||| ||||||| |||||||
Db 1 AGTCTGGGATTACAGGCATGAGCCAC 27

RESULT 289
LOCUS AX118160 27 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 3283 from Patent WO0129262.
ACCESSION AX118160
VERSION AX118160.1 GI:14035111
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 3283 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES
Location/Qualifiers
source
1..27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"
misc_feature
1..27
/note="n = C3 linker"

Query Match      1.0%; Score 22.8; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 6.7e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2332 TCGGCTCCCAAAGTCTGGGATTACA 2358
||||| ||||||| ||||||| ||||||| |||||||
Db 1 TTGGCTCNCACAGTGTCTGGGATTACA 27

RESULT 290
LOCUS AX116662 30 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 1785 from Patent WO0129262.
ACCESSION AX116662
VERSION AX116662.1 GI:14033604
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 1785 26-APR-2001;
Orchid Biosciences, Inc. (US)
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FEATURES
source
Location/Qualifiers
1..30
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match
Best Local Similarity 1.0%; Score 22.8; DB 1; Length 30;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2250 TTTTGTGACTTTAGTAGACAGG 2275
|||||
Db 5 TTTTGTGACTTTAGTAGACGG 30
|||||

RESULT 291
AR051440/c
LOCUS
DEFINITION Sequence 6 from patent US 5830670.
ACCESSION AR051440
VERSION AR051440.1 GI:5974804
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS de la Monte,S. and Wands,J.R.
TITLE Neural thread protein gene expression and detection of Alzheimer's disease
JOURNAL Patent: US 5830670-A 6 03-NOV-1998;
FEATURES Location/Qualifiers
source
1..30
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.0%; Score 22.6; DB 1; Length 30;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2179 TTCGACCATTCCTCGCTCAGCTCCC 2207
|||||
Db 30 TTCAGCGATTCTCTCGCTCAGCTCCC 2
|||||

RESULT 292
AR072580/c
LOCUS
DEFINITION Sequence 6 from patent US 5948634.
ACCESSION AR072580
VERSION AR072580.1 GI:9999344
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS de la Monte,S. and Wands,J.R.
TITLE Neural thread protein gene expression and detection of Alzheimer's disease
JOURNAL Patent: US 5948634-A 6 07-SEP-1999;
FEATURES Location/Qualifiers
source
1..30
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.0%; Score 22.6; DB 1; Length 30;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2179 TTCGACCATTCCTCGCTCAGCTCCC 2207
|||||
Db 30 TTCAGCGATTCTCTCGCTCAGCTCCC 2
|||||

RESULT 293
AR073125/c
LOCUS
DEFINITION Sequence 6 from patent US 5948888.
ACCESSION AR073125
VERSION AR073125.1 GI:9999888
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS de la Monte,S. and Wands,J.R.
TITLE Neural thread protein gene expression and detection of Alzheimer's disease
JOURNAL Patent: US 5948888-A 6 07-SEP-1999;
FEATURES Location/Qualifiers
source
1..30
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.0%; Score 22.6; DB 1; Length 30;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2179 TTCGACCATTCCTCGCTCAGCTCCC 2207
|||||
Db 30 TTCAGCGATTCTCTCGCTCAGCTCCC 2
|||||

RESULT 294
AX092647
LOCUS
DEFINITION Sequence 59 from Patent WO0115676.
ACCESSION AX092647
VERSION AX092647.1 GI:13444704
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Hayden,M.R., Brooks-Wilson,A.R., Pimstone,S.N. and Clee,S.M.
TITLE Compositions and methods for modulating hdl cholesterol and triglyceride levels
JOURNAL Patent: WO 0115676-A 59 08-MAR-2001;
FEATURES Location/Qualifiers
source
1..24
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.9%; Score 22.4; DB 1; Length 24;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2301 CTCGATCTCTGACCTCGTGATCC 2324
|||||
Db 1 CTCGATCTCTGACCTCGTGATCC 24
|||||

RESULT 295
AR322085/c
LOCUS
DEFINITION Sequence 10 from patent US 6566053.
ACCESSION AR322085
VERSION AR322085.1 GI:33707625
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)

AUTHORS Perucho,M., Peinado,M.A., Ionov,Y., Malkhosyan,S., McClelland,M. and Welsh,J.
 TITLE Identification of neoplasms by detection of genetic insertions and deletions
 JOURNAL Patent: US 6566053-A 10 20-MAY-2003;
 FEATURES Location/Qualifiers
 source
 1. .25
 /organism="unknown"
 /mol_type="mRNA"

Query Match 0.9%; Score 22.4; DB 1; Length 25;
 Best Local Similarity 95.8%; Pred. No. 6.7e+02;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGACAGAGGCTTTCACC 2283
 |||||
 Db 24 TTTTAGTAGACAGAGGCTTTCACC 1

RESULT 296
 AX184030/c
 LOCUS AX184030 29 bp DNA linear PAT 06-AUG-2001
 DEFINITION Sequence 1783 from Patent WO0142511.
 ACCESSION AX184030
 VERSION AX184030.1 GI:15135366
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 AUTHORS Daly,M., Hudson,T.J., Lander,E.S., Rioux,J. and Siminovitch,K.
 TITLE Ibd-related polymorphisms
 JOURNAL Patent: WO 0142511-A 1783 14-JUN-2001;
 WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
 Biotherapeutics Corporation (CA)
 FEATURES Location/Qualifiers
 source
 1. .29
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.9%; Score 22.4; DB 1; Length 29;
 Best Local Similarity 92.0%; Pred. No. 7.1e+02;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2230 CTGCCACCACCTGGCTAATTTT 2254
 |||||
 Db 25 CTGCCACCACCTGGCTAATTTT 1

RESULT 297
 AR044033
 LOCUS AR044033 22 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 1 from patent US 5817462.
 ACCESSION AR044033
 VERSION AR044033.1 GI:5965498
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 1 (bases 1 to 22)
 REFERENCE Garini,Y., Cabib,D., Buckwald,R.A., Ried,T. and Soenksen,D.G.
 AUTHORS Method for simultaneous detection of multiple fluorophores for in
 TITLE situ hybridization and multicolor chromosome painting and banding
 JOURNAL Patent: US 5817462-A 1 06-OCT-1998;
 FEATURES Location/Qualifiers
 source
 1. .22
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.9%; Score 22; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2338 TCCCAAAGTCTGGGATTACAG 2359
 |||||
 Db 1 TCCCAAAGTCTGGGATTACAG 22

RESULT 298
 AR208403/c
 LOCUS AR208403 22 bp DNA linear PAT 20-JUN-2002
 DEFINITION Sequence 19 from patent US 6383752.
 ACCESSION AR208403
 VERSION AR208403.1 GI:21509548
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 1 (bases 1 to 22)
 REFERENCE 1 (bases 1 to 22)
 AUTHORS Agrawal,S. and Kandimalia,E.R.
 TITLE Pseudo-cyclic oligonucleobases
 JOURNAL Patent: US 6383752-A 19 07-MAY-2002;
 FEATURES Location/Qualifiers
 source
 1. .22
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.9%; Score 22; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 679 GTGAGAACAGGTGTCACTTGA 700
 |||||
 Db 22 GTGAGAACAGGTGTCACTTGA 1

RESULT 299
 AR300896
 LOCUS AR300896 22 bp DNA linear PAT 12-JUN-2003
 DEFINITION Sequence 3 from patent US 6537984.
 ACCESSION AR300896
 VERSION AR300896.1 GI:31688463
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 1 (bases 1 to 22)
 REFERENCE 1 (bases 1 to 22)
 AUTHORS Rosen,G.D., Lennox,E.S. and Musser,J.H.
 TITLE Uses of diterpenoid triepoxides as an anti-proliferative agent
 JOURNAL Patent: US 6537984-A 3 25-MAR-2003;
 FEATURES Location/Qualifiers
 source
 1. .22
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 0.9%; Score 22; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 639 GTCATCAGCAGGAATCATCGG 660
 |||||
 Db 1 GTCATCAGCAGGAATCATCGG 22

RESULT 300
 AR361045
 LOCUS AR361045 22 bp DNA linear PAT 17-AUG-2003
 DEFINITION Sequence 3 from patent US 6599499.
 ACCESSION AR361045
 VERSION AR361045.1 GI:33768612
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.

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REFERENCE 1 (bases 1 to 22)
AUTHORS Rosen,G.D., Lennox,E.S. and Musser,J.H.
TITLE Uses of diterpenoid triepoxides as an anti-proliferative agent
JOURNAL Patent: US 659499-A 3 29-JUL-2003;
FEATURES
    source
        1..22
            /organism="unknown"
            /mol_type="genomic DNA"
Query Match 0.9%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 639 GTCATCAGCAGGATCATCGG 660
Db 1 GTCATCAGCAGGATCATCGG 22

RESULT 301
LOCUS AR393736/c 22 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 275 from patent US 6617122.
ACCESSION AR393736
VERSION AR393736.1 GI:40120580
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Hayden,M.R., Brooks-Wilson,A.R. and Pimstone,S.N.
TITLE Process for identifying modulators of ABC1 activity
JOURNAL Patent: US 6617122-A 275 09-SEP-2003;
FEATURES
    source
        1..22
            /organism="unknown"
            /mol_type="genomic DNA"
Query Match 0.9%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2188 TTCTCTGCTCAGCTCCCAA 2209
Db 22 TTCTCTGCTCAGCTCCCAA 1

RESULT 302
LOCUS AX693017 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5749 from Patent EP1281758.
ACCESSION AX693017
VERSION AX693017.1 GI:29415980
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5749 05-FEB-2003;
FEATURES
    source
        1..25
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match 0.9%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2274 GGTTTTCACCGTGTAGCCAG 2295
Db 4 GGTTTTCACCGTGTAGCCAG 25

RESULT 303
LOCUS E50643/c 25 bp DNA linear PAT 31-JAN-2002
DEFINITION Simple detection method of drug-metabolizing synthetase gene polymorphism.
ACCESSION E50643
VERSION E50643.1 GI:18629424
KEYWORDS JP 2001017185-A/7.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 25)
AUTHORS Mizugaki,M. and Hiratauka,M.
TITLE Simple detection method of drug-metabolizing synthetase gene
JOURNAL Patent: JP 2001017185-A 7 23-JAN-2001;
COMMENT OTSUKA PHARMACEUT CO LTD
OS Unidentified
PN JP 2001017185-A/7
PD 23-JAN-2001
PE 10-DEC-1999 JP 1999351610
PR MICHINAO MIZUGAKI, MASAHIRO HIRATSUKA
PI C12N15/09,C12Q1/68,C12Q1/68,C12N15/00
PC CC
FH Key Location/Qualifiers
FT source 1..25
FT /organism='Unidentified'.
FEATURES
    source
        1..25
            Location/Qualifiers
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"
Query Match 0.9%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 7.2e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2269 AGACAGGTTTACCGTGTAGCCA 2293
Db 25 AGACAGGTTTACCATGTGGCCA 1

RESULT 304
LOCUS AX614112 25 bp DNA linear PAT 17-FEB-2003
DEFINITION Sequence 5137 from Patent WO02072882.
ACCESSION AX614112
VERSION AX614112.1 GI:28409541
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Cullen,P. and Seedorf,U.
TITLE Coronary chip
JOURNAL Patent: WO 02072882-A 5137 19-SEP-2002;
FEATURES
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Query Match 0.9%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 7.2e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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AX692928					
ACCESSION	AX692928.1 GI:29415891				
VERSION					
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE					
AUTHORS	Shannon,M., Gu,Y. and Nguyen,C.T.				
TITLE	Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12				
JOURNAL	Patent: EP 1281758-A 5660 05-FEB-2003;				
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source	Aeomica, Inc. (US) Location/Qualifiers 1..25 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"				
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Oy	2183 CACCATTCTCCTGCCTCAGCTGCC 2207				
Db	 1 CACCATTCTCCTGCTTCAGTCTGCC 25				
RESULT 308					
AX692991	AX692991 25 bp DNA linear PAT 31-MAR-2003				
LOCUS	Sequence 5723 from Patent EPI281758.				
DEFINITION	AX692991				
ACCESSION	AX692991.1 GI:29415954				
VERSION					
KEYWORDS	Homo sapiens (human)				
SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE					
AUTHORS	Shannon,M., Gu,Y. and Nguyen,C.T.				
TITLE	Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12				
JOURNAL	Patent: EP 1281758-A 5723 05-FEB-2003;				
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Best Local Similarity 92.0%; Pred.No. 7.2e+02;					
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
Oy	2246 CTAATTTTGTACTTTTAGTAGAG 2270				
Db	 1 CTAATATTTTGATTTTTAGTAGAG 25				
RESULT 309					
AX692992	AX692992 25 bp DNA linear PAT 31-MAR-2003				
LOCUS	Sequence 5724 from Patent EPI281758.				
DEFINITION	AX692992				
ACCESSION	AX692992.1 GI:29415955				
VERSION					
KEYWORDS	Homo sapiens (human)				
SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE					
AUTHORS	Shannon,M., Gu,Y. and Nguyen,C.T.				

TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12

JOURNAL Patent: EP 1281758-A 5724 05-FEB-2003;

Acemica, Inc. (US)

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 21.8; DB 1; Length 25;
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QY 2247 TAATTTTGTGACTTTTAGTAGAGA 2271

Db 1 TAATATTGTGATTATTTTAGTAGAGA 25

RESULT 310
AX692993
LOCUS AX692993 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5725 from Patent EP1281758.
ACCESSION AX692993
VERSION AX692993.1 GI:29415956
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12

JOURNAL Patent: EP 1281758-A 5725 05-FEB-2003;
Acemica, Inc. (US)

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/db_xref="taxon:9606"

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QY 2248 AATTTTGTGACTTTTAGTAGAGAC 2272

Db 1 AATATTGTGATTATTTTAGTAGAGAC 25

RESULT 311
AX692997
LOCUS AX692997 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5729 from Patent EP1281758.
ACCESSION AX692997
VERSION AX692997.1 GI:29415960
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12

JOURNAL Patent: EP 1281758-A 5729 05-FEB-2003;
Acemica, Inc. (US)

FEATURES

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/mol_type="unassigned DNA"
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QY 2252 TTTTGACTTTTAGTAGAGACGGG 2276

Db 1 TTTTGATTATTAGTAGAGACGGG 25

RESULT 312
AX184125
LOCUS AX184125 27 bp DNA linear PAT 06-AUG-2001
DEFINITION Sequence 1878 from Patent WO0142511.
ACCESSION AX184125
VERSION AX184125.1 GI:15135465
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Daly,M., Hudson,T.J., Lander,E.S., Rioux,J. and Siminovitch,K.
TITLE Ibd-related polymorphisms
JOURNAL Patent: WO 0142511-A 1878 14-JUN-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
Biotherapeutics Corporation (CA)
Location/Qualifiers

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1. .27
/organism="Homo sapiens"
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/db_xref="taxon:9606"

Query Match 0.9%; Score 21.8; DB 1; Length 27;
Best Local Similarity 88.5%; Pred. No. 7.3e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAGTCTCGGATTACAGG 2360

Db 1 GCCTCCCAAGTGCNAGGATTACAGG 26

RESULT 313
AX9272
LOCUS AX9272 28 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 2 from Patent EP0714987.
ACCESSION AX9272
VERSION AX9272.1 GI:2302795
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE 1 (bases 1 to 28)
AUTHORS Haemmerle,T.D., Falkner,F.D., Kohl,J.D., Himmelsbach,M.D. and Dörner,F.P.
TITLE Method for quantifying genomic DNA
JOURNAL Patent: EP 0714987-A 2 05-JUN-1996;
IMMUNO AG (AT)
COMMENT Other publication AT 401270 960725
Other publication JP 8105887 960423
Other publication CA 2159043 960327
Other publication AT 183094 951215.

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/organism="unidentified"
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Query Match 0.9%; Score 21.6; DB 1; Length 28;
Best Local Similarity 85.7%; Pred. No. 7.6e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2100 GAGACCGAGTCTGCTCTGTACCCAGG 2127


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Db 1 GAGACAGAGTCTCGCTCTGTGCGCCAGG 28

RESULT 314
AR122136
LOCUS AR122136 28 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 8 from patent US 6165711.
ACCESSION AR122136
VERSION AR122136.1 GI:14106453
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Dörner, F., Barrett, N. and Eibl, J.
TITLE Process for disintegrating nucleic acids and preparing biological
JOURNAL products of guaranteed quality
PATENT: US 6165711-A 8 26-DEC-2000;
FEATURES Location/Qualifiers
source 1..28
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 21.6; DB 1; Length 28;
Best Local Similarity 95.7%; Pred. No. 7.6e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2100 GAGACGAGTCTGCTCTGTATCCAGG 2127
||||| ||||| ||||| ||||| |||||
Db 1 GAGACAGAGTCTCGCTCTGTGCGCCAGG 28

RESULT 315
AR345149/c
LOCUS AR345149 23 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 30 from patent US 6583112.
ACCESSION AR345149
VERSION AR345149.1 GI:33741785
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Fu, Y.-H., Yu, C.-E., Oshima, J., Mulligan, J.T. and Schellenberg, G.D.
TITLE Gene products related to werner's syndrome
JOURNAL Patent: US 6583112-A 30 24-JUN-2003;
FEATURES Location/Qualifiers
source 1..23
/mol_type="unknown"
/mol_type="genomic DNA"

Query Match 0.9%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 7.2e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2336 CCTCCCAAGTCTGGGATTACA 2358
||||| ||||| ||||| ||||| |||||
Db 23 CCTCCCAAGTGTGGGATTACA 1

RESULT 316
AX823487
LOCUS AX823487 23 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 260 from Patent WO02068647.
ACCESSION AX823487
VERSION AX823487.1 GI:39749947
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS

JOURNAL Patent: WO 0200933-A 15 03-JAN-2002;
Interleukin Genetics, Inc. (US)
FEATURES Location/Qualifiers
source 1..25
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/note="Primer"

JOURNAL Patent: WO 02068647-A 260 06-SBP-2002;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..23
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: PCR Primer Sequence"

Query Match 0.9%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 7.2e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2097 TTTGACGCGAGTCTTGCTCTGT 2119
||||| ||||| ||||| ||||| |||||
Db 1 TTTGACGCGAGTCTTGCTCTGT 23

RESULT 317
A82465
LOCUS A82465 25 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 3 from Patent WO9854359.
ACCESSION A82465
VERSION A82465.1 GI:67322209
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 25)
AUTHORS Duff, G. and Cox, A.
TITLE PREDICTION OF INFLAMMATORY DISEASE ASSOCIATED WITH IL-1 GENELOC1
JOURNAL Patent: WO 9854359-A 3 03-DEC-1998;
DUFF GORDON (GB); COX ANGELA (GB)
FEATURES Location/Qualifiers
source 1..25
/mol_type="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.9%; Score 21.4; DB 1; Length 25;
Best Local Similarity 95.7%; Pred. No. 7.4e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2350 GGGATTACAGGCGTGAGCCACCG 2372
||||| ||||| ||||| ||||| |||||
Db 1 GGGATTACAGGCGTGAGCCACCG 23

RESULT 318
AX360029
LOCUS AX360029 25 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 15 from Patent WO0200933.
ACCESSION AX360029
VERSION AX360029.1 GI:18675655
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Duff, G.W. and Kornman, K.S.
TITLE Screening assays for identifying modulators of the inflammatory or
JOURNAL immune responses
PATENT: WO 0200933-A 15 03-JAN-2002;
Interleukin Genetics, Inc. (US)
FEATURES Location/Qualifiers
source 1..25
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/note="Primer"

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Query Match      0.9%; Score 21.2; DB 1; Length 27;
Best Local Similarity 85.2%; Pred. No. 7.8e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2344 AGTGTGGGATTACAGGCATGACCCAC 2370
      ||||| ||||| ||||| ||||| |||||
Db 1 AGTGCTGAATTACAGNCGTGAGCCAC 27

RESULT 323
LOCUS AR208405/c 21 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 21 from patent US 6383752.
ACCESSION AR208405
VERSION AR208405.1 GI:21509551
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Agrawal,S. and Kandimala,E.R.
TITLE Pseudo-cyclic oligonucleobases
JOURNAL Patent: US 6383752-A 21 07-MAY-2002;
FEATURES
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      /mol_type="unassigned DNA"

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 726 GTACAAGAGCTTCAGGAAGAG 746
      ||||| ||||| ||||| ||||| |||||
Db 21 GTACAAGAGCTTCAGGAAGAG 1

RESULT 324
LOCUS AX117999 21 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 3122 from Patent WO0129262.
ACCESSION AX117999
VERSION AX117999.1 GI:14034950
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 3122 26-APR-2001;
FEATURES
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      /db_xref="taxon:32630"
      /note="Primer"

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2286 GTTAGCCAGGATGGTCTCGAT 2306
      ||||| ||||| ||||| ||||| |||||
Db 1 GTTAGCCAGGATGGTCTCGAT 21

RESULT 325
LOCUS AX190635/c 21 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 53 from Patent WO0144287.

ACCESSION AX190635
VERSION AX190635.1 GI:15143914
SOURCE
ORGANISM
REFERENCE
AUTHORS Shimkets,R.A.
TITLE Novel polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0144287-A 53 21-JUN-2001;
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      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="2826468 expression forward primer"

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2300 TCTCGATCTCTGACCTCGTG 2320
      ||||| ||||| ||||| ||||| |||||
Db 21 TCTCGATCTCTGACCTCGTG 1

RESULT 326
LOCUS AX800306 21 bp DNA linear PAT 13-OCT-2003
DEFINITION Sequence 68 from Patent WO0305595.
ACCESSION AX800306
VERSION AX800306.1 GI:37653543
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Wen,X.Y., Stewart,A.K., Tsui,L.C. and Hegele,R.A.
TITLE Lipase genes and proteins
JOURNAL Patent: WO 0305595-A 68 10-JUL-2003;
FEATURES
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      /db_xref="taxon:9606"

Query Match      0.9%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2346 TGCTGGGATTACAGGCATGAG 2366
      ||||| ||||| ||||| ||||| |||||
Db 1 TGCTGGGATTACAGGCATGAG 21

RESULT 327
LOCUS BD073983 21 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073983
VERSION BD073983.1 GI:22619586
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Chen,J., Agrawal,S. and Zhang,R.
TITLE Antisense oligonucleotide specific to MDM2
JOURNAL Patent: JP 2001513996-A 22 11-SEP-2001;
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Query Match      0.9%; Score 21; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 7.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2188 TTCTCTCGCTCAGCTCCCAA 2209
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Db 22 TTCTCTCGCTCAGCTCCCAA 1

RESULT 331
AX693016
LOCUS AX693016 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5748 from Patent EPI281758.
ACCESSION AX693016
VERSION AX693016.1 GI:29415979
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Shannon.M., Gu.Y. and Nguyen.C.T.
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
TITLE mdz12
JOURNAL Patent: EP 1281758-A 5748 05-FEB-2003;
Aeomica, Inc. (US)
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Query Match      0.9%; Score 21; DB 1; Length 25;
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2274 GGGTTTCACCGTGTAGCCAG 2294
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Db 5 GGGTTTCACCGTGTAGCCAG 25

RESULT 332
CQ828992/c
LOCUS CQ828992 24 bp DNA linear PAT 05-JUL-2004
DEFINITION Sequence 710 from Patent WO2004053120.
ACCESSION CQ828992
VERSION CQ828992.1 GI:49732475
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Weihe,E., Bieller,A. and Schaefer,M.K.
AUTHORS Regulatory elements in the 5' region of the vrl gene
TITLE Patent: WO 2004053120-A 710 24-JUN-2004;
Gruenenthal GmbH (DE)
JOURNAL
FEATURES
source Location/Qualifiers
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/db_xref="taxon:9606"
/notes="V$GF11 01"

Query Match      0.9%; Score 20.8; DB 1; Length 24;
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Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2340 CCAAGTGTGGGATTACAGCAT 2363
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Db 24 CCAAGTGTGGGATTACAGCGT 1

Query Match      0.9%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 7.8e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2293 AGGATGGTCTCGATCTCTGACCT 2316
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Db 1 AGGCTGGTCTCGAATCTCTGACCT 24

RESULT 333
AX092602
LOCUS AX092602 24 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 14 from Patent WO0115676.
ACCESSION AX092602
VERSION AX092602.1 GI:13444659
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Hayden,M.R., Brooks-Wilson,A.R., Pimstone,S.N. and Clee,S.M.
AUTHORS Compositions and methods for modulating hdl cholesterol and
TITLE triglyceride levels
JOURNAL Patent: WO 0115676-A 14 08-MAR-2001;
University of British Columbia (CA) ; Xenon Genetics Inc. (CA)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.9%; Score 20.8; DB 1; Length 24;
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Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2293 AGGATGGTCTCGATCTCTGACCT 2316
|||||
Db 1 AGGCTGGTCTCGAATCTCTGACCT 24

RESULT 334
AX092650
LOCUS AX092650 24 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 62 from Patent WO0115676.
ACCESSION AX092650
VERSION AX092650.1 GI:13444707
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Hayden,M.R., Brooks-Wilson,A.R., Pimstone,S.N. and Clee,S.M.
AUTHORS Compositions and methods for modulating hdl cholesterol and
TITLE triglyceride levels
JOURNAL Patent: WO 0115676-A 62 08-MAR-2001;
University of British Columbia (CA) ; Xenon Genetics Inc. (CA)
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Query Match      0.9%; Score 20.8; DB 1; Length 24;
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Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2301 CTCGATCTCTGACCTCGTGATCC 2324
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Db 1 CTCGATTTCTTGACCTCGTGATCC 24

RESULT 335
AX662968
LOCUS AX662968 24 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 55 from Patent WO02066681.
ACCESSION AX662968
VERSION AX662968.1 GI:29163549
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .24

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

/note="Sense primer for PSF promoter"

Query Match 0.9%; Score 20.8; DB 1; Length 24;

Best Local Similarity 91.7%; Pred. No. 7.8e+02;

Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2342 AAGTGTGGGATTACAGCGTGA 2365

Db 1 AAGTGTGGGATTACAGCGTGA 24

RESULT 336

AX797527/C

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .24

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="PCR primer"

Query Match 0.9%; Score 20.8; DB 1; Length 24;

Best Local Similarity 91.7%; Pred. No. 7.8e+02;

Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2114 CTCGTACCCAGGCTGGAGTGA 2137

Db 24 CTCGTACCCAGGCTGGAGTGA 1

RESULT 337

AX817219/C

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .24

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="Primer"

Query Match 0.9%; Score 20.8; DB 1; Length 25;

Best Local Similarity 91.7%; Pred. No. 7.9e+02;

Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

source

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/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="Beschreibung der kuenstlichen Sequenz: Primer fur PCR-Reaktion zur Amplifikation von M30 des Menschen"

Query Match 0.9%; Score 20.8; DB 1; Length 24;

Best Local Similarity 91.7%; Pred. No. 7.8e+02;

Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2106 GAGTCTTGCTCTGTATCCAGGCT 2129

Db 24 GAGTCTTGCTCTGTATCCAGGCT 1

RESULT 338

AX115904

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .25

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="Primer"

Query Match 0.9%; Score 20.8; DB 1; Length 25;

Best Local Similarity 91.7%; Pred. No. 7.9e+02;

Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2249 ATTTTGTGCTTTTAGTAGAGAC 2272

Db 1 ATTTTGTGCTTTTAGTAGAGAC 24

RESULT 339

AX116344

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .25

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="Primer"

Query Match 0.9%; Score 20.8; DB 1; Length 25;

Best Local Similarity 91.7%; Pred. No. 7.9e+02;

Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2249 ATTGTTTGTACTTTTAGTAGAGAC 2272
 Db 1 AATTTTGTATTTTAGTAGAGAC 24

RESULT 340
 AX692917
 LOCUS 25 bp DNA linear PAT 31-MAR-2003
 DEFINITION Sequence 5649 from Patent EP1281758.
 ACCESSION AX692917
 VERSION AX692917.1 GI:29415880
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
 JOURNAL Patent: EP 1281758-A 5649 05-FEB-2003;
 Aeomica, Inc. (US)
 FEATURES
 source Location/Qualifiers
 1..25
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.9%; Score 20.8; DB 1; Length 25;
 Best Local Similarity 91.7%; Pred. No. 7.9e+02;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2173 CCGGGTTCGACCACTTCTCTGC 2196
 Db 2 CCTGGGTTACACCACTTCTCTGC 25

RESULT 341
 AX692918
 LOCUS 25 bp DNA linear PAT 31-MAR-2003
 DEFINITION Sequence 5650 from Patent EP1281758.
 ACCESSION AX692918
 VERSION AX692918.1 GI:29415881
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
 JOURNAL Patent: EP 1281758-A 5650 05-FEB-2003;
 Aeomica, Inc. (US)
 FEATURES
 source Location/Qualifiers
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 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.9%; Score 20.8; DB 1; Length 25;
 Best Local Similarity 91.7%; Pred. No. 7.9e+02;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2173 CCGGGTTCGACCACTTCTCTGC 2196
 Db 1 CCTGGGTTACACCACTTCTCTGC 24

RESULT 342
 AX692920
 LOCUS 25 bp DNA linear PAT 31-MAR-2003
 DEFINITION Sequence 5652 from Patent EP1281758.

ACCESSION AX692920
 VERSION AX692920.1 GI:29415883
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
 JOURNAL Patent: EP 1281758-A 5652 05-FEB-2003;
 Aeomica, Inc. (US)
 FEATURES
 source Location/Qualifiers
 1..25
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.9%; Score 20.8; DB 1; Length 25;
 Best Local Similarity 91.7%; Pred. No. 7.9e+02;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2176 GGGTTCGACCACTTCTCTGCCTC 2199
 Db 2 GGGTTCACACCACTTCTCTGCCTC 25

RESULT 343
 AX692923
 LOCUS 25 bp DNA linear PAT 31-MAR-2003
 DEFINITION Sequence 5655 from Patent EP1281758.
 ACCESSION AX692923
 VERSION AX692923.1 GI:29415886
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
 JOURNAL Patent: EP 1281758-A 5655 05-FEB-2003;
 Aeomica, Inc. (US)
 FEATURES
 source Location/Qualifiers
 1..25
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.9%; Score 20.8; DB 1; Length 25;
 Best Local Similarity 91.7%; Pred. No. 7.9e+02;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2178 GTTCGACCACTTCTCTGCCTCAG 2201
 Db 1 GTTCACCACTTCTCTGCCTCAG 24

RESULT 344
 AX692927
 LOCUS 25 bp DNA linear PAT 31-MAR-2003
 DEFINITION Sequence 5659 from Patent EP1281758.
 ACCESSION AX692927
 VERSION AX692927.1 GI:29415890
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.

TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12

JOURNAL Patent: EP 1281758-A 5659 05-FEB-2003;

AEOMICA, Inc. (US)

FEATURES Location/Qualifiers

source
1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 7.9e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2183 CACGATTCCTCGCTCAGCTCC 2206

Db 2 CACGATTCCTCGCTCAGCTCC 25

RESULT 345
AX692929
LOCUS AX692929 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5661 from Patent EP1281758.
ACCESSION AX692929
VERSION AX692929.1 GI:29415892

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

Shannon, M., Gu, Y. and Nguyen, C.T.

Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and

mdz12

Patent: EP 1281758-A 5661 05-FEB-2003;

AEOMICA, Inc. (US)

FEATURES Location/Qualifiers

source

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/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 7.9e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2184 ACCATTCCTCGCTCAGCTCCC 2207

Db 1 ACCATTCCTCGCTCAGCTCCC 24

RESULT 346
AX692990
LOCUS AX692990 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5722 from Patent EP1281758.
ACCESSION AX692990
VERSION AX692990.1 GI:29415953

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

Shannon, M., Gu, Y. and Nguyen, C.T.

Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and

mdz12

Patent: EP 1281758-A 5722 05-FEB-2003;

AEOMICA, Inc. (US)

FEATURES Location/Qualifiers

source

1..25

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 7.9e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2246 CTAATTTTGTACTTTTAGTAGA 2269

Db 2 CTAATTTTGTACTTTTAGTAGA 25

RESULT 347
AX692994
LOCUS AX692994 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5726 from Patent EP1281758.
ACCESSION AX692994
VERSION AX692994.1 GI:29415957

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

Shannon, M., Gu, Y. and Nguyen, C.T.

Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and

mdz12

Patent: EP 1281758-A 5726 05-FEB-2003;

AEOMICA, Inc. (US)

FEATURES Location/Qualifiers

source

1..25

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 7.9e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2249 ATTTTGTACTTTTAGTAGAGAC 2272

Db 1 ATTTTGTACTTTTAGTAGAGAC 24

RESULT 348
AX692996
LOCUS AX692996 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5728 from Patent EP1281758.
ACCESSION AX692996
VERSION AX692996.1 GI:29415959

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

Shannon, M., Gu, Y. and Nguyen, C.T.

Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and

mdz12

Patent: EP 1281758-A 5728 05-FEB-2003;

AEOMICA, Inc. (US)

FEATURES Location/Qualifiers

source

1..25

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 7.9e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2252 TTTTGTACTTTTAGTAGAGACGG 2275

Db 2 TTTTGTACTTTTAGTAGAGACGG 25


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RESULT 349
AX692998
LOCUS AX692998 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5730 from Patent EPI281758.
ACCESSION AX692998
VERSION AX692998.1 GI:29415961
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5730 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.9%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 7.9e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2253 TTGTACTTTTACTAGACAGGG 2276
|||||
Db 1 TTGTATTTTGTAGACGGGG 24
|||||

RESULT 350
AR381743/C
LOCUS AR381743 27 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 18 from patent US 6610285.
ACCESSION AR381743
VERSION AR381743.1 GI:40089939
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
AUTHORS Hirata,Y.
TITLE Cytokine-like proteins that promote cell proliferation
JOURNAL Patent: US 6610285-A 18-26-AUG-2003;
FEATURES
source
1..27
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.9%; Score 20.8; DB 1; Length 27;
Best Local Similarity 91.7%; Pred. No. 8.1e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2192 CCTGCCTCAGCTCCCAATTAGCT 2215
|||||
Db 27 CCTGCCTCAGCTCCCAAGCAGCT 4
|||||

RESULT 351
AX116940
LOCUS AX116940 27 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 2063 from Patent WO0129262.
ACCESSION AX116940
VERSION AX116940.1 GI:14033882
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Picoult-Newburg,L. and Pohl,M.

```

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TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 2063 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES
source
1..27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/misc_feature
1..27
/note="Primer"
/note="n = C3 linker"
Query Match 0.9%; Score 20.8; DB 1; Length 27;
Best Local Similarity 84.6%; Pred. No. 8.1e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2346 TGCTGGATTACAGGATGAGCCACC 2371
|||||
Db 1 TGCTGNGATTATAGNCAGGCCACC 26
|||||

RESULT 352
AX183893/C
LOCUS AX183893 27 bp DNA linear PAT 06-AUG-2001
DEFINITION Sequence 1646 from Patent WO0142511.
ACCESSION AX183893
VERSION AX183893.1 GI:15135224
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Daly,M., Hudson,T.J., Lander,E.S., Rioux,J. and Siminovitch,K.
TITLE Ibd-related polymorphisms
JOURNAL Patent: WO 0142511-A 1646 14-JUN-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
Biotherapeutics Corporation (CA)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.9%; Score 20.8; DB 1; Length 27;
Best Local Similarity 88.0%; Pred. No. 8.1e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2185 CCATTCTCCTCGCTCAGCCTCCCAA 2209
|||||
Db 25 CGATTCTCNGCCTCAGCCTCCCAA 1
|||||

RESULT 353
AX095325
LOCUS AX095325 21 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 503 from Patent WO0118250.
ACCESSION AX095325
VERSION AX095325.1 GI:13511528
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Lander,E.S., Gargill,M., Ireland,J.S., Bolck,S., Daley,G.Q. and McCarthy,J.J.
TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: WO 0118250-A 503 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
Pharmaceuticals, Inc. (US)
FEATURES
source
1..21
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.9%; Score 20.6; DB 1; Length 21;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2336 CCTCCCAAGTCTGGGATTA 2356
Db 1 CCTCCCAAGTCTGGGATTA 21

RESULT 354
AX709011 AX709011 27 bp DNA linear PAT 04-APR-2003
LOCUS AR242944/c
DEFINITION Sequence 35 from Patent WO03008443.
ACCESSION AX709011
VERSION AX709011.1 GI:29564684
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Averbach,P.A.
TITLE Peptides effective in the treatment of tumors and other conditions
JOURNAL requiring the removal or destruction of cells
JOURNAL Patent: WO 03008443-A 35 30-JAN-2003;
JOURNAL Nymox Corporation (CA)
FEATURES
source
1..27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

Query Match
Best Local Similarity 0.9%; Score 20.6; DB 1; Length 27;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2331 CTGGCCTCCCAAGTCTGGGATTAC 2357
Db 1 CTCAGCCTCCCAAGCAGCTGGGATTAC 27

RESULT 355
E50641/c
LOCUS AR242948/c
DEFINITION Sequence 22 bp DNA linear PAT 31-JAN-2002
ACCESSION AR242948
VERSION AR242948.1 GI:18629422
KEYWORDS simple detection method of drug-metabolizing synthetase gene
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 22)
AUTHORS Mizugaki,M. and Hiratsuka,M.
TITLE Simple detection method of drug-metabolizing synthetase gene
JOURNAL Patent: JP 2001017185-A 5 23-JAN-2001;
JOURNAL OTSUKA PHARMACEUT CO LTD
COMMENT OS Unidentified
PN JP 2001017185-A/5
PD 23-JAN-2001
PF 10-DEC-1999 JP 1999351610
PR MICHINAO MIZUGAKI, MASAHIRO HIRATSUKA
PC C12N15/09,C12Q1/68,C12Q1/68,C12N15/00
CC
FH Key
FT source
FT 1..22
/organism="Unidentified".
/organism="Unidentified".
Location/Qualifiers

Query Match
Best Local Similarity 0.9%; Score 20.6; DB 1; Length 21;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2336 CCTCCCAAGTCTGGGATTA 2356
Db 1 CCTCCCAAGTCTGGGATTA 21

RESULT 354
AX709011 AX709011 27 bp DNA linear PAT 04-APR-2003
LOCUS AR242944/c
DEFINITION Sequence 35 from Patent WO03008443.
ACCESSION AX709011
VERSION AX709011.1 GI:29564684
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Averbach,P.A.
TITLE Peptides effective in the treatment of tumors and other conditions
JOURNAL requiring the removal or destruction of cells
JOURNAL Patent: WO 03008443-A 35 30-JAN-2003;
JOURNAL Nymox Corporation (CA)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

Query Match
Best Local Similarity 0.9%; Score 20.6; DB 1; Length 27;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2331 CTGGCCTCCCAAGTCTGGGATTAC 2357
Db 1 CTCAGCCTCCCAAGCAGCTGGGATTAC 27

RESULT 355
E50641/c
LOCUS AR242948/c
DEFINITION Sequence 22 bp DNA linear PAT 31-JAN-2002
ACCESSION AR242948
VERSION AR242948.1 GI:18629422
KEYWORDS simple detection method of drug-metabolizing synthetase gene
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 22)
AUTHORS Mizugaki,M. and Hiratsuka,M.
TITLE Simple detection method of drug-metabolizing synthetase gene
JOURNAL Patent: JP 2001017185-A 5 23-JAN-2001;
JOURNAL OTSUKA PHARMACEUT CO LTD
COMMENT OS Unidentified
PN JP 2001017185-A/5
PD 23-JAN-2001
PF 10-DEC-1999 JP 1999351610
PR MICHINAO MIZUGAKI, MASAHIRO HIRATSUKA
PC C12N15/09,C12Q1/68,C12Q1/68,C12N15/00
CC
FH Key
FT source
FT 1..22
/organism="Unidentified".
/organism="Unidentified".
Location/Qualifiers

Query Match
Best Local Similarity 0.9%; Score 20.4; DB 1; Length 22;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2344 AGTCTGGGATTACAGGCATGA 2365
Db 22 AATGCTGGGATTACAGGCATGA 1

RESULT 356
AR242944/c
LOCUS AR242944
DEFINITION Sequence 90 from patent US 6475739.
ACCESSION AR242944
VERSION AR242944.1 GI:27289606
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Brunkow,M.E., Proll,S., Paepfer,B. and Staehling-Hampton,K.
TITLE Methods for identifying genomic deletions
JOURNAL Patent: US 6475739-A 90 05-NOV-2002;
JOURNAL Location/Qualifiers
FEATURES
source
1..22
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.9%; Score 20.4; DB 1; Length 22;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2187 ATTCTCTGCTCAGCTCCCA 2208
Db 22 ATTCTCTGCTCAGCTCCCA 1

RESULT 357
AR242948/c
LOCUS AR242948
DEFINITION Sequence 94 from patent US 6475739.
ACCESSION AR242948
VERSION AR242948.1 GI:27289610
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Brunkow,M.E., Proll,S., Paepfer,B. and Staehling-Hampton,K.
TITLE Methods for identifying genomic deletions
JOURNAL Patent: US 6475739-A 94 05-NOV-2002;
JOURNAL Location/Qualifiers
FEATURES
source
1..22
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.9%; Score 20.4; DB 1; Length 22;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2187 ATTCTCTGCTCAGCTCCCA 2208
Db 22 ATTCTCTGCTCAGCTCCCA 1

RESULT 358
AR393735/c
LOCUS AR393735
DEFINITION Sequence 22 bp DNA linear PAT 18-DEC-2003

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Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2109 TCTTGCTCTGTACCCAGGCTG 2130
 Db 1 TCTTGCTCTGTACCCAGGCTG 22

RESULT 363
 AX115271
 LOCUS AX115271 25 bp DNA linear PAT 11-MAY-2001
 DEFINITION Sequence 394 from Patent WO0129262.
 ACCESSION AX115271
 VERSION AX115271.1 GI:14032213
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Picoult-Newburg, L. and Pohl, M.
 TITLE Genotyping reagents, kits and methods of use thereof
 JOURNAL Patent: WO 0129262-A 394 26-APR-2001;
 Orchid Biosciences, Inc. (US)
 FEATURES Location/Qualifiers
 source
 1..25
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Primer"

Query Match 0.9%; Score 20.2; DB 1; Length 25;
 Best Local Similarity 88.0%; Pred. No. 8.3e+02;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2090 TATTTTTTTGAGCCGAGTCTTGC 2114
 Db 1 TTTTTTTTTCAGATGGAGTCTTGC 25

RESULT 364
 AX115532
 LOCUS AX115532 25 bp DNA linear PAT 11-MAY-2001
 DEFINITION Sequence 655 from Patent WO0129262.
 ACCESSION AX115532
 VERSION AX115532.1 GI:14032474
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Picoult-Newburg, L. and Pohl, M.
 TITLE Genotyping reagents, kits and methods of use thereof
 JOURNAL Patent: WO 0129262-A 655 26-APR-2001;
 Orchid Biosciences, Inc. (US)
 FEATURES Location/Qualifiers
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 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Primer"

Query Match 0.9%; Score 20.2; DB 1; Length 25;
 Best Local Similarity 88.0%; Pred. No. 8.3e+02;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2339 CCCAAAGTCTGGGATTACAGGCAT 2363
 Db 1 CCCAAATAGCTGGGATTACAGGAT 25

RESULT 365
 AX116096
 LOCUS AX116096 25 bp DNA linear PAT 11-MAY-2001
 DEFINITION Sequence 1219 from Patent WO0129262.

ACCESSION AX116096
 VERSION AX116096.1 GI:14033038
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Picoult-Newburg, L. and Pohl, M.
 TITLE Genotyping reagents, kits and methods of use thereof
 JOURNAL Patent: WO 0129262-A 1219 26-APR-2001;
 Orchid Biosciences, Inc. (US)
 FEATURES Location/Qualifiers
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 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Primer"

Query Match 0.9%; Score 20.2; DB 1; Length 25;
 Best Local Similarity 88.0%; Pred. No. 8.3e+02;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2185 CCATTCTCTGCTCAGCTCCCA 2209
 Db 1 CAATTCTCTGCTCAGCTCCCA 25

RESULT 366
 AX116664/c
 LOCUS AX116664 25 bp DNA linear PAT 11-MAY-2001
 DEFINITION Sequence 1787 from Patent WO0129262.
 ACCESSION AX116664
 VERSION AX116664.1 GI:14033606
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Picoult-Newburg, L. and Pohl, M.
 TITLE Genotyping reagents, kits and methods of use thereof
 JOURNAL Patent: WO 0129262-A 1787 26-APR-2001;
 Orchid Biosciences, Inc. (US)
 FEATURES Location/Qualifiers
 source
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 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Primer"

Query Match 0.9%; Score 20.2; DB 1; Length 25;
 Best Local Similarity 88.0%; Pred. No. 8.3e+02;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2326 CCCACCTCGCCCTCCCAAGTGCTG 2350
 Db 25 CCCGCTTGACCTCCCAAGTGCTG 1

RESULT 367
 AX117740/c
 LOCUS AX117740 25 bp DNA linear PAT 11-MAY-2001
 DEFINITION Sequence 2863 from Patent WO0129262.
 ACCESSION AX117740
 VERSION AX117740.1 GI:14034691
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Picoult-Newburg, L. and Pohl, M.
 TITLE Genotyping reagents, kits and methods of use thereof
 JOURNAL Patent: WO 0129262-A 2863 26-APR-2001;
 Orchid Biosciences, Inc. (US)

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        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Primer"

Query Match
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  Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2188 TTCTCCTGCCTCAGCCTCCCAATTA 2212
Db 25 TTCTCCTGCCTCAGCCTCCCGAGTA 1

RESULT 368
AX118236/c
LOCUS AX118236 25 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 3359 from Patent WO0129262.
ACCESSION AX118236
VERSION AX118236.1 GI:14035187
KEYWORDS
SOURCE
  ORGANISM
    Homo sapiens
  REFERENCE
    1 Picoult-Newburg, L. and Pohl, M.
    AUTHORS
    Genotyping reagents, kits and methods of use thereof
    TITLE
    Patent: WO 0129262-A 3359 26-APR-2001;
    JOURNAL
    Orchid BioSciences, Inc. (US)
  FEATURES
    source
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        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Primer"

Query Match
  Best Local Similarity 88.0%; Score 20.2; DB 1; Length 25;
  Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2188 TTCTCCTGCCTCAGCCTCCCAATTA 2212
Db 25 TTCTCCTGCCTCAGCCTCCCGAGTA 1

RESULT 369
AX692832
LOCUS AX692832 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5564 from Patent EP1281758.
ACCESSION AX692832
VERSION AX692832.1 GI:29415795
KEYWORDS
SOURCE
  ORGANISM
    Homo sapiens
  REFERENCE
    1 Shannon, M., Gu, Y. and Nguyen, C.T.
    AUTHORS
    Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
    TITLE
    Patent: EP 1281758-A 5564 05-FEB-2003;
    JOURNAL
    Aeomica, Inc. (US)
  FEATURES
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        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
  Best Local Similarity 88.0%; Score 20.2; DB 1; Length 25;
  Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2188 TTCTCCTGCCTCAGCCTCCCAATTA 2212
Db 25 TTCTCCTGCCTCAGCCTCCCGAGTA 1

RESULT 370
AX692833
LOCUS AX692833 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5565 from Patent EP1281758.
ACCESSION AX692833
VERSION AX692833.1 GI:29415796
KEYWORDS
SOURCE
  ORGANISM
    Homo sapiens
  REFERENCE
    1 Shannon, M., Gu, Y. and Nguyen, C.T.
    AUTHORS
    Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
    TITLE
    Patent: EP 1281758-A 5565 05-FEB-2003;
    JOURNAL
    Aeomica, Inc. (US)
  FEATURES
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        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
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  Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2086 TTATTATTTTGTGACCGAGTC 2110
Db 1 TTTTATTTTGTGACGAGATC 25

RESULT 371
AX692838
LOCUS AX692838 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5570 from Patent EP1281758.
ACCESSION AX692838
VERSION AX692838.1 GI:29415801
KEYWORDS
SOURCE
  ORGANISM
    Homo sapiens
  REFERENCE
    1 Shannon, M., Gu, Y. and Nguyen, C.T.
    AUTHORS
    Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
    TITLE
    Patent: EP 1281758-A 5570 05-FEB-2003;
    JOURNAL
    Aeomica, Inc. (US)
  FEATURES
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        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
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  Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2087 TATTATTTTGTGACCGAGTC 2111
Db 1 TTTTATTTTGTGACGAGATC 25

RESULT 372
AX692839
LOCUS AX692839 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5571 from Patent EP1281758.
ACCESSION AX692839
VERSION AX692839.1 GI:29415802
KEYWORDS
SOURCE
  ORGANISM
    Homo sapiens
  REFERENCE
    1 Shannon, M., Gu, Y. and Nguyen, C.T.
    AUTHORS
    Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
    TITLE
    Patent: EP 1281758-A 5571 05-FEB-2003;
    JOURNAL
    Aeomica, Inc. (US)
  FEATURES
    source
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        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
  Best Local Similarity 88.0%; Score 20.2; DB 1; Length 25;
  Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2092 TTTTATTTTGTGACCGAGTC 2116
Db 1 TTTTATTTTGTGACGAGATC 25

RESULT 373
AX692840
LOCUS AX692840 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5572 from Patent EP1281758.
ACCESSION AX692840
VERSION AX692840.1 GI:29415803
KEYWORDS
SOURCE
  ORGANISM
    Homo sapiens
  REFERENCE
    1 Shannon, M., Gu, Y. and Nguyen, C.T.
    AUTHORS
    Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
    TITLE
    Patent: EP 1281758-A 5572 05-FEB-2003;
    JOURNAL
    Aeomica, Inc. (US)
  FEATURES
    source
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        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
  Best Local Similarity 88.0%; Score 20.2; DB 1; Length 25;
  Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2093 TTTTATTTTGTGACCGAGTC 2117
Db 1 TTTTATTTTGTGACGAGATC 25

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DEFINITION Sequence 5571 from Patent EP1281758.
ACCESSION AX692839
VERSION AX692839.1 GI:29415802
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Shannon,M., Gu,Y. and Nguyen,C.T.
JOURNAL Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
PATENT: EP 1281758-A 5571 05-FEB-2003;
MDZ12
FEATURES
source Location/Qualifiers
1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 8.3e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2093 TTTTGTGAGACCGAGTCTTGCTCT 2117
|||||
Db 1 TTTTGTGAGACGAGTCTGCTCT 25

RESULT 373
AX692919
LOCUS AX692919 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5651 from Patent EP1281758.
ACCESSION AX692919
VERSION AX692919.1 GI:29415882
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Shannon,M., Gu,Y. and Nguyen,C.T.
JOURNAL Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
PATENT: EP 1281758-A 5651 05-FEB-2003;
MDZ12
FEATURES
source Location/Qualifiers
1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 8.3e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2174 CCGGTTGCGACCATTCCTCGCT 2198
|||||
Db 1 CTGGTTGACACCATTCCTGCTT 25

RESULT 374
AX692924
LOCUS AX692924 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5656 from Patent EP1281758.
ACCESSION AX692924
VERSION AX692924.1 GI:29415887
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Shannon,M., Gu,Y. and Nguyen,C.T.
JOURNAL Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
PATENT: EP 1281758-A 5656 05-FEB-2003;
MDZ12
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
MDZ12
JOURNAL Patent: EP 1281758-A 5656 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 8.3e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2179 TTCGACCATTCCTCGCTCAGCC 2203
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Db 1 TTCACACCATTCCTGCTTCAGTC 25

RESULT 375
AX692925
LOCUS AX692925 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5657 from Patent EP1281758.
ACCESSION AX692925
VERSION AX692925.1 GI:29415888
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Shannon,M., Gu,Y. and Nguyen,C.T.
JOURNAL Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
PATENT: EP 1281758-A 5657 05-FEB-2003;
MDZ12
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 8.3e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2180 TCGCACCATTCTCTGCTCAGCCT 2204
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Db 1 TCACACCATTCCTGCTTCAGTCT 25

RESULT 376
AX692926
LOCUS AX692926 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5658 from Patent EP1281758.
ACCESSION AX692926
VERSION AX692926.1 GI:29415889
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Shannon,M., Gu,Y. and Nguyen,C.T.
JOURNAL Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
PATENT: EP 1281758-A 5658 05-FEB-2003;
MDZ12
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"

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Query Match	0.9%;	Score 20.2;	DB 1;	Length 25;
Best Local Similarity	88.0%;	Pred. No. 8.3e+02;		
Matches	22;	Conservative	0;	Mismatches 3;
			Indels	0;
Gaps				0;
QY	2250	TTTTTTGTACTTTT	TAGTAGACAG	2274
DB	1	TATTTTGTATTTT	TAGTAGACGG	25

RESULT	381
AX183618	
LOCUS	AX183618
DEFINITION	Sequence 1371 from Patent WO0142511.
ACCESSION	AX183618
VERSION	AX183618.1
KEYWORDS	GI:15134938
	linear
	26 bp DNA
	PAT 06-AUG-2001

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Daly, M., Hudson, T.J., Lander, E.S., Rioux, J. and Siminovitch, K.
AUTHORS Ibd-related polymorphisms
TITLE Patent: WO 0142511-A 1371 14-JUN-2001;
JOURNAL WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
Biotherapeutics Corporation (CA)
FEATURES Location/Qualifiers
source 1..26
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.9%; Score 20.2; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 8.4e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2345 GTGCTGGGATTACAGGCATGAGCCAC 2370
Db 1 GTGCTGGGATTANAGGTGTAACCAC 26
AX183704.1 GI:15135027
RESULT 382
LOCUS AX183704 26 bp DNA linear PAT 06-AUG-2001
DEFINITION Sequence 1457 from Patent WO0142511.
ACCESSION AX183704
VERSION AX183704.1
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Daly, M., Hudson, T.J., Lander, E.S., Rioux, J. and Siminovitch, K.
AUTHORS Ibd-related polymorphisms
TITLE Patent: WO 0142511-A 1457 14-JUN-2001;
JOURNAL WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
Biotherapeutics Corporation (CA)
FEATURES Location/Qualifiers
source 1..26
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.9%; Score 20.2; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 8.4e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2345 GTGCTGGGATTACAGGCATGAGCCAC 2370
Db 26 GTGCTGGGATTGCANGTGTGAGCCAC 1
AX154586/c
RESULT 383
LOCUS AX154586 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 3 from patent US 6238921.
ACCESSION AR154586
VERSION AR154586.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia, L.J., Nero, P., Graham, M.J. and Monia, B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 3 29-MAY-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unassigned DNA"
/mol_type="unassigned DNA"
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCACCGCGCGAGCTTGGCTG 20
Db 20 GCACCGCGCGAGCTTGGCTG 1
AX154587/c
RESULT 384
LOCUS AR154587 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 4 from patent US 6238921.
ACCESSION AR154587
VERSION AR154587.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia, L.J., Nero, P., Graham, M.J. and Monia, B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 4 29-MAY-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unassigned DNA"
/mol_type="unassigned DNA"
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY .37 GGCCCTGTGTGTCGGAAGA 56
Db 20 GGCCCTGTGTGTCGGAAGA 1
AR154588/c
RESULT 385
LOCUS AR154588 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 5 from patent US 6238921.
ACCESSION AR154588
VERSION AR154588.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia, L.J., Nero, P., Graham, M.J. and Monia, B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 5 29-MAY-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unassigned DNA"
/mol_type="unassigned DNA"
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 95 CTCTGACCGAGATCCTGCTG 114
Db 20 CTCTGACCGAGATCCTGCTG 1
AR154589/c
RESULT 386
LOCUS AR154589 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 6 from patent US 6238921.
ACCESSION AR154589

/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCACCGCGCGAGCTTGGCTG 20
Db 20 GCACCGCGCGAGCTTGGCTG 1
AR154587/c
RESULT 384
LOCUS AR154587 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 4 from patent US 6238921.
ACCESSION AR154587
VERSION AR154587.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia, L.J., Nero, P., Graham, M.J. and Monia, B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 4 29-MAY-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY .37 GGCCCTGTGTGTCGGAAGA 56
Db 20 GGCCCTGTGTGTCGGAAGA 1
AR154588/c
RESULT 385
LOCUS AR154588 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 5 from patent US 6238921.
ACCESSION AR154588
VERSION AR154588.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia, L.J., Nero, P., Graham, M.J. and Monia, B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 5 29-MAY-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 95 CTCTGACCGAGATCCTGCTG 114
Db 20 CTCTGACCGAGATCCTGCTG 1
AR154589/c
RESULT 386
LOCUS AR154589 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 6 from patent US 6238921.
ACCESSION AR154589


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VERSION AR154589.1 GI:15122642
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 6 29-MAY-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 147 ATTAGTCGTCAGCGCCCC 166
Db 20 ATTAGTCGTCAGCGCCCC 1

RESULT 387
AR154590/c
LOCUS AR154590 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 7 from patent US 6238921.
ACCESSION AR154590
VERSION AR154590.1 GI:15122643
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 7 29-MAY-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 181 GAGAGTCGAATGATCCCCGA 200
Db 20 GAGAGTCGAATGATCCCCGA 1

RESULT 388
AR154591/c
LOCUS AR154591 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 8 from patent US 6238921.
ACCESSION AR154591
VERSION AR154591.1 GI:15122644
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 8 29-MAY-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 303 AGCAGGCAATGTGCAATAC 322
Db 20 AGCAGGCAATGTGCAATAC 1

RESULT 391
AR154594/c
LOCUS AR154594 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 11 from patent US 6238921.
ACCESSION AR154594
VERSION AR154594.1 GI:15122647
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)

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Qy 273 CTCCAAGCGGAAACCCCG 292
Db 20 CTCCAAGCGGAAACCCCG 1

RESULT 389
AR154592/c
LOCUS AR154592 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 9 from patent US 6238921.
ACCESSION AR154592
VERSION AR154592.1 GI:15122645
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 9 29-MAY-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 295 TGGTGAGGAGCAGGCAATG 314
Db 20 TGGTGAGGAGCAGGCAATG 1

RESULT 390
AR154593/c
LOCUS AR154593 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 10 from patent US 6238921.
ACCESSION AR154593
VERSION AR154593.1 GI:15122646
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 10 29-MAY-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 303 AGCAGGCAATGTGCAATAC 322
Db 20 AGCAGGCAATGTGCAATAC 1

RESULT 391
AR154594/c
LOCUS AR154594 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 11 from patent US 6238921.
ACCESSION AR154594
VERSION AR154594.1 GI:15122647
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)

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AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 11 29-MAY-2001;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 331 CTGTACCTACTGATGGTGCT 350
Db 20 CTGTACCTACTGATGGTGCT 1

RESULT 392
ARI54595/c
LOCUS ARI54595 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 12 from patent US 6238921.
ACCESSION ARI54595
VERSION ARI54595.1 GI:15122648
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 12 29-MAY-2001;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 617 GATCTACAGGAACCTTGCTAG 636
Db 20 GATCTACAGGAACCTTGCTAG 1

RESULT 393
ARI54596/c
LOCUS ARI54596 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 13 from patent US 6238921.
ACCESSION ARI54596
VERSION ARI54596.1 GI:15122649
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 13 29-MAY-2001;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1047 AGTGAGAAATTGAAGTTGA 1066
Db 20 AGTGAGAAATTGAAGTTGA 1

RESULT 394
ARI54597/c
LOCUS ARI54597 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 14 from patent US 6238921.
ACCESSION ARI54597
VERSION ARI54597.1 GI:15122650
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 14 29-MAY-2001;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1381 TTGATGTTCTCTGATTGTAAA 1400
Db 20 TTGATGTTCTCTGATTGTAAA 1

RESULT 395
ARI54598/c
LOCUS ARI54598 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 15 from patent US 6238921.
ACCESSION ARI54598
VERSION ARI54598.1 GI:15122651
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 15 29-MAY-2001;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1695 TTTACATGTGCAAGAAGCT 1714
Db 20 TTTACATGTGCAAGAAGCT 1

RESULT 396
ARI54599/c
LOCUS ARI54599 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 16 from patent US 6238921.
ACCESSION ARI54599
VERSION ARI54599.1 GI:15122652
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 16 29-MAY-2001;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"

/mol_type="unassigned DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1776 TATTTCCTCCCTAGTTGACCTG 1795
|||||
Db 20 TATTTCCTCCCTAGTTGACCTG 1

RESULT 397
AR154600/c

LOCUS AR154600 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 17 from patent US 6238921.
ACCESSION AR154600
VERSION AR154600.1 GI:15122653

KEYWORDS
SOURCE Unknown.

ORGANISM
Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 17 29-MAY-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1785 TACTTGACCTCTCTATAAGA 1804
|||||
Db 20 TACTTGACCTCTCTATAAGA 1

RESULT 398
AR154601/c

LOCUS AR154601 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 18 from patent US 6238921.
ACCESSION AR154601
VERSION AR154601.1 GI:15122654

KEYWORDS
SOURCE Unknown.

ORGANISM
Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 18 29-MAY-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1818 CTAACCTATATAACCTAGGA 1837
|||||
Db 20 CTAACCTATATAACCTAGGA 1

RESULT 399
AR154602/c

LOCUS AR154602 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 19 from patent US 6238921.
ACCESSION AR154602
VERSION AR154602.1 GI:15122655

KEYWORDS

SOURCE Unknown.

ORGANISM
Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 19 29-MAY-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

QY 1934 TAGTGGAAATAGTGAATCTT 1953
|||||
Db 20 TAGTGGAAATAGTGAATCTT 1

Query Match 0.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 400
AR154603/c

LOCUS AR154603 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 20 from patent US 6238921.
ACCESSION AR154603
VERSION AR154603.1 GI:15122656

KEYWORDS
SOURCE Unknown.

ORGANISM
Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 20 29-MAY-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

QY 2132 AGTCAGTCGGTCATCTTG 2151
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Db 20 AGTCAGTCGGTCATCTTG 1

Query Match 0.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 401
AR154604/c

LOCUS AR154604 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 21 from patent US 6238921.
ACCESSION AR154604
VERSION AR154604.1 GI:15122657

KEYWORDS
SOURCE Unknown.

ORGANISM
Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 21 29-MAY-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

QY 2132 AGTCAGTCGGTCATCTTG 2151
|||||
Db 20 AGTCAGTCGGTCATCTTG 1

Query Match 0.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

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Qy      2349 TGGATTACAGGCATGAGCC 2368
Db      1 TGGATTACAGGCATGAGCC 20

RESULT 406
LOCUS   CQ784281.1 20 bp DNA linear PAT 17-MAR-2004
DEFINITION Sequence 4421 from Patent EP1396543.
ACCESSION CQ784281
VERSION   CQ784281.1 GI:45538769
KEYWORDS .
SOURCE   synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS  Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
          Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
          Koga,H.
TITLE    Primers for synthesizing full length cDNA clones and their use
JOURNAL  Patent: Ep 1396543-A 4421 10-MAR-2004;
          Research Association for Biotechnology (JP)
FEATURES
source   1..20
          /organism="synthetic construct"
          /mol_type="unassigned DNA"
          /db_xref="taxon:32630"
          /note="Description of Artificial Sequence: an artificially
          synthesized primer sequence"

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2341 CAAAGTCTGGGATTACAGG 2360
Db      20 CAAAGTCTGGGATTACAGG 1

RESULT 407
LOCUS   CQ786097 20 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 21 from Patent WO2004018711.
ACCESSION CQ786097
VERSION   CQ786097.1 GI:45721200
KEYWORDS .
SOURCE   synthetic construct
ORGANISM synthetic construct
          artificial sequences.

REFERENCE 1
AUTHORS  Ming-Qing,D.
TITLE    Diagnostic test
JOURNAL  Patent: WO 2004018711-A 21 04-MAR-2004;
          University College London (GB)
FEATURES
source   1..20
          /organism="synthetic construct"
          /mol_type="unassigned DNA"
          /db_xref="taxon:32630"
          /note="primer for amplification of D6S105"

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2340 CCAAGTCTGGGATTACAG 2359
Db      1 CCAAGTCTGGGATTACAG 20

RESULT 408
LOCUS   E31877/c 20 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 3 from patent US 6465247.
ACCESSION AR236783
VERSION   AR236783.1 GI:27280976
KEYWORDS .
SOURCE   synthetic construct
ORGANISM synthetic construct
          artificial sequences.

REFERENCE 1
AUTHORS  Nario,O.
TITLE    Method for anticipating risk of Alzheimer's disease
JOURNAL  Patent: JP 199908996-A 10 09-NOV-1999;
          SRL INC
COMMENT     OS Unidentified
           PN JP 1999308996-A/10
           PD 09-NOV-1999
           PF 28-APR-1998 JP 1998134578
           PR NARIO OTA
           PC C12N15/09,C12Q1/68,C12N15/00
           CC Key Location/Qualifiers
           FH Key 1..20
           FT source /organism='Unidentified'.
           FT Location/Qualifiers
              1..20
              /organism="unidentified"
              /mol_type="genomic DNA"
              /db_xref="taxon:32644"

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2263 TAGTAGAGACAGGTTTCAC 2282
Db      20 TAGTAGAGACAGGTTTCAC 1

RESULT 409
LOCUS   AR208406/c 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 22 from patent US 6383752.
ACCESSION AR208406
VERSION   AR208406.1 GI:21509552
KEYWORDS .
SOURCE   Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS  Agrawal,S. and Kandimala,E.R.
TITLE    Pseudo-cyclic oligonucleobases
JOURNAL  Patent: US 6383752-A 22 07-MAY-2002;
          Location/Qualifiers
FEATURES
source   1..20
          /organism="unknown"
          /mol_type="unassigned DNA"

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      675 GTGAGTGAGACAGGTGTCA 694
Db      20 GTGAGTGAGACAGGTGTCA 1

RESULT 410
LOCUS   AR236783/c 20 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 3 from patent US 6465247.
ACCESSION AR236783
VERSION   AR236783.1 GI:27280976
KEYWORDS .
SOURCE   synthetic construct
ORGANISM synthetic construct
          artificial sequences.

REFERENCE 1
AUTHORS  Nario,O.
TITLE    Method for anticipating risk of Alzheimer's disease
JOURNAL  Patent: JP 199908996-A 10 09-NOV-1999;
          SRL INC
COMMENT     OS Unidentified
           PN JP 1999308996-A/10
           PD 09-NOV-1999
           PF 28-APR-1998 JP 1998134578
           PR NARIO OTA
           PC C12N15/09,C12Q1/68,C12N15/00
           CC Key Location/Qualifiers
           FH Key 1..20
           FT source /organism='Unidentified'.
           FT Location/Qualifiers
              1..20
              /organism="unidentified"
              /mol_type="genomic DNA"
              /db_xref="taxon:32644"

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      675 GTGAGTGAGACAGGTGTCA 694
Db      20 GTGAGTGAGACAGGTGTCA 1

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KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Weissman,I.L., Traver,D.J. and Akashi,K.
TITLE Mammalian myeloid progenitor cell subsets
JOURNAL Patent: US 6465247-A 3 15-OCT-2002;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2344 AGTCTGGGATTACAGGCAT 2363
Db 20 AGTCTGGGATTACAGGCAT 1

RESULT 413
AR310706/c
LOCUS AR310706 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 2 from patent US 6559279.
ACCESSION AR310706
VERSION AR310706.1 GI:31703861
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Manoharan,M. and Guzaev,A.P.
TITLE Process for preparing peptide derivatized oligomeric compounds
JOURNAL Patent: US 6559279-A 2 06-MAY-2003;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1695 TTTCATGTGCAAGAAGCT 1714
Db 20 TTTCATGTGCAAGAAGCT 1

RESULT 414
AR321577/c
LOCUS AR321577 20 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 1 from patent US 6562959.
ACCESSION AR321577
VERSION AR321577.1 GI:33706806
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cherif,D.
TITLE Detection of altered expression of genes regulating cell proliferation
JOURNAL Patent: US 6562959-A 1 13-MAY-2003;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2122 CCAGGCTGGAGTGCGAGTGG 2141
Db 20 CCAGGCTGGAGTGCGAGTGG 1

RESULT 415
AR337145
LOCUS AR337145 20 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 70 from patent US 6566135.
ACCESSION AR337145
VERSION AR337145.1 GI:33722999
KEYWORDS
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KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Weissman,I.L., Traver,D.J. and Akashi,K.
TITLE Mammalian myeloid progenitor cell subsets
JOURNAL Patent: US 6465247-A 3 15-OCT-2002;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2344 AGTCTGGGATTACAGGCAT 2363
Db 20 AGTCTGGGATTACAGGCAT 1

RESULT 411
AR305303/c
LOCUS AR305303 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 257 from patent US 6545137.
ACCESSION AR305303
VERSION AR305303.1 GI:31694613
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Todd,J.A., Hess,J.W., Caskey,C.T., Cox,R.D., Gerhold,D.,
Hammond,H., Hey,P., Kawaguchi,Y., Merriam,T.R., Metzker,M.L.,
Nakagawa,Y., Phillips,M.S. and Twells,R.C.J.
TITLE Receptor
JOURNAL Patent: US 6545137-A 257 08-APR-2003;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2344 AGTCTGGGATTACAGGCAT 2363
Db 20 AGTCTGGGATTACAGGCAT 1

RESULT 412
AR309407/c
LOCUS AR309407 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 257 from patent US 6555654.
ACCESSION AR309407
VERSION AR309407.1 GI:31701412
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Todd,J.A., Hess,J.W., Caskey,C.T., Cox,R.D., Gerhold,D.,
Hammond,H., Hey,P., Kawaguchi,Y., Merriam,T.R., Metzker,M.L.,
Nakagawa,Y., Phillips,M.S. and Twells,R.C.J.
TITLE LDL-receptor
JOURNAL Patent: US 6555654-A 257 29-APR-2003;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="genomic DNA"
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SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Watt,A.T.
TITLE        Antisense modulation of caspase 6 expression
JOURNAL      Patent: US 6566135-A 70 20-MAY-2003;
FEATURES     Location/Qualifiers
             source
               1. .20
               /organism="unknown"
               /mol_type="genomic DNA"

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2340 CCAAAGTGTGGGATTACAG 2359
LOCUS   AR370250/c                      20 bp      DNA      linear      PAT 12-SEP-2003
DEFINITION Sequence 71 from patent US 6300132.
ACCESSION AR370250
VERSION   AR370250.1 GI:34606756
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS   Monia,B.P. and Cowseert,L.M.
TITLE     Antisense inhibition of telomeric repeat binding factor 2
          expression
JOURNAL   Patent: US 6300132-A 71 09-OCT-2001;
FEATURES  Location/Qualifiers
             source
               1. .20
               /organism="unknown"
               /mol_type="genomic DNA"

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2292 CAGGATGGTCTCGATCTCCT 2311
LOCUS   AR370252/c                      20 bp      DNA      linear      PAT 12-SEP-2003
DEFINITION Sequence 73 from patent US 6300132.
ACCESSION AR370252
VERSION   AR370252.1 GI:34606758
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS   Monia,B.P. and Cowseert,L.M.
TITLE     Antisense inhibition of telomeric repeat binding factor 2
          expression
JOURNAL   Patent: US 6300132-A 73 09-OCT-2001;
FEATURES  Location/Qualifiers
             source
               1. .20
               /organism="unknown"
               /mol_type="genomic DNA"

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2338 TCCCAAAGTGTGGGATTAC 2357
LOCUS   AX116275                      20 bp      DNA      linear      PAT 11-MAY-2001
DEFINITION Sequence 1398 from Patent WO0129262.
ACCESSION AX116275
VERSION   AX116275.1 GI:14033217
KEYWORDS
SOURCE    synthetic construct

SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Watt,A.T.
TITLE        Antisense modulation of caspase 6 expression
JOURNAL      Patent: US 6566135-A 70 20-MAY-2003;
FEATURES     Location/Qualifiers
             source
               1. .20
               /organism="unknown"
               /mol_type="genomic DNA"

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2346 TGCTGGGATTACAGCATGA 2365
LOCUS   AR435741/c                      20 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION Sequence 7 from patent US 6656730.
ACCESSION AR435741
VERSION   AR435741.1 GI:40198823
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS   Manoharan,M.
TITLE     Oligonucleotides conjugated to protein-binding drugs
          Patent: US 6656730-A 7 02-DEC-2003;
FEATURES  Location/Qualifiers
             source
               1. .20
               /organism="unknown"
               /mol_type="genomic DNA"

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1695 TTTACATGTGCAAGAAGCT 1714
LOCUS   AX115919                      20 bp      DNA      linear      PAT 11-MAY-2001
DEFINITION Sequence 1042 from Patent WO0129262.
ACCESSION AX115919
VERSION   AX115919.1 GI:14032861
KEYWORDS
SOURCE    synthetic construct
          synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS   Picoult-Newburg,L. and Pohl,M.
TITLE     Genotyping reagents, kits and methods of use thereof
          Patent: WO 0129262-A 1042 26-APR-2001;
          Orchid Biosciences, Inc. (US)
FEATURES  Location/Qualifiers
             source
               1. .20
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Primer"

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2338 TCCCAAAGTGTGGGATTAC 2357
LOCUS   AX116275                      20 bp      DNA      linear      PAT 11-MAY-2001
DEFINITION Sequence 1398 from Patent WO0129262.
ACCESSION AX116275
VERSION   AX116275.1 GI:14033217
KEYWORDS
SOURCE    synthetic construct

SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Watt,A.T.
TITLE        Antisense modulation of caspase 6 expression
JOURNAL      Patent: US 6566135-A 70 20-MAY-2003;
FEATURES     Location/Qualifiers
             source
               1. .20
               /organism="unknown"
               /mol_type="genomic DNA"

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2340 CCAAAGTGTGGGATTACAG 2359
LOCUS   AR370250/c                      20 bp      DNA      linear      PAT 12-SEP-2003
DEFINITION Sequence 71 from patent US 6300132.
ACCESSION AR370250
VERSION   AR370250.1 GI:34606756
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS   Monia,B.P. and Cowseert,L.M.
TITLE     Antisense inhibition of telomeric repeat binding factor 2
          expression
JOURNAL   Patent: US 6300132-A 71 09-OCT-2001;
FEATURES  Location/Qualifiers
             source
               1. .20
               /organism="unknown"
               /mol_type="genomic DNA"

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2292 CAGGATGGTCTCGATCTCCT 2311
LOCUS   AR370252/c                      20 bp      DNA      linear      PAT 12-SEP-2003
DEFINITION Sequence 73 from patent US 6300132.
ACCESSION AR370252
VERSION   AR370252.1 GI:34606758
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS   Monia,B.P. and Cowseert,L.M.
TITLE     Antisense inhibition of telomeric repeat binding factor 2
          expression
JOURNAL   Patent: US 6300132-A 73 09-OCT-2001;
FEATURES  Location/Qualifiers
             source
               1. .20
               /organism="unknown"
               /mol_type="genomic DNA"

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2338 TCCCAAAGTGTGGGATTAC 2357
LOCUS   AX116275                      20 bp      DNA      linear      PAT 11-MAY-2001
DEFINITION Sequence 1398 from Patent WO0129262.
ACCESSION AX116275
VERSION   AX116275.1 GI:14033217
KEYWORDS
SOURCE    synthetic construct

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ORGANISM      synthetic construct
REFERENCE      artificial sequences.
1
AUTHORS      Picoult-Newburg,L. and Pohl,M.
JOURNAL      Genotyping reagents, kits and methods of use thereof
              Patent: WO 0129262-A 1398 26-APR-2001;
              Orchard BioSciences, Inc. (US)
FEATURES      Location/Qualifiers
              source
                1..20
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Primer"

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2352 GATTACAGGCATGAGCCACC 2371
Db      1 GATTACAGGCATGAGCCACC 20

RESULT 421
AX146647/c
LOCUS      AX146647      20 bp      DNA      linear      PAT 31-MAY-2001
DEFINITION      Sequence 1 from Patent WO0134093.
ACCESSION      AX146647
VERSION      AX146647.1 GI:14285040
KEYWORDS
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
1
REFERENCE
AUTHORS      Agrawal,S.
TITLE      Potentiation of prodrg efficacy
JOURNAL      Patent: WO 0134093-A 1 17-MAY-2001;
            HYBRIDON, INC. (US)
FEATURES      Location/Qualifiers
              source
                1..20
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Oligonucleotide sequence"

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      675 GTGAGTGAGAACAGGTGTCA 694
Db      20 GTGAGTGAGAACAGGTGTCA 1

RESULT 422
AX657359
LOCUS      AX657359      20 bp      DNA      linear      PAT 22-MAR-2003
DEFINITION      Sequence 72 from Patent WO02100896.
ACCESSION      AX657359
VERSION      AX657359.1 GI:29160099
KEYWORDS
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
1
REFERENCE
AUTHORS      dalla Venezia,N.L., Magnard,C.M., Lenoir,G.M. and
            Sinelnikova-Brard,O.
TITLE      Method for diagnosing cancer susceptibility
JOURNAL      Patent: WO 02100896-A 72 19-DEC-2002;
            CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR);
            UNIVERSITE CLAUDE BERNARD - LYON 1 (FR)
FEATURES      Location/Qualifiers
              source
                1..20

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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="amorce PCR"

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2338 TCCCAAAGTGTGGGATTAC 2357
Db      1 TCCCAAAGTGTGGGATTAC 20

RESULT 423
BD073963
LOCUS      BD073963      20 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION      Antisense oligonucleotide specific to MDM2.
ACCESSION      BD073963
VERSION      BD073963.1 GI:22619566
KEYWORDS      JP 2001513996-A/2.
SOURCE      unidentified
            unidentified
            unclassified.
1 (bases 1 to 20)
REFERENCE
AUTHORS      Chen,J., Agrawal,S. and Zhang,R.
TITLE      Antisense oligonucleotide specific to MDM2
JOURNAL      Patent: JP 2001513996-A 2 11-SEP-2001;
            HYBRIDON INC
COMMENT      OS Unidentified
            PN JP 2001513996-A/2
            PD 11-SEP-2001
            PF 18-AUG-1998 JP 2000507794
            PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
            PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
            C12N15/00
            CC Strandedness: Both;
            CC Topology: Linear;
            CC Antisense oligonucleotide specific to MDM2
            FH Key Location/Qualifiers
            FT source 1..20
            FT /organism='Unidentified'.
            FT Location/Qualifiers
              source
                1..20
                /organism="unidentified"
                /mol_type="genomic DNA"
                /db_xref="taxon:32644"

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      481 TTGGCCAGTATATTATGACT 500
Db      1 TTGGCCAGTATATTATGACT 20

RESULT 424
BD073964
LOCUS      BD073964      20 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION      Antisense oligonucleotide specific to MDM2.
ACCESSION      BD073964
VERSION      BD073964.1 GI:22619567
KEYWORDS      JP 2001513996-A/3.
SOURCE      unidentified
            unidentified
            unclassified.
1 (bases 1 to 20)
REFERENCE
AUTHORS      Chen,J., Agrawal,S. and Zhang,R.
TITLE      Antisense oligonucleotide specific to MDM2
JOURNAL      Patent: JP 2001513996-A 3 11-SEP-2001;
            HYBRIDON INC

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COMMENT      OS      Unidentified
              PN      JP 2001513996-A/3
              PD      11-SEP-2001
              PF      18-AUG-1998 JP 2000507794
              PR      22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
              JIANDONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
              PC      C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
              PC      C12N15/00
              CC      Strandedness: Both;
              CC      Topology: Linear;
              CC      Antisense oligonucleotide specific to MDM2
              FH      Key      Location/Qualifiers
              FT      source      1..20
              FT      Location/Qualifiers
              FT      1..20
              FT      /organism='Unidentified'.
              FT      /mol_type='genomic DNA'
              FT      /db_xref='taxon:32644'

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      695 CCTGAAGGTGGGAGTGATC 714
      |||||||
Db      1 CCTGAAGGTGGGAGTGATC 20

RESULT 425
BD073965
LOCUS      BD073965      20 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION      Antisense oligonucleotide specific to MDM2.
ACCESSION      BD073965
VERSION      BD073965.1 GI:22619568
KEYWORDS      JP 2001513996-A/4.
SOURCE      unidentified
ORGANISM      unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Chen,J., Agrawal,S. and Zhang,R.
TITLE      Antisense oligonucleotide specific to MDM2
JOURNAL      Patent: JP 2001513996-A 4 11-SEP-2001;
              HYBRIDON INC
COMMENT      OS      Unidentified
              PN      JP 2001513996-A/4
              PD      11-SEP-2001
              PF      18-AUG-1998 JP 2000507794
              PR      22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
              JIANDONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
              PC      C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
              PC      C12N15/00
              CC      Strandedness: Both;
              CC      Topology: Linear;
              CC      Antisense oligonucleotide specific to MDM2
              FH      Key      Location/Qualifiers
              FT      source      1..20
              FT      Location/Qualifiers
              FT      1..20
              FT      /organism='Unidentified'.
              FT      /mol_type='genomic DNA'
              FT      /db_xref='taxon:32644'

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1018 TGGATCAGGATTCAGTTTCA 1037
      |||||||
Db      1 TGGATCAGGATTCAGTTTCA 20

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RESULT 426
BD073968
LOCUS      BD073968      20 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION      Antisense oligonucleotide specific to MDM2.
ACCESSION      BD073968
VERSION      BD073968.1 GI:22619571
KEYWORDS      JP 2001513996-A/7.
SOURCE      unidentified
ORGANISM      unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Chen,J., Agrawal,S. and Zhang,R.
TITLE      Antisense oligonucleotide specific to MDM2
JOURNAL      Patent: JP 2001513996-A 7 11-SEP-2001;
              HYBRIDON INC
COMMENT      OS      Unidentified
              PN      JP 2001513996-A/7
              PD      11-SEP-2001
              PF      18-AUG-1998 JP 2000507794
              PR      22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
              JIANDONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
              PC      C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
              PC      C12N15/00
              CC      Strandedness: Both;
              CC      Topology: Linear;
              CC      Antisense oligonucleotide specific to MDM2
              FH      Key      Location/Qualifiers
              FT      source      1..20
              FT      Location/Qualifiers
              FT      1..20
              FT      /organism='Unidentified'.

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      357 ACCTCAGATTCACGCTTC 376
      |||||||
Db      1 ACCTCAGATTCACGCTTC 20

RESULT 427
BD073969
LOCUS      BD073969      20 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION      Antisense oligonucleotide specific to MDM2.
ACCESSION      BD073969
VERSION      BD073969.1 GI:22619572
KEYWORDS      JP 2001513996-A/8.
SOURCE      unidentified
ORGANISM      unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Chen,J., Agrawal,S. and Zhang,R.
TITLE      Antisense oligonucleotide specific to MDM2
JOURNAL      Patent: JP 2001513996-A 8 11-SEP-2001;
              HYBRIDON INC
COMMENT      OS      Unidentified
              PN      JP 2001513996-A/8
              PD      11-SEP-2001
              PF      18-AUG-1998 JP 2000507794
              PR      22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
              JIANDONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
              PC      C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
              PC      C12N15/00
              CC      Strandedness: Both;
              CC      Topology: Linear;
              CC      Antisense oligonucleotide specific to MDM2
              FH      Key      Location/Qualifiers
              FT      source      1..20
              FT      Location/Qualifiers
              FT      1..20
              FT      /organism='Unidentified'.

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FEATURES	Location/Qualifiers	source
OS	Unidentified	
PN	JP 2001513996-A/10	
PD	11-SEP-2001	
PF	18-AUG-1998 JP 2000507794	
PR	22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI	
PC	C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,	
PC	C12N15/00	
CC	Strandedness: Both;	
CC	Topology: Linear;	
CC	Antisense oligonucleotide specific to MDM2	
FH	Key Location/Qualifiers	
FT	source 1..20 /organism='Unidentified'.	
FEATURES	Location/Qualifiers	
source	1..20 /organism='unidentified' /mol_type='genomic DNA' /db_xref='taxon:32644'	
Query Match	0.8%; Score 20; DB 1; Length 20;	
Best Local Similarity	100.0%; Pred. No. 7.9e+02;	
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1203 TCCTTAGCTGACTATTGGAA 1222	
Db	1 TCCTTAGCTGACTATTGGAA 20	
RESULT 430		
BD073972		
LOCUS	BD073972 20 bp DNA linear	PAT 27-AUG-2002
DEFINITION	Antisense oligonucleotide specific to MDM2.	
ACCESSION	BD073972	
VERSION	BD073972.1 GI:22619575	
KEYWORDS	JP 2001513996-A/11.	
SOURCE	unidentified	
ORGANISM	unclassified.	
REFERENCE	1 (bases 1 to 20)	
AUTHORS	Chen,J., Agrawal,S. and Zhang,R.	
TITLE	Antisense oligonucleotide specific to MDM2	
JOURNAL	Patent: JP 2001513996-A 11 11-SEP-2001;	
COMMENT	HYBRIDON INC	
OS	Unidentified	
PN	JP 2001513996-A/11	
PD	11-SEP-2001	
PF	18-AUG-1998 JP 2000507794	
PR	22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI	
PC	C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,	
PC	C12N15/00	
CC	Strandedness: Both;	
CC	Topology: Linear;	
CC	Antisense oligonucleotide specific to MDM2	
FH	Key Location/Qualifiers	
FT	source 1..20 /organism='Unidentified'.	
FEATURES	Location/Qualifiers	
source	1..20 /organism='unidentified' /mol_type='genomic DNA' /db_xref='taxon:32644'	
Query Match	0.8%; Score 20; DB 1; Length 20;	
Best Local Similarity	100.0%; Pred. No. 7.9e+02;	
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	780 TCTACCTCATCTAGAGGAG 799	
Db	1 TCTACCTCATCTAGAGGAG 20	
RESULT 429		
BD073971		
LOCUS	BD073971 20 bp DNA linear	PAT 27-AUG-2002
DEFINITION	Antisense oligonucleotide specific to MDM2.	
ACCESSION	BD073971	
VERSION	BD073971.1 GI:22619574	
KEYWORDS	JP 2001513996-A/10.	
SOURCE	unidentified	
ORGANISM	unclassified.	
REFERENCE	1 (bases 1 to 20)	
AUTHORS	Chen,J., Agrawal,S. and Zhang,R.	
TITLE	Antisense oligonucleotide specific to MDM2	
JOURNAL	Patent: JP 2001513996-A 10 11-SEP-2001;	

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RESULT 431
BD073974
LOCUS          BD073974          20 bp    DNA    linear    PAT 27-AUG-2002
DEFINITION     Antisense oligonucleotide specific to MDM2.
ACCESSION      BD073974
VERSION        BD073974.1 GI:22619577
KEYWORDS       JP 2001513996-A/13.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS       Chen,J., Agrawal,S. and Zhang,R.
TITLE         Antisense oligonucleotide specific to MDM2
JOURNAL       Patent: JP 2001513996-A 13 11-SEP-2001;
              HYBRIDON INC
COMMENT        OS Unidentified
              PN JP 2001513996-A/13
              PD 11-SEP-2001
              PF 18-AUG-1998 JP 2000507794
              PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
              PC C12N15/09,A61K31/47,A61K48/00,A61P35/00,C07H21/00,
              PC C12N15/00
              CC Strandedness: Both;
              CC Topology: Linear;
              CC Antisense oligonucleotide specific to MDM2
              FH Key Location/Qualifiers
              FT source 1..20
              FT /organism='Unidentified'.

FEATURES
  source      Location/Qualifiers
            1..20
            /organism='unidentified'
            /mol_type='genomic DNA'
            /db_xref='taxon:32644'

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 669 ACATCTGTGAGTGAGACAG 688
      |||||
      1 ACATCTGTGAGTGAGACAG 20
Db

RESULT 432
BD073975
LOCUS          BD073975          20 bp    DNA    linear    PAT 27-AUG-2002
DEFINITION     Antisense oligonucleotide specific to MDM2.
ACCESSION      BD073975
VERSION        BD073975.1 GI:22619578
KEYWORDS       JP 2001513996-A/14.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS       Chen,J., Agrawal,S. and Zhang,R.
TITLE         Antisense oligonucleotide specific to MDM2
JOURNAL       Patent: JP 2001513996-A 14 11-SEP-2001;
              HYBRIDON INC
COMMENT        OS Unidentified
              PN JP 2001513996-A/14
              PD 11-SEP-2001
              PF 18-AUG-1998 JP 2000507794
              PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
              PC C12N15/09,A61K31/47,A61K48/00,A61P35/00,C07H21/00,
              PC C12N15/00
              CC Strandedness: Both;
              CC Topology: Linear;
              CC Antisense oligonucleotide specific to MDM2
              FH Key Location/Qualifiers
              FT source 1..20
              FT /organism='Unidentified'.

FEATURES
  source      Location/Qualifiers
            1..20
            /organism='unidentified'
            /mol_type='genomic DNA'
            /db_xref='taxon:32644'

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 669 ACATCTGTGAGTGAGACAG 688
      |||||
      1 ACATCTGTGAGTGAGACAG 20
Db

RESULT 433
BD073976
LOCUS          BD073976          20 bp    DNA    linear    PAT 27-AUG-2002
DEFINITION     Antisense oligonucleotide specific to MDM2.
ACCESSION      BD073976
VERSION        BD073976.1 GI:22619579
KEYWORDS       JP 2001513996-A/15.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS       Chen,J., Agrawal,S. and Zhang,R.
TITLE         Antisense oligonucleotide specific to MDM2
JOURNAL       Patent: JP 2001513996-A 15 11-SEP-2001;
              HYBRIDON INC
COMMENT        OS Unidentified
              PN JP 2001513996-A/15
              PD 11-SEP-2001
              PF 18-AUG-1998 JP 2000507794
              PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
              PC C12N15/09,A61K31/47,A61K48/00,A61P35/00,C07H21/00,
              PC C12N15/00
              CC Strandedness: Both;
              CC Topology: Linear;
              CC Antisense oligonucleotide specific to MDM2
              FH Key Location/Qualifiers
              FT source 1..20
              FT /organism='Unidentified'.

FEATURES
  source      Location/Qualifiers
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            /mol_type='genomic DNA'
            /db_xref='taxon:32644'

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTGAGAACAGGTGTCA 694
      |||||
      1 GTGAGTGAGAACAGGTGTCA 20
Db

RESULT 434
BD073977
LOCUS          BD073977          20 bp    DNA    linear    PAT 27-AUG-2002
DEFINITION     Antisense oligonucleotide specific to MDM2.
ACCESSION      BD073977
VERSION        BD073977.1 GI:22619580
KEYWORDS       JP 2001513996-A/16.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS       Chen,J., Agrawal,S. and Zhang,R.
TITLE         Antisense oligonucleotide specific to MDM2
JOURNAL       Patent: JP 2001513996-A 16 11-SEP-2001;
              HYBRIDON INC
COMMENT        OS Unidentified
              PN JP 2001513996-A/16
              PD 11-SEP-2001
              PF 18-AUG-1998 JP 2000507794
              PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
              PC C12N15/09,A61K31/47,A61K48/00,A61P35/00,C07H21/00,
              PC C12N15/00
              CC Strandedness: Both;
              CC Topology: Linear;
              CC Antisense oligonucleotide specific to MDM2
              FH Key Location/Qualifiers
              FT source 1..20
              FT /organism='Unidentified'.

FEATURES
  source      Location/Qualifiers
            1..20
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            /mol_type='genomic DNA'
            /db_xref='taxon:32644'

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 680 TGAGAACAGGTGTCACTTG 699
      |||||
      1 TGAGAACAGGTGTCACTTG 20
Db

RESULT 435
BD073978
LOCUS          BD073978          20 bp    DNA    linear    PAT 27-AUG-2002
DEFINITION     Antisense oligonucleotide specific to MDM2.
ACCESSION      BD073978
VERSION        BD073978.1 GI:22619581
KEYWORDS       JP 2001513996-A/17.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS       Chen,J., Agrawal,S. and Zhang,R.
TITLE         Antisense oligonucleotide specific to MDM2
JOURNAL       Patent: JP 2001513996-A 17 11-SEP-2001;
              HYBRIDON INC
COMMENT        OS Unidentified
              PN JP 2001513996-A/17
              PD 11-SEP-2001
              PF 18-AUG-1998 JP 2000507794
              PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
              PC C12N15/09,A61K31/47,A61K48/00,A61P35/00,C07H21/00,
              PC C12N15/00
              CC Strandedness: Both;
              CC Topology: Linear;
              CC Antisense oligonucleotide specific to MDM2
              FH Key Location/Qualifiers
              FT source 1..20
              FT /organism='Unidentified'.

FEATURES
  source      Location/Qualifiers
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            /mol_type='genomic DNA'
            /db_xref='taxon:32644'

Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 680 TGAGAACAGGTGTCACTTG 699
      |||||
      1 TGAGAACAGGTGTCACTTG 20
Db

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JOURNAL      Patent: JP 2001513996-A 16 11-SEP-2001;
COMMENT      HYBRIDON INC
OS           Unidentified
PN          JP 2001513996-A/16
PD          11-SEP-2001
PF          18-AUG-1998 JP 2000507794
PR          22-AUG-1997 US 08/916384, 06-MAY-1998 US 09/073567 PI
JIANJONG CHEN, SUDHIR AGRAWAL, RUIWEN ZHANG
PC          C12N15/09, A61K31/47, A61K31/7088, A61K48/00, A61P35/00, C07H21/00,
PC          C12N15/00
CC          Strandedness: Both;
CC          Topology: Linear;
CC          Antisense oligonucleotide specific to MDM2
FH          Key Location/Qualifiers
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FT          /db_xref='taxon:32644'

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source
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/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      685 ACAGGTGTCACCTTGAAGGT 704
      |||||||
Db      1 ACAGGTGTCACCTTGAAGGT 20

RESULT 435
BD073978
LOCUS      20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073978
VERSION BD073978.1 GI:22619581
KEYWORDS JP 2001513996-A/17.
SOURCE      unidentified
ORGANISM      unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Chen, J., Agrawal, S. and Zhang, R.
TITLE        Antisense oligonucleotide specific to MDM2
JOURNAL      Patent: JP 2001513996-A 17 11-SEP-2001;
HYBRIDON INC
COMMENT      OS Unidentified
PN          JP 2001513996-A/17
PD          11-SEP-2001
PF          18-AUG-1998 JP 2000507794
PR          22-AUG-1997 US 08/916384, 06-MAY-1998 US 09/073567 PI
JIANJONG CHEN, SUDHIR AGRAWAL, RUIWEN ZHANG
PC          C12N15/09, A61K31/47, A61K31/7088, A61K48/00, A61P35/00, C07H21/00,
PC          C12N15/00
CC          Strandedness: Both;
CC          Topology: Linear;
CC          Antisense oligonucleotide specific to MDM2
FH          Key Location/Qualifiers
FT          1. .20
FT          Location/Qualifiers
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FT          /mol_type='genomic DNA'
FT          /db_xref='taxon:32644'

FEATURES
source
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/mol_type='genomic DNA'
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Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      704 TGGGAGTGATCAAAAGGACC 723
      |||||||
Db      1 TGGGAGTGATCAAAAGGACC 20

JOURNAL      Patent: JP 2001513996-A 16 11-SEP-2001;
COMMENT      HYBRIDON INC
OS           Unidentified
PN          JP 2001513996-A/16
PD          11-SEP-2001
PF          18-AUG-1998 JP 2000507794
PR          22-AUG-1997 US 08/916384, 06-MAY-1998 US 09/073567 PI
JIANJONG CHEN, SUDHIR AGRAWAL, RUIWEN ZHANG
PC          C12N15/09, A61K31/47, A61K31/7088, A61K48/00, A61P35/00, C07H21/00,
PC          C12N15/00
CC          Strandedness: Both;
CC          Topology: Linear;
CC          Antisense oligonucleotide specific to MDM2
FH          Key Location/Qualifiers
FT          1. .20
FT          Location/Qualifiers
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FT          /db_xref='taxon:32644'

FEATURES
source
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/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      704 TGGGAGTGATCAAAAGGACC 723
      |||||||
Db      1 TGGGAGTGATCAAAAGGACC 20

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RESULT 436
BD073979
LOCUS      20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073979
VERSION BD073979.1 GI:22619582
KEYWORDS JP 2001513996-A/18.
SOURCE      unidentified
ORGANISM      unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Chen, J., Agrawal, S. and Zhang, R.
TITLE        Antisense oligonucleotide specific to MDM2
JOURNAL      Patent: JP 2001513996-A 18 11-SEP-2001;
HYBRIDON INC
COMMENT      OS Unidentified
PN          JP 2001513996-A/18
PD          11-SEP-2001
PF          18-AUG-1998 JP 2000507794
PR          22-AUG-1997 US 08/916384, 06-MAY-1998 US 09/073567 PI
JIANJONG CHEN, SUDHIR AGRAWAL, RUIWEN ZHANG
PC          C12N15/09, A61K31/47, A61K31/7088, A61K48/00, A61P35/00, C07H21/00,
PC          C12N15/00
CC          Strandedness: Both;
CC          Topology: Linear;
CC          Antisense oligonucleotide specific to MDM2
FH          Key Location/Qualifiers
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FT          Location/Qualifiers
FT          1. .20
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FT          /db_xref='taxon:32644'

FEATURES
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/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      709 GTGATCAAAAGGACCTTGTA 728
      |||||||
Db      1 GTGATCAAAAGGACCTTGTA 20

RESULT 437
BD073980
LOCUS      20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073980
VERSION BD073980.1 GI:22619583
KEYWORDS JP 2001513996-A/19.
SOURCE      unidentified
ORGANISM      unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Chen, J., Agrawal, S. and Zhang, R.
TITLE        Antisense oligonucleotide specific to MDM2
JOURNAL      Patent: JP 2001513996-A 19 11-SEP-2001;
HYBRIDON INC
COMMENT      OS Unidentified
PN          JP 2001513996-A/19
PD          11-SEP-2001
PF          18-AUG-1998 JP 2000507794
PR          22-AUG-1997 US 08/916384, 06-MAY-1998 US 09/073567 PI
JIANJONG CHEN, SUDHIR AGRAWAL, RUIWEN ZHANG
PC          C12N15/09, A61K31/47, A61K31/7088, A61K48/00, A61P35/00, C07H21/00,
PC          C12N15/00
CC          Strandedness: Both;
CC          Topology: Linear;
CC          Antisense oligonucleotide specific to MDM2
FH          Key Location/Qualifiers

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FT source 1..20
FT /organism='Unidentified'.
FEATURES
  source
    Location/Qualifiers
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      /db_xref='taxon:32644'

Query Match
Best Local Similarity 0.8%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 717 AAGGACCTTGACAGAGCT 736
    |||||
Db 1 AAGGACCTTGACAGAGCT 20

RESULT 438
LOCUS BD073981 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073981
VERSION BD073981.1 GI:22619584
KEYWORDS JP 2001513996-A/20.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Chen,J., Agrawal,S. and Zhang,R.
TITLE Antisense oligonucleotide specific to MDM2
JOURNAL Patent: JP 2001513996-A 20 11-SEP-2001;
COMMENT HYBRIDON INC
OS Unidentified
PN JP 2001513996-A/20
PD 11-SEP-2001
PR 18-AUG-1998 JP 2000507794
PT 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PT
PC C12N15/09,A61K31/47,A61K48/00,A61P35/00,C07H21/00,
PC C12N15/00
CC Strandedness: Both;
CC Topology: Linear;
CC Antisense oligonucleotide specific to MDM2
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Unidentified'.

FEATURES
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      /db_xref='taxon:32644'

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1003 ATTCAGGTGATTGGTGGAT 1022
    |||||
Db 1 ATTCAGGTGATTGGTGGAT 20

RESULT 440
LOCUS BD073984 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073984
VERSION BD073984.1 GI:22619587
KEYWORDS JP 2001513996-A/23.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Chen,J., Agrawal,S. and Zhang,R.
TITLE Antisense oligonucleotide specific to MDM2
JOURNAL Patent: JP 2001513996-A 23 11-SEP-2001;
COMMENT HYBRIDON INC
OS Unidentified
PN JP 2001513996-A/23
PD 11-SEP-2001
PR 18-AUG-1998 JP 2000507794
PT 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PT
PC C12N15/09,A61K31/47,A61K48/00,A61P35/00,C07H21/00,
PC C12N15/00
CC Strandedness: Both;
CC Topology: Linear;
CC Antisense oligonucleotide specific to MDM2
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Unidentified'.

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      /db_xref='taxon:32644'

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 998 TGAACATTCAGGTGATTGGT 1017
    |||||
Db 1 TGAACATTCAGGTGATTGGT 20

RESULT 439
LOCUS BD073982 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073982
VERSION BD073982.1 GI:22619585
KEYWORDS JP 2001513996-A/21.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Chen,J., Agrawal,S. and Zhang,R.

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Db      1  ATTCAGTTTCAGATCAGTTT 20

RESULT 441
LOCUS   BD073985
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073985
VERSION   BD073985.1 GI:22619588
KEYWORDS  JP 2001513996-A/24.
SOURCE    unidentified
ORGANISM  unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS   Chen,J., Agrawal,S. and Zhang,R.
TITLE      Antisense oligonucleotide specific to MDM2
JOURNAL    Patent: JP 2001513996-A 24 11-SEP-2001;
            HYBRIDON INC
COMMENT    OS Unidentified
            PN JP 2001513996-A/24
            PD 11-SEP-2001
            PF 18-AUG-1998 JP 2000507794
            PR 22-AUG-1997 US 08/916384, 06-MAY-1998 US 09/073567 PI
            PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
            PC C12N15/00
            CC Strandedness: Both;
            CC Topology: Linear;
            CC Antisense oligonucleotide specific to MDM2
            FH Key Location/Qualifiers
            FT source 1..20
            FT /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source           1..20
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                     /db_xref="taxon:32644"
Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1038  GATCAGTTTAGTGTAGAAATT 1057
          |||||
Db      1  GATCAGTTTAGTGTAGAAATT 20

RESULT 442
LOCUS   BD073988/c
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073988
VERSION   BD073988.1 GI:22619591
KEYWORDS  JP 2001513996-A/27.
SOURCE    unidentified
ORGANISM  unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS   Chen,J., Agrawal,S. and Zhang,R.
TITLE      Antisense oligonucleotide specific to MDM2
JOURNAL    Patent: JP 2001513996-A 27 11-SEP-2001;
            HYBRIDON INC
COMMENT    OS Unidentified
            PN JP 2001513996-A/27
            PD 11-SEP-2001
            PF 18-AUG-1998 JP 2000507794
            PR 22-AUG-1997 US 08/916384, 06-MAY-1998 US 09/073567 PI
            PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
            PC C12N15/00
            CC Strandedness: Both;
            CC Topology: Linear;
            CC Antisense oligonucleotide specific to MDM2
            FH Key Location/Qualifiers
            FT source 1..20
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            FT /db_xref="taxon:32644"
Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1038  GATCAGTTTAGTGTAGAAATT 1057
          |||||
Db      1  GATCAGTTTAGTGTAGAAATT 20

RESULT 443
LOCUS   BD073989/c
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073989
VERSION   BD073989.1 GI:22619592
KEYWORDS  JP 2001513996-A/28.
SOURCE    unidentified
ORGANISM  unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS   Chen,J., Agrawal,S. and Zhang,R.
TITLE      Antisense oligonucleotide specific to MDM2
JOURNAL    Patent: JP 2001513996-A 28 11-SEP-2001;
            HYBRIDON INC
COMMENT    OS Unidentified
            PN JP 2001513996-A/28
            PD 11-SEP-2001
            PF 18-AUG-1998 JP 2000507794
            PR 22-AUG-1997 US 08/916384, 06-MAY-1998 US 09/073567 PI
            PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
            PC C12N15/00
            CC Strandedness: Both;
            CC Topology: Linear;
            CC Antisense oligonucleotide specific to MDM2
            FH Key Location/Qualifiers
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            FT /organism="Unidentified".
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
Query Match          0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      695  CCTTGAAGGTGGAGTGATC 714
          |||||
Db      20  CCTTGAAGGTGGAGTGATC 1

RESULT 444
LOCUS   BD073990/c
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073990
VERSION   BD073990.1 GI:22619593
KEYWORDS  JP 2001513996-A/29.
SOURCE    unidentified
ORGANISM  unclassified.
REFERENCE 1 (bases 1 to 20)

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AUTHORS      Chen,J., Agrawal,S. and Zhang,R.
TITLE        Antisense oligonucleotide specific to MDM2
JOURNAL      Patent: JP 2001513996-A 29 11-SEP-2001;
COMMENT      HYBRIDON INC
OS           Unidentified
PN           JP 2001513996-A/29
PD           11-SEP-2001
PF           18-AUG-1998 JP 2000507794
PR           22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
JIAN DONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
PC           C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
PC           C12N15/00
CC           Strandedness: Both;
CC           Topology: Linear;
CC           Antisense oligonucleotide specific to MDM2
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              /db_xref='taxon:32644'

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1018 TGGATCAGGATTCAGTTTCA 1037
Db      20 TGGATCAGGATTCAGTTTCA 1

RESULT 445
LOCUS      BD073991/c
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION  BD073991
VERSION     BD073991.1 GI:22619594
KEYWORDS    JP 2001513996-A/30.
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Chen,J., Agrawal,S. and Zhang,R.
TITLE       Antisense oligonucleotide specific to MDM2
JOURNAL     Patent: JP 2001513996-A 30 11-SEP-2001;
COMMENT     HYBRIDON INC
OS           Unidentified
PN           JP 2001513996-A/30
PD           11-SEP-2001
PF           18-AUG-1998 JP 2000507794
PR           22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
JIAN DONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
PC           C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
PC           C12N15/00
CC           Strandedness: Both;
CC           Topology: Linear;
CC           Antisense oligonucleotide specific to MDM2
FH           Key Location/Qualifiers
FT           source 1..20 /organism='Unidentified'.
FEATURES
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              /mol_type='genomic DNA'
              /db_xref='taxon:32644'

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1018 TGGATCAGGATTCAGTTTCA 1037
Db      20 TGGATCAGGATTCAGTTTCA 1

RESULT 446
LOCUS      BD073992/c
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION  BD073992
VERSION     BD073992.1 GI:22619595
KEYWORDS    JP 2001513996-A/31.
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Chen,J., Agrawal,S. and Zhang,R.
TITLE       Antisense oligonucleotide specific to MDM2
JOURNAL     Patent: JP 2001513996-A 31 11-SEP-2001;
COMMENT     HYBRIDON INC
OS           Unidentified
PN           JP 2001513996-A/31
PD           11-SEP-2001
PF           18-AUG-1998 JP 2000507794
PR           22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
JIAN DONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
PC           C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
PC           C12N15/00
CC           Strandedness: Both;
CC           Topology: Linear;
CC           Antisense oligonucleotide specific to MDM2
FH           Key Location/Qualifiers
FT           source 1..20 /organism='Unidentified'.
FEATURES
  source      Location/Qualifiers
              1..20
              /organism='unidentified'
              /mol_type='genomic DNA'
              /db_xref='taxon:32644'

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      369 CCAGCTTCGACACAGAGAC 388
Db      20 CCAGCTTCGACACAGAGAC 1

RESULT 447
LOCUS      BD073993/c
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION  BD073993
VERSION     BD073993.1 GI:22619596
KEYWORDS    JP 2001513996-A/32.
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Chen,J., Agrawal,S. and Zhang,R.
TITLE       Antisense oligonucleotide specific to MDM2
JOURNAL     Patent: JP 2001513996-A 32 11-SEP-2001;
COMMENT     HYBRIDON INC
OS           Unidentified
PN           JP 2001513996-A/32
PD           11-SEP-2001
PF           18-AUG-1998 JP 2000507794
PR           22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
JIAN DONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
PC           C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
PC           C12N15/00
CC           Strandedness: Both;
CC           Topology: Linear;
CC           Antisense oligonucleotide specific to MDM2
FH           Key Location/Qualifiers
FT           source 1..20 /organism='Unidentified'.
FEATURES
  source      Location/Qualifiers
              1..20
              /organism='unidentified'
              /mol_type='genomic DNA'
              /db_xref='taxon:32644'

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      357 ACCTCACAGATTCAGCTTC 376

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CC Antisense oligonucleotide specific to MDM2
FH Key Location/Qualifiers
FT source
  Location/Qualifiers
  1..20
  /organism="unidentified"
  /mol_type="genomic DNA"
  /db_xref="taxon:32644"

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 780 TCTACCTCATCTAGAGGAG 799
Db 20 TCTACCTCATCTAGAGGAG 1

RESULT 448
BD073994/c
LOCUS BD073994 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073994
VERSION BD073994.1 GI:22619597
KEYWORDS JP 2001513996-A/33.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Chen,J., Agrawal,S. and Zhang,R.
TITLE Antisense oligonucleotide specific to MDM2
JOURNAL Patent: JP 2001513996-A 33 11-SEP-2001;
HYBRIDON INC
OS Unidentified
PN JP 2001513996-A/33
PD 11-SEP-2001
PF 18-AUG-1998 JP 2000507794
PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
JIANDONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
PC C12N15/00
CC Strandedness: Both;
CC Topology: Linear;
CC Antisense oligonucleotide specific to MDM2
FH Key Location/Qualifiers
FT source
  Location/Qualifiers
  1..20
  /organism="unidentified"
  /mol_type="genomic DNA"
  /db_xref="taxon:32644"

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1203 TCCTTAGCTGACTATTGGAA 1222
Db 20 TCCTTAGCTGACTATTGGAA 1

RESULT 449
BD073995/c
LOCUS BD073995 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073995
VERSION BD073995.1 GI:22619598
KEYWORDS JP 2001513996-A/34.
SOURCE unidentified
ORGANISM unclassified.

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REFERENCE 1 (bases 1 to 20)
AUTHORS Chen,J., Agrawal,S. and Zhang,R.
TITLE Antisense oligonucleotide specific to MDM2
JOURNAL Patent: JP 2001513996-A 34 11-SEP-2001;
HYBRIDON INC
COMMENT OS Unidentified
PN JP 2001513996-A/34
PD 11-SEP-2001
PF 18-AUG-1998 JP 2000507794
PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
JIANDONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
PC C12N15/00
CC Strandedness: Both;
CC Topology: Linear;
CC Antisense oligonucleotide specific to MDM2
FH Key Location/Qualifiers
FT source
  Location/Qualifiers
  1..20
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  /mol_type="genomic DNA"
  /db_xref="taxon:32644"

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1230 TCATGCAATGAATGAATCC 1249
Db 20 TCATGCAATGAATGAATCC 1

RESULT 450
BD073996/c
LOCUS BD073996 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD073996
VERSION BD073996.1 GI:22619599
KEYWORDS JP 2001513996-A/35.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Chen,J., Agrawal,S. and Zhang,R.
TITLE Antisense oligonucleotide specific to MDM2
JOURNAL Patent: JP 2001513996-A 35 11-SEP-2001;
HYBRIDON INC
COMMENT OS Unidentified
PN JP 2001513996-A/35
PD 11-SEP-2001
PF 18-AUG-1998 JP 2000507794
PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
JIANDONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
PC C12N15/00
CC Strandedness: Both;
CC Topology: Linear;
CC Antisense oligonucleotide specific to MDM2
FH Key Location/Qualifiers
FT source
  Location/Qualifiers
  1..20
  /organism="unidentified"
  /mol_type="genomic DNA"
  /db_xref="taxon:32644"

Query Match      0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 669 ACATCTGTGAGTGAGAACAG 688
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 Db 20 ACATCTGTGAGTGAGAACAG 1

RESULT 451

BD073997/c
 LOCUS BD073997 20 bp DNA linear PAT 27-AUG-2002
 DEFINITION Antisense oligonucleotide specific to MDM2.
 ACCESSION BD073997

VERSION BD073997.1 GI:22619600
 KEYWORDS JP 2001513996-A/36.
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 20)

AUTHORS Chen,J., Agrawal,S. and Zhang,R.

TITLE Antisense oligonucleotide specific to MDM2

JOURNAL Patent: JP 2001513996-A 36 11-SEP-2001;

COMMENT HYBRIDON INC

OS Unidentified

PN JP 2001513996-A/36

PD 11-SEP-2001

PF 18-AUG-1998 JP 2000507794

PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI

PC JIANDONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG

PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,

PC C12N15/00

CC Strandedness: Both;

CC Topology: Linear;

CC Antisense oligonucleotide specific to MDM2

FF Key Location/Qualifiers

FT source 1..20

FT /organism='Unidentified'.

FEATURES

source

1..20

/organism='unidentified'

/mol_type='genomic DNA'

/db_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 7.9e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTGAGAACAGGTGTCA 694

||||||||||||||||

Db 20 GTGAGTGAGAACAGGTGTCA 1

RESULT 452

BD073998/c
 LOCUS BD073998 20 bp DNA linear PAT 27-AUG-2002
 DEFINITION Antisense oligonucleotide specific to MDM2.
 ACCESSION BD073998

VERSION BD073998.1 GI:22619601

KEYWORDS JP 2001513996-A/37.

SOURCE unidentified

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 20)

AUTHORS Chen,J., Agrawal,S. and Zhang,R.

TITLE Antisense oligonucleotide specific to MDM2

JOURNAL Patent: JP 2001513996-A 37 11-SEP-2001;

COMMENT HYBRIDON INC

OS Unidentified

PN JP 2001513996-A/37

PD 11-SEP-2001

PF 18-AUG-1998 JP 2000507794

PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI

PC JIANDONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG

PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,

PC C12N15/00

CC Strandedness: Both;

CC Topology: Linear;

CC Antisense oligonucleotide specific to MDM2

FF Key Location/Qualifiers

FT source 1..20

FT /organism='Unidentified'.

CC Topology: Linear;
 CC Antisense oligonucleotide specific to MDM2
 FH Key Location/Qualifiers
 FT source 1..20
 FT /organism='Unidentified'.

FEATURES

source

1..20

/organism='unidentified'

/mol_type='genomic DNA'

/db_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 7.9e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 680 TGAGAACAGGTGTCACTTG 699

||||||||||||||||

Db 20 TGAGAACAGGTGTCACTTG 1

RESULT 453

BD073999/c

LOCUS BD073999 20 bp DNA linear PAT 27-AUG-2002

DEFINITION Antisense oligonucleotide specific to MDM2.

ACCESSION BD073999

VERSION BD073999.1 GI:22619602

KEYWORDS JP 2001513996-A/38.

SOURCE unidentified

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 20)

AUTHORS Chen,J., Agrawal,S. and Zhang,R.

TITLE Antisense oligonucleotide specific to MDM2

JOURNAL Patent: JP 2001513996-A 38 11-SEP-2001;

COMMENT HYBRIDON INC

OS Unidentified

PN JP 2001513996-A/38

PD 11-SEP-2001

PF 18-AUG-1998 JP 2000507794

PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI

PC JIANDONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG

PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,

PC C12N15/00

CC Strandedness: Both;

CC Topology: Linear;

CC Antisense oligonucleotide specific to MDM2

FF Key Location/Qualifiers

FT source 1..20

FT /organism='Unidentified'.

FEATURES

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1..20

/organism='unidentified'

/mol_type='genomic DNA'

/db_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 7.9e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 685 ACAGGTGTCACTTGAAGGT 704

||||||||||||||||

Db 20 ACAGGTGTCACTTGAAGGT 1

RESULT 454

BD074000/c

LOCUS BD074000 20 bp DNA linear PAT 27-AUG-2002

DEFINITION Antisense oligonucleotide specific to MDM2.

ACCESSION BD074000

VERSION BD074000.1 GI:22619603

KEYWORDS JP 2001513996-A/39.

SOURCE unidentified

ORGANISM unclassified

Qy	709	GTGATCAAAAGGACCTTGTA	728
Db	20	GTGATCAAAAGGACCTTGTA	1
RESULT 456			
BD074002/c			
LOCUS	BD074002	20 bp DNA linear	PAT 27-AUG-2002
DEFINITION	Antisense oligonucleotide specific to MDM2.		
ACCESSION	BD074002		
VERSION	BD074002.1	GI:22619605	
KEYWORDS	JP 2001513996-A/41.		
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 20)		
AUTHORS	Chen,J., Agrawal,S. and Zhang,R.		
TITLE	Antisense oligonucleotide specific to MDM2		
JOURNAL	Patent: JP 2001513996-A 41 11-SEP-2001;		
COMMENT	HYBRIDON INC		
	OS Unidentified		
	FN JP 2001513996-A/41		
	PD 11-SEP-2001		
	PF 18-AUG-1998 JP 2000507794		
	PR 22-AUG-1997 US 08/916384,06-MAY-1998 US	09/073567 PI	
	PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,		
	CC C12N15/00		
	CC Strandedness: Both;		
	CC Topology: Linear;		
	CC Antisense oligonucleotide specific to MDM2		
FH Key	Location/Qualifiers		
FT source	1..20		
FT	/organism='Unidentified'.		
FEATURES			
source	1..20		
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	/db_xref="taxon:32644"		
Query Match	0.8%; Score 20; DB 1; Length 20;		
Best Local Similarity	100.0%; Pred. No. 7.9e+02;		
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	717	AAGGACCTTGTACAAGACT	736
Db	20	AAGGACCTTGTACAAGACT	1
RESULT 457			
BD074003/c			
LOCUS	BD074003	20 bp DNA linear	PAT 27-AUG-2002
DEFINITION	Antisense oligonucleotide specific to MDM2.		
ACCESSION	BD074003		
VERSION	BD074003.1	GI:22619606	
KEYWORDS	JP 2001513996-A/42.		
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 20)		
AUTHORS	Chen,J., Agrawal,S. and Zhang,R.		
TITLE	Antisense oligonucleotide specific to MDM2		
JOURNAL	Patent: JP 2001513996-A 42 11-SEP-2001;		
COMMENT	HYBRIDON INC		
	OS Unidentified		
	FN JP 2001513996-A/42		
	PD 11-SEP-2001		
	PF 18-AUG-1998 JP 2000507794		
	PR 22-AUG-1997 US 08/916384,06-MAY-1998 US	09/073567 PI	
	PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,		
	CC C12N15/00		

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CC Strandedness: Both;
CC Topology: Linear;
CC Antisense oligonucleotide specific to MDM2
PH Key Location/Qualifiers
FT source 1..20
FT /organism='Unidentified'.

FEATURES
source
Location/Qualifiers
1..20
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/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 998 TGAACATTCAGGTGATTGGT 1017
|||||
Db 20 TGAACATTCAGGTGATTGGT 1

RESULT 458
BD074004/c
LOCUS BD074004 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD074004
VERSION BD074004.1 GI:22619607
KEYWORDS JP 2001513996-A/43.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Chen,J., Agrawal,S. and Zhang,R.
TITLE Antisense oligonucleotide specific to MDM2
JOURNAL Patent: JP 2001513996-A 43 11-SEP-2001;
HYBRIDON INC
COMMENT OS Unidentified
PN JP 2001513996-A/43
PD 11-SEP-2001
PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
JIANJONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
PC C12N15/00
CC Strandedness: Both;
CC Topology: Linear;
CC Antisense oligonucleotide specific to MDM2
PH Key Location/Qualifiers
FT source 1..20
FT /organism='Unidentified'.

FEATURES
source
Location/Qualifiers
1..20
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1027 ATTCAGTTTCAGATCAGTTT 1046
|||||
Db 20 ATTCAGTTTCAGATCAGTTT 1

RESULT 460
BD074007/c
LOCUS BD074007 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD074007
VERSION BD074007.1 GI:22619610
KEYWORDS JP 2001513996-A/46.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Chen,J., Agrawal,S. and Zhang,R.
TITLE Antisense oligonucleotide specific to MDM2
JOURNAL Patent: JP 2001513996-A 46 11-SEP-2001;
HYBRIDON INC
COMMENT OS Unidentified
PN JP 2001513996-A/46
PD 11-SEP-2001
PR 22-AUG-1997 US 08/916384,06-MAY-1998 US 09/073567 PI
JIANJONG CHEN,SUDHIR AGRAWAL,RUIWEN ZHANG
PC C12N15/09,A61K31/47,A61K31/7088,A61K48/00,A61P35/00,C07H21/00,
PC C12N15/00
CC Strandedness: Both;
CC Topology: Linear;
CC Antisense oligonucleotide specific to MDM2
PH Key Location/Qualifiers
FT source 1..20
FT /organism='Unidentified'.

FEATURES
source
Location/Qualifiers
1..20
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1003 ATTCAGGTGATTGGTTGGAT 1022
|||||
Db 20 ATTCAGGTGATTGGTTGGAT 1

RESULT 459
BD074006/c
LOCUS BD074006 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD074006
VERSION BD074006.1 GI:22619609
KEYWORDS JP 2001513996-A/45.
SOURCE unidentified

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1038 GATCAGTTAGTGTAGATT 1057
Db 20 GATCAGTTAGTGTAGATT 1

RESULT 461
BD074008/c
LOCUS BD074008 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD074008
VERSION BD074008.1 GI:22619611
KEYWORDS JP 2001513996-A/47.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Chen, J., Agrawal, S. and Zhang, R.
TITLE Antisense oligonucleotide specific to MDM2
JOURNAL Patent: JP 2001513996-A 47 11-SEP-2001;
HYBRIDON INC
COMMENT OS Unidentified
PN JP 2001513996-A/47
PD 11-SEP-2001
PF 18-SEP-1998 JP 2000507794
PR 18-AUG-1997 US 08/916384, 06-MAY-1998 US 09/073567 PI
JI JIANGDONG CHEN, SUDHIR AGRAWAL, RUIWEN ZHANG
PC C12N15/09, A61K31/47, A61K31/7086, A61K48/00, A61P35/00, C07H21/00,
PC C12N15/00
CC Strandedness: Both;
CC Topology: linear;
CC Antisense oligonucleotide specific to MDM2
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Unidentified'.
FEATURES
source
1..20
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTGAGACAGGTGTCA 694
Db 20 GTGAGTGAGACAGGTGTCA 1

RESULT 462
BD088804
LOCUS BD088804 20 bp DNA linear PAT 27-AUG-2002
DEFINITION A method of arraying genome clone.
ACCESSION BD088804
VERSION BD088804.1 GI:22634414
KEYWORDS JP 2001321190-A/1048.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Soeda, E.
TITLE A method of arraying genome clone
JOURNAL Patent: JP 2001321190-A 1048 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
GENOTECHS
OS Artificial Sequence
PN JP 2001321190-A/1048
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EIICHI SOEDA
PC C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N33/53, G01N33/566, PC

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1038 GATCAGTTAGTGTAGATT 1057
Db 20 GATCAGTTAGTGTAGATT 1

RESULT 461
BD074008/c
LOCUS BD074008 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide specific to MDM2.
ACCESSION BD074008
VERSION BD074008.1 GI:22619611
KEYWORDS JP 2001513996-A/47.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Chen, J., Agrawal, S. and Zhang, R.
TITLE Antisense oligonucleotide specific to MDM2
JOURNAL Patent: JP 2001513996-A 47 11-SEP-2001;
HYBRIDON INC
COMMENT OS Unidentified
PN JP 2001513996-A/47
PD 11-SEP-2001
PF 18-SEP-1998 JP 2000507794
PR 18-AUG-1997 US 08/916384, 06-MAY-1998 US 09/073567 PI
JI JIANGDONG CHEN, SUDHIR AGRAWAL, RUIWEN ZHANG
PC C12N15/09, A61K31/47, A61K31/7086, A61K48/00, A61P35/00, C07H21/00,
PC C12N15/00
CC Strandedness: Both;
CC Topology: linear;
CC Antisense oligonucleotide specific to MDM2
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Unidentified'.
FEATURES
source
1..20
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 675 GTGAGTGAGACAGGTGTCA 694
Db 20 GTGAGTGAGACAGGTGTCA 1

RESULT 462
BD088804
LOCUS BD088804 20 bp DNA linear PAT 27-AUG-2002
DEFINITION A method of arraying genome clone.
ACCESSION BD088804
VERSION BD088804.1 GI:22634414
KEYWORDS JP 2001321190-A/1048.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Soeda, E.
TITLE A method of arraying genome clone
JOURNAL Patent: JP 2001321190-A 1048 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
GENOTECHS
OS Artificial Sequence
PN JP 2001321190-A/1048
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EIICHI SOEDA
PC C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N33/53, G01N33/566, PC

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C12N15/00,
PC C12N15/00
CC Description of Artificial Sequence:Synthetic DNA FH Key
Location/Qualifiers
FT source 1..20
FT /organism='Artificial Sequence'.
FEATURES
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1..20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2337 CTCCCAAAGTCTGGGATTA 2356
Db 1 CTCCCAAAGTCTGGGATTA 20

RESULT 463
BD089238/c
LOCUS BD089238 20 bp DNA linear PAT 27-AUG-2002
DEFINITION A method of arraying genome clone.
ACCESSION BD089238
VERSION BD089238.1 GI:22634848
KEYWORDS JP 2001321190-A/1482.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Soeda, E.
TITLE A method of arraying genome clone
JOURNAL Patent: JP 2001321190-A 1482 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
GENOTECHS
OS Artificial Sequence
PN JP 2001321190-A/1482
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EIICHI SOEDA
PC C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N33/53, G01N33/566, PC
C12N15/00
CC Description of Artificial Sequence:Synthetic DNA FH Key
Location/Qualifiers
FT source 1..20
FT /organism='Artificial Sequence'.
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1..20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2142 GTGATCTTGGCTCAGTGCAA 2161
Db 20 GTGATCTTGGCTCAGTGCAA 1

RESULT 464
BD106214/c
LOCUS BD106214 20 bp DNA linear PAT 18-SEP-2002
DEFINITION Novel LDL-receptor.
ACCESSION BD106214
VERSION BD106214.1 GI:23201032
KEYWORDS JP 2002501376-A/229.
SOURCE Chlamydia sp.
ORGANISM Chlamydia sp.

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REFERENCE 1 (bases 1 to 20)
 AUTHORS Todd,J.A., Hess,J.W., Caskey,C.T., Cox,R.D., Gerhold,D., Hammond,H. and Hey,P.
 TITLE Novel LDL-receptor
 JOURNAL Patent: JP 2002501376-A 229 15-JAN-2002;
 THE WELLCOME TRUST LTD AS TRUSTEE TO THE WELLCOME TRUST, MERCK & CO INC

COMMENT PN JP 2002501376-A/229
 PD 15-JAN-2002
 PF 15-APR-1998 JP 1998543635
 PR 15-APR-1997 US 60/043553,05-JUN-1997 US 60/048740 PI
 JOHN ANDREW TODD,JOHN WILFRED HESS,CHARLES
 THOMAS CASKEY,ROGER
 PI DAVID COX,
 PI DAVID GERHOLD,HOLLY HAMMOND,PATRICIA HEY

PC C12N15/12,C12N15/11,C12Q1/68,C07K14/705,C07K16/28,A61K38/17,
 PC A61K39/395,
 PC A61K48/00
 CC Strandedness: Single;
 CC Topology: Linear;
 FH Key Location/Qualifiers.

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 : /mol_type="genomic DNA"
 : /db_xref="taxon:35827"

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2344 AGTGCTGGGATTACAGGCAT 2363
 |||||
 Db 20 AGTGCTGGGATTACAGGCAT 1

RESULT 465
 BD128205/c
 LOCUS 20 bp DNA linear PAT 18-SEP-2002
 DEFINITION Primer for synthesizing full-length cDNA and use thereof.
 ACCESSION BD128205
 VERSION BD128205.1 GI:232233150
 KEYWORDS JP 2002017375-A/3636.
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 20)
 AUTHORS Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and Koga,H.
 TITLE Primer for synthesizing full-length cDNA and use thereof
 JOURNAL Patent: JP 2002017375-A 3636 22-JAN-2002;
 HELIX RESEARCH INSTITUTE
 OS Unidentified

COMMENT PN JP 2002017375-A/3636
 PD 22-JAN-2002
 PF 07-JUL-2000 JP 2000253172
 PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
 PI ISHII,
 PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
 SHINICHI KOJIMA,
 PI TETSUJI OTSUKI,HISASHI KOGA

PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/PC
 10,
 PC C12P21/02,C12Q1/68/C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
 Description of Artificial Sequence: an artificially CC
 synthesized primer
 CC sequence
 FH Key Location/Qualifiers
 FT source 1..20
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FEATURES
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 : /organism="unidentified"
 : /mol_type="genomic DNA"
 : /db_xref="taxon:32644"
 Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2341 CAAAGTCTGGGATTACAGG 2360
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 Db 20 CAAAGTCTGGGATTACAGG 1

RESULT 466
 BD138077/c
 LOCUS 20 bp DNA linear PAT 18-SEP-2002
 DEFINITION Antisense modulation of human MDM2 expression.
 ACCESSION BD138077
 VERSION BD138077.1 GI:23233022
 KEYWORDS JP 2002508944-A/3.
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 20)
 AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsett,L.M.
 TITLE Antisense modulation of human MDM2 expression
 JOURNAL Patent: JP 2002508944-A 3 26-MAR-2002;
 ISIS PHARMACEUTICALS INC
 OS Unidentified
 COMMENT PN JP 2002508944-A/3
 PD 26-MAR-2002
 PF 26-MAR-1999 JP 2000538025
 PR 26-MAR-1998 US 09/048810
 PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI COWSERT
 PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04///
 PC C12Q1/68,
 PC C12N15/00
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 CC Topology: Linear;
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 : /mol_type="genomic DNA"
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 Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGGAGCTTGGCTG 20
 |||||
 Db 20 GCACCGCGGAGCTTGGCTG 1

RESULT 467
 BD138078/c
 LOCUS 20 bp DNA linear PAT 18-SEP-2002
 DEFINITION Antisense modulation of human MDM2 expression.
 ACCESSION BD138078
 VERSION BD138078.1 GI:23233023
 KEYWORDS JP 2002508944-A/4.
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 20)

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AUTHORS      Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE        Antisense modulation of human MDM2 expression
JOURNAL      Patent: JP 2002508944-A 4 26-MAR-2002;
              ISIS PHARMACEUTICALS INC
COMMENT      OS Unidentified
              PN JP 2002508944-A/4
              PD 26-MAR-2002
              PF 26-MAR-1999 JP 2000538025
              PR 26-MAR-1998 US 09/048810
              PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI COWSEERT
PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04///
PC C12Q1/68,
PC C12N15/00
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CC Topology: linear;
CC Antisense modulation of human MDM2 expression FH Key
CC Location/Qualifiers
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FT Location/Qualifiers
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   /mol_type='genomic DNA'
   /db_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 GGCCTGTGTGTCGGAAGA 56
Db 20 GGCCTGTGTGTCGGAAGA 1

RESULT 468
BD138079/c
LOCUS      BD138079
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION  BD138079
VERSION     JP 2002508944-A/5.
KEYWORDS   JP 2002508944-A/5.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE      Antisense modulation of human MDM2 expression
JOURNAL    Patent: JP 2002508944-A 5 26-MAR-2002;
            ISIS PHARMACEUTICALS INC
COMMENT    OS Unidentified
            PN JP 2002508944-A/5
            PD 26-MAR-2002
            PF 26-MAR-1999 JP 2000538025
            PR 26-MAR-1998 US 09/048810
            PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI COWSEERT
PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04///
PC C12Q1/68,
PC C12N15/00
CC Strandedness: Single;
CC Topology: linear;
CC Antisense modulation of human MDM2 expression FH Key
CC Location/Qualifiers
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FT Location/Qualifiers
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Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 GGCCTGTGTGTCGGAAGA 56
Db 20 GGCCTGTGTGTCGGAAGA 1

RESULT 468
BD138079/c
LOCUS      BD138079
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION  BD138079
VERSION     JP 2002508944-A/5.
KEYWORDS   JP 2002508944-A/5.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE      Antisense modulation of human MDM2 expression
JOURNAL    Patent: JP 2002508944-A 5 26-MAR-2002;
            ISIS PHARMACEUTICALS INC
COMMENT    OS Unidentified
            PN JP 2002508944-A/5
            PD 26-MAR-2002
            PF 26-MAR-1999 JP 2000538025
            PR 26-MAR-1998 US 09/048810
            PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI COWSEERT
PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04///
PC C12Q1/68,
PC C12N15/00
CC Strandedness: Single;
CC Topology: linear;
CC Antisense modulation of human MDM2 expression FH Key
CC Location/Qualifiers
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   /mol_type='genomic DNA'
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Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 ATTAGTGGGTACGAGCGCCC 166
Db 20 ATTAGTGGGTACGAGCGCCC 1

RESULT 470
BD138081/c
LOCUS      BD138081
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION  BD138081
VERSION     BD138081.1 GI:23233026
KEYWORDS   JP 2002508944-A/7.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE      Antisense modulation of human MDM2 expression
JOURNAL    Patent: JP 2002508944-A 7 26-MAR-2002;
            ISIS PHARMACEUTICALS INC
COMMENT    OS Unidentified

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Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 CTCTGACCGAGATCCTGCTG 114
Db 20 CTCTGACCGAGATCCTGCTG 1

RESULT 469
BD138080/c
LOCUS      BD138080
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION  BD138080
VERSION     BD138080.1 GI:23233025
KEYWORDS   JP 2002508944-A/6.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE      Antisense modulation of human MDM2 expression
JOURNAL    Patent: JP 2002508944-A 6 26-MAR-2002;
            ISIS PHARMACEUTICALS INC
COMMENT    OS Unidentified
            PN JP 2002508944-A/6
            PD 26-MAR-2002
            PF 26-MAR-1999 JP 2000538025
            PR 26-MAR-1998 US 09/048810
            PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI COWSEERT
PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04///
PC C12Q1/68,
PC C12N15/00
CC Strandedness: Single;
CC Topology: linear;
CC Antisense modulation of human MDM2 expression FH Key
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   /organism='unidentified'
   /mol_type='genomic DNA'
   /db_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 ATTAGTGGGTACGAGCGCCC 166
Db 20 ATTAGTGGGTACGAGCGCCC 1

RESULT 470
BD138081/c
LOCUS      BD138081
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION  BD138081
VERSION     BD138081.1 GI:23233026
KEYWORDS   JP 2002508944-A/7.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE      Antisense modulation of human MDM2 expression
JOURNAL    Patent: JP 2002508944-A 7 26-MAR-2002;
            ISIS PHARMACEUTICALS INC
COMMENT    OS Unidentified

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PN JP 2002508944-A/7
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

PI CONSENT
PC C12N15/09, A61K48/00, A61P9/10, A61P17/06, A61P35/00, C07H21/04//
PC C12Q1/68,
PC C12N15/00
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CC Topology: Linear;
CC Antisense modulation of human MDM2 expression FH Key
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   /mol_type='genomic DNA'
   /db_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 GAGAGTGGATGATCCCCGA 200
Db 20 GAGAGTGGATGATCCCCGA 1

RESULT 471
BD138082/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Miraglia, L.J., Nero, P., Graham, M.J., Monia, B.P. and Cowser, L.M.
Antisense modulation of human MDM2 expression
Patent: JP 2002508944-A 8 26-MAR-2002;
ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/8
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

PI CONSENT
PC C12N15/09, A61K48/00, A61P9/10, A61P17/06, A61P35/00, C07H21/04//
PC C12Q1/68,
PC C12N15/00
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CC Topology: Linear;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PN JP 2002508944-A/7
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

PI CONSENT
PC C12N15/09, A61K48/00, A61P9/10, A61P17/06, A61P35/00, C07H21/04//
PC C12Q1/68,
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Antisense modulation of human MDM2 expression FH Key
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   /mol_type='genomic DNA'
   /db_xref='taxon:32644'

Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 273 CTCGAAGCGCGAAACCCCG 292
Db 20 CTCGAAGCGCGAAACCCCG 1

RESULT 472
BD138083/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Miraglia, L.J., Nero, P., Graham, M.J., Monia, B.P. and Cowser, L.M.
Antisense modulation of human MDM2 expression
Patent: JP 2002508944-A 9 26-MAR-2002;
ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/9
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

PI CONSENT
PC C12N15/09, A61K48/00, A61P9/10, A61P17/06, A61P35/00, C07H21/04//
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CC Topology: Linear;
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Query Match 0.8%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 295 TGGTGAGGAGCGCAAAATG 314
Db 20 TGGTGAGGAGCGCAAAATG 1

RESULT 473
BD138084/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Miraglia, L.J., Nero, P., Graham, M.J., Monia, B.P. and Cowser, L.M.
Antisense modulation of human MDM2 expression
Patent: JP 2002508944-A 10 26-MAR-2002;
ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/10
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

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PI COWSERT
 PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//
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 CC Strandedness: Single;
 CC Topology: linear;
 CC Antisense modulation of human MDM2 expression FH Key
 CC Location/Qualifiers
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 FT Location/Qualifiers
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 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 ACCAGGCAAAATGTGCAATAC 322
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 Db 20 ACCAGGCAAAATGTGCAATAC 1

RESULT 474
 BDI38085/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 unclassified.
 1 (bases 1 to 20)
 Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsert,L.M.
 Antisense modulation of human MDM2 expression
 Patent: JP 2002508944-A 11 26-MAR-2002;
 ISIS PHARMACEUTICALS INC
 OS Unidentified
 PN JP 2002508944-A/11
 PD 26-MAR-2002
 PF 26-MAR-1999 JP 2000538025
 PR 26-MAR-1998 US 09/048810
 PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

BDI38085 20 bp DNA linear PAT 18-SEP-2002
 Antisense modulation of human MDM2 expression.
 BDI38085
 BDI38085.1 GI:23233030
 JP 2002508944-A/11.
 unclassified
 unclassified
 unclassified
 1 (bases 1 to 20)
 Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsert,L.M.
 Antisense modulation of human MDM2 expression
 Patent: JP 2002508944-A 11 26-MAR-2002;
 ISIS PHARMACEUTICALS INC
 OS Unidentified
 PN JP 2002508944-A/11
 PD 26-MAR-2002
 PF 26-MAR-1999 JP 2000538025
 PR 26-MAR-1998 US 09/048810
 PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

PI COWSERT
 PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//
 PC C12Q1/68,
 PC C12N15/00
 CC Strandedness: Single;
 CC Topology: linear;
 CC Antisense modulation of human MDM2 expression FH Key
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 FT Location/Qualifiers
 1 (bases 1 to 20)
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 /organism="unidentified"
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 /db_xref="taxon:32644"

Query Match 0.8%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 331 CTGTACCTACTGATGGTCT 350
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 Db 20 CTGTACCTACTGATGGTCT 1

RESULT 475
 BDI38086/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
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 1 (bases 1 to 20)
 Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsert,L.M.
 Antisense modulation of human MDM2 expression
 Patent: JP 2002508944-A 12 26-MAR-2002;
 ISIS PHARMACEUTICALS INC
 OS Unidentified
 PN JP 2002508944-A/12
 PD 26-MAR-2002
 PF 26-MAR-1999 JP 2000538025
 PR 26-MAR-1998 US 09/048810
 PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

BDI38086 20 bp DNA linear PAT 18-SEP-2002
 Antisense modulation of human MDM2 expression.
 BDI38086
 BDI38086.1 GI:23233031
 JP 2002508944-A/12.
 unclassified
 unclassified
 unclassified
 1 (bases 1 to 20)
 Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsert,L.M.
 Antisense modulation of human MDM2 expression
 Patent: JP 2002508944-A 12 26-MAR-2002;
 ISIS PHARMACEUTICALS INC
 OS Unidentified
 PN JP 2002508944-A/12
 PD 26-MAR-2002
 PF 26-MAR-1999 JP 2000538025
 PR 26-MAR-1998 US 09/048810
 PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

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 PC C12Q1/68,
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QY 617 GATCTACGGAAGCTTGCTAG 636
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 Antisense modulation of human MDM2 expression
 Patent: JP 2002508944-A 13 26-MAR-2002;
 ISIS PHARMACEUTICALS INC
 OS Unidentified
 PN JP 2002508944-A/13
 PD 26-MAR-2002
 PF 26-MAR-1999 JP 2000538025
 PR 26-MAR-1998 US 09/048810
 PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

BDI38087 20 bp DNA linear PAT 18-SEP-2002
 Antisense modulation of human MDM2 expression.
 BDI38087
 BDI38087.1 GI:23233032
 JP 2002508944-A/13.
 unclassified
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 Antisense modulation of human MDM2 expression
 Patent: JP 2002508944-A 13 26-MAR-2002;
 ISIS PHARMACEUTICALS INC
 OS Unidentified
 PN JP 2002508944-A/13
 PD 26-MAR-2002
 PF 26-MAR-1999 JP 2000538025
 PR 26-MAR-1998 US 09/048810
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CC Antisense modulation of human MDM2 expression FH Key
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DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138088
VERSION BD138088.1 GI:23233033
KEYWORDS JP 2002508944-A/14.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsett,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 14 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/14
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
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DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138089

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VERSION BD138089.1 GI:23233034
KEYWORDS JP 2002508944-A/15.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsett,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 15 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/15
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
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DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138090
VERSION BD138090.1 GI:23233035
KEYWORDS JP 2002508944-A/16.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsett,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 16 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/16
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M
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PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//
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PC C12N15/00
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CC Antisense modulation of human MDM2 expression FH Key
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REFERENCE	1 (bases 1 to 20)
AUTHORS	Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsett,L.M.
TITLE	Antisense modulation of human MDM2 expression
JOURNAL	Patent: JP 2002508944-A 18 26-MAR-2002;
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CC	Antisense modulation of human MDM2 expression FH Key
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DB	20 CTAACCTATATACCCCTAGGA 1
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LOCUS	BD138093 20 bp DNA linear PAT 18-SEP-2002
DEFINITION	Antisense modulation of human MDM2 expression.
ACCESSION	BD138093
VERSION	BD138093.1 GI:23233038
KEYWORDS	JP 2002508944-A/19.
SOURCE	unidentified
ORGANISM	unclassified. 1 (bases 1 to 20) Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsett,L.M.
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AUTHORS	Antisense modulation of human MDM2 expression
TITLE	Patent: JP 2002508944-A 19 26-MAR-2002;
JOURNAL	ISIS PHARMACEUTICALS INC
COMMENT	OS Unidentified PN JP 2002508944-A/19 PD 26-MAR-2002 PF 26-MAR-1999 JP 2000538025 PR 26-MAR-1998 US 09/048810 PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M
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Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1934 TAGTGAATAGTGAATCTT 1953
Db 20 TAGTGAATAGTGAATCTT 1

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LOCUS BD138094 20 bp DNA linear PAT 18-SEP-2002
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138094
VERSION BD138094.1 GI:23233039
KEYWORDS JP 2002508944-A/20.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 20 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/20
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI CONSERT
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2224 AGTCATCTGCCACACCT 2243
Db 20 AGTCATCTGCCACACCT 1

RESULT 485
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LOCUS BD138096 20 bp DNA linear PAT 18-SEP-2002
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138096
VERSION BD138096.1 GI:23233041
KEYWORDS JP 2002508944-A/22.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 22 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/22
PD 26-MAR-2002
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PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

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ACCESSION BD138095
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KEYWORDS JP 2002508944-A/21.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 21 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC

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QY 2256 GTACTTTTAGTAGACAGG 2275
Db 20 GTACTTTTAGTAGACAGG 1

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DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138099
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KEYWORDS JP 2002508944-A/25.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 25 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC
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PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

QY 37 GGCCCTGTGTGCGAAGA 56
Db 20 GGCCCTGTGTGCGAAGA 1

RESULT 487
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LOCUS BD138107 20 bp DNA linear PAT 18-SEP-2002
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138107
VERSION BD138107.1 GI:23233052
KEYWORDS JP 2002508944-A/33.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 33 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/33
PD 26-MAR-2002
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Db 20 CCGCGCGAGCTTGGCTGCTT 1

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DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138108
VERSION BD138108.1 GI:23233053
KEYWORDS JP 2002508944-A/34.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 34 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/34
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
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ACCESSION      BD138112
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KEYWORDS       JP 2002508944-A/38.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS       Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE         Antisense modulation of human MDM2 expression
JOURNAL       Patent: JP 2002508944-A 38 26-MAR-2002;
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DEFINITION   Antisense modulation of human MDM2 expression.
ACCESSION    BD138113
VERSION      BD138113.1  GI:23233058
KEYWORDS     JP 2002508944-A/39.
SOURCE       unidentified
ORGANISM     unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE       Antisense modulation of human MDM2 expression
JOURNAL     Patent: JP 2002508944-A 39 26-MAR-2002;
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CC Topology: Linear;
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DEFINITION   Antisense modulation of human MDM2 expression.
ACCESSION    BD138113
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SOURCE       unidentified
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AUTHORS     Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
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QY 62 CAAGAAGCCGAGCCGAGGG 81
DB 20 CAAGAAGCCGAGCCGAGGG 1

RESULT 495
BD138115/C
LOCUS         BD138115
DEFINITION   Antisense modulation of human MDM2 expression.
ACCESSION    BD138115
VERSION      BD138115.1  GI:23233060
KEYWORDS     JP 2002508944-A/41.
SOURCE       unidentified
ORGANISM     unidentified

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1 (bases 1 to 20)
REFERENCE
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowser,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 41 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/41
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI COWSERT
PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04///
PC C12Q1/68,
PC C12N15/00
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QY 70 CGAGCCCGAGGGCGGCCG 89
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Db 20 CGAGCCCGAGGGCGGCCG 1

RESULT 496
BD138116/c
LOCUS
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138116
VERSION BD138116.1 GI:23233061
KEYWORDS JP 2002508944-A/42.
SOURCE unidentified
ORGANISM unclassified.
1 (bases 1 to 20)
REFERENCE
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowser,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 42 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/42
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
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PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

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AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowser,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 41 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/41
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI COWSERT
PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04///
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Db 20 TGACCGAGATCCCTGCTGCTT 1

RESULT 497
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LOCUS
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138117
VERSION BD138117.1 GI:23233062
KEYWORDS JP 2002508944-A/43.
SOURCE unidentified
ORGANISM unclassified.
1 (bases 1 to 20)
REFERENCE
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowser,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 43 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/43
PD 26-MAR-2002
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PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

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PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04///
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Db 20 GATCCTGCTGCTTTCGAGC 1

RESULT 498
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LOCUS
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138118
VERSION BD138118.1 GI:23233063
KEYWORDS JP 2002508944-A/44.
SOURCE unidentified
ORGANISM unclassified.
1 (bases 1 to 20)
REFERENCE
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowser,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 44 26-MAR-2002;

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PI	LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M								
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DEFINITION	Antisense modulation of human MDM2 expression.								
ACCESSION	BD138119								
VERSION	BD138119.1 GI:23233064								
KEYWORDS	JP 2002508944-A/45.								
SOURCE	unidentified								
ORGANISM	unclassified.								
REFERENCE	1 (bases 1 to 20)								
AUTHORS	Miraglia, L.J., Nero, P., Graham, M.J., Monia, B.P. and Cowsert, L.M.								
TITLE	Antisense modulation of human MDM2 expression								
JOURNAL	Patent: JP 2002508944-A 45 26-MAR-2002;								
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AUTHORS	Miraglia, L.J., Nero, P., Graham, M.J., Monia, B.P. and Cowsert, L.M.								
TITLE	Antisense modulation of human MDM2 expression								
JOURNAL	Patent: JP 2002508944-A 45 26-MAR-2002;								
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OS	Unidentified								
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PR 26-MAR-1998 US 09/048810
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RESULT 502

BD138122/c
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 DEFINITION Antisense modulation of human MDM2 expression.
 ACCESSION BD138122

VERSION BD138122.1 GI:232333067
 KEYWORDS JP 2002508944-A/48.
 SOURCE unidentified
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REFERENCE 1 (bases 1 to 20)
 AUTHORS Miraglia, L.J., Nero, P., Graham, M.J., Monia, B.P. and Cowsert, L.M.
 TITLE Antisense modulation of human MDM2 expression
 JOURNAL Patent: JP 2002508944-A 48 26-MAR-2002;
 COMMENT ISIS PHARMACEUTICALS INC

OS Unidentified
 PN JP 2002508944-A/48
 PD 26-MAR-2002
 PF 26-MAR-1999 JP 2000538025
 PR 26-MAR-1998 US 09/048810
 PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

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Qy 165 CCAGTGCCTGGCCCGAGA 184
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RESULT 503

BD138123/c
 LOCUS 20 bp DNA linear PAT 18-SEP-2002
 DEFINITION Antisense modulation of human MDM2 expression.
 ACCESSION BD138123

VERSION BD138123.1 GI:232333068
 KEYWORDS JP 2002508944-A/49.
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 20)
 AUTHORS Miraglia, L.J., Nero, P., Graham, M.J., Monia, B.P. and Cowsert, L.M.
 TITLE Antisense modulation of human MDM2 expression
 JOURNAL Patent: JP 2002508944-A 49 26-MAR-2002;
 COMMENT ISIS PHARMACEUTICALS INC

OS Unidentified
 PN JP 2002508944-A/49
 PD 26-MAR-2002
 PF 26-MAR-1999 JP 2000538025
 PR 26-MAR-1998 US 09/048810
 PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

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Qy 174 TGGCCCGAGAGTGGGAATGA 193
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RESULT 504

BD138124/c
 LOCUS 20 bp DNA linear PAT 18-SEP-2002
 DEFINITION Antisense modulation of human MDM2 expression.
 ACCESSION BD138124

VERSION BD138124.1 GI:232333069
 KEYWORDS JP 2002508944-A/50.
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 20)
 AUTHORS Miraglia, L.J., Nero, P., Graham, M.J., Monia, B.P. and Cowsert, L.M.
 TITLE Antisense modulation of human MDM2 expression
 JOURNAL Patent: JP 2002508944-A 50 26-MAR-2002;
 COMMENT ISIS PHARMACEUTICALS INC

OS Unidentified
 PN JP 2002508944-A/50
 PD 26-MAR-2002
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 PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

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PC C12Q1/68,
PC C12N15/00
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RESULT 505
BD138125/c
LOCUS BD138125 20 bp DNA linear PAT 18-SEP-2002
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138125
VERSION BD138125.1 GI:23233070
KEYWORDS JP 2002508944-A/51.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 51 26-MAR-2002;
ISIS PHARMACEUTICALS INC
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PN JP 2002508944-A/51
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI COWSERT
PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04///
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RESULT 506
BD138126/c
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DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138126
VERSION BD138126.1 GI:23233071
KEYWORDS JP 2002508944-A/52.
SOURCE unidentified
ORGANISM unidentified
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REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 52 26-MAR-2002;
ISIS PHARMACEUTICALS INC
COMMENT OS Unidentified
PN JP 2002508944-A/52
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
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PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

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CC Topology: Linear;
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Query Match 0.8%; Score 20; DB 1; Length 20;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 217 CTTCCGCGAGTAGTCAGTCCC 236
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LOCUS BD138127 20 bp DNA linear PAT 18-SEP-2002
DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138127
VERSION BD138127.1 GI:23233072
KEYWORDS JP 2002508944-A/53.
SOURCE unidentified
ORGANISM unidentified
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REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 53 26-MAR-2002;
ISIS PHARMACEUTICALS INC
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CC Topology: Linear;
CC Antisense modulation of human MDM2 expression FH Key

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DB 20 ATGGTGAGGAGCGCAAT 1

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DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138131
VERSION BD138131.1 GI:23233076
KEYWORDS JP 2002508944-A/57.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 57 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC
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PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

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RESULT 513
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DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138133
VERSION BD138133.1 GI:23233078
KEYWORDS JP 2002508944-A/59.
SOURCE unidentified
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REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 59 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC
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PN JP 2002508944-A/59
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

PI COWSEERT
PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//
PC C12Q1/68,
CC Strandedness: Single;
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DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138132
VERSION BD138132.1 GI:23233077
KEYWORDS JP 2002508944-A/58.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowseert,L.M.
TITLE Antisense modulation of human MDM2 expression

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RESULT 514
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DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138134
VERSION BD138134.1 GI:23233079
KEYWORDS JP 2002508944-A/60.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1. (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowser,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 60 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/60
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

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DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138136
VERSION BD138136.1 GI:23233081
KEYWORDS JP 2002508944-A/62.
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1. (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowser,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 62 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/62
PD 26-MAR-2002
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PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

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ACCESSION BD138135
VERSION BD138135.1 GI:23233080
KEYWORDS JP 2002508944-A/61.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1. (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowser,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 61 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC
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PF 26-MAR-1999 JP 2000538025
PR 26-MAR-1998 US 09/048810
PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

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DEFINITION Antisense modulation of human MDM2 expression.
ACCESSION BD138136
VERSION BD138136.1 GI:23233081
KEYWORDS JP 2002508944-A/62.
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1. (bases 1 to 20)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowser,L.M.
TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 62 26-MAR-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2002508944-A/62
PD 26-MAR-2002
PF 26-MAR-1999 JP 2000538025
PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

PI COWSERT
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DEFINITION	Antisense modulation of human MDM2 expression.		
ACCESSION	BD138142		
VERSION	BD138142.1 GI:23233087		
KEYWORDS	JP 2002508944-A/68.		
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1. (bases 1 to 20)		
AUTHORS	Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowser,L.M.		
TITLE	Antisense modulation of human MDM2 expression		
JOURNAL	Patent: JP 2002508944-A 68 26-MAR-2002;		
COMMENT	ISIS PHARMACEUTICALS INC		
OS	Unidentified		
PN	JP 2002508944-A/68		
PD	26-MAR-2002		
PF	26-MAR-1999 JP 2000538025		
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PI	LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M		
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DEFINITION	Antisense modulation of human MDM2 expression.		
ACCESSION	BD138143		
VERSION	BD138143.1 GI:23233088		
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